# Richard A Neher

List of Publications by Year
in descending order

| 76 | 10,511 | 76326 | 71685 |
|---|---|---|---|
| papers | citations | 40 | 76 |
| | | h-index | g-index |

| 135 | 135 | 135 | 15195 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Nextstrain: real-time tracking of pathogen evolution. Bioinformatics, 2018, 34, 4121-4123. | 4.1 | 2,287 |
| 2 | TreeTime: Maximum-likelihood phylodynamic analysis. Virus Evolution, 2018, 4, vex042. | 4.9 | 883 |
| 3 | Nextclade: clade assignment, mutation calling and quality control for viral genomes. Journal of Open Source Software, 2021, 6, 3773. | 4.6 | 496 |
| 4 | COVID-19 epidemic in Switzerland: on the importance of testing, contact tracing and isolation. Swiss Medical Weekly, 2020, 150, w20225. | 1.6 | 367 |
| 5 | Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. Nature, 2021, 595, 707-712. | 27.8 | 363 |
| 6 | Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. Cell, 2020, 181, 990-996.e5. | 28.9 | 321 |
| 7 | panX: pan-genome analysis and exploration. Nucleic Acids Research, 2018, 46, e5-e5. | 14.5 | 241 |
| 8 | Potential impact of seasonal forcing on a SARS-CoV-2 pandemic. Swiss Medical Weekly, 2020, 150, w20224. | 1.6 | 223 |
| 9 | SARS-CoV-2 Variants of Interest and Concern naming scheme conducive for global discourse. Nature Microbiology, 2021, 6, 821-823. | 13.3 | 221 |
| 10 | Cryptic transmission of SARS-CoV-2 in Washington state. Science, 2020, 370, 571-575. | 12.6 | 217 |
| 11 | Population genomics of intrapatient HIV-1 evolution. ELife, 2015, 4, . | 6.0 | 206 |
| 12 | 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 |
| 13 | Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. PLoS Biology, 2021, 19, e3001236. | 5.6 | 200 |
| 14 | Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. Eurosurveillance, 2020, 25, . | 7.0 | 186 |
| 15 | Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1701-9. | 7.1 | 165 |
| 16 | Genetic Draft, Selective Interference, and Population Genetics of Rapid Adaptation. Annual Review of Ecology, Evolution, and Systematics, 2013, 44, 195-215. | 8.3 | 161 |
| 17 | Predicting evolution from the shape of genealogical trees. ELife, 2014, 3, . | 6.0 | 159 |
| 18 | Recombination Rate and Selection Strength in HIV Intra-patient Evolution. PLoS Computational Biology, 2010, 6, e1000660. | 3.2 | 154 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | nextflu: real-time tracking of seasonal influenza virus evolution in humans. Bioinformatics, 2015, 31, 3546-3548. | 4.1 | 153 |
| 20 | Arabidopsis thaliana and Pseudomonas Pathogens Exhibit Stable Associations over Evolutionary Timescales. Cell Host and Microbe, 2018, 24, 168-179.e4. | 11.0 | 145 |
| 21 | 2019-novel Coronavirus (2019-nCoV): estimating the case fatality rate â€" a word of caution. Swiss Medical Weekly, 2020, 150, w20203. | 1.6 | 135 |
| 22 | Augur: a bioinformatics toolkit for phylogenetic analyses of human pathogens. Journal of Open Source Software, 2021, 6, 2906. | 4.6 | 129 |
| 23 | Establishment and stability of the latent HIV-1 DNA reservoir. ELife, 2016, 5, . | 6.0 | 119 |
| 24 | Blind Source Separation Techniques for the Decomposition of Multiply Labeled Fluorescence Images. Biophysical Journal, 2009, 96, 3791-3800. | 0.5 | 113 |
| 25 | 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 |
| 26 | Dynamic Mutationâ€"Selection Balance as an Evolutionary Attractor. Genetics, 2012, 191, 1309-1319. | 2.9 | 96 |
| 27 | Genetic Diversity in the Interference Selection Limit. PLoS Genetics, 2014, 10, e1004222. | 3.5 | 96 |
| 28 | Temporal dynamics of gene expression and histone marks at the Arabidopsis shoot meristem during flowering. Nature Communications, 2017, 8, 15120. | 12.8 | 96 |
| 29 | Predictive Modeling of Influenza Shows the Promise of Applied Evolutionary Biology. Trends in Microbiology, 2018, 26, 102-118. | 7.7 | 95 |
| 30 | Statistical genetics and evolution of quantitative traits. Reviews of Modern Physics, 2011, 83, 1283-1300. | 45.6 | 87 |
| 31 | *In vivo* mutation rates and the landscape of fitness costs of HIV-1. Virus Evolution, 2017, 3, vex003. | 4.9 | 85 |
| 32 | Characterization of Genetic Diversity in the Nematode *Pristionchus pacificus* from Population-Scale Resequencing Data. Genetics, 2014, 196, 1153-1165. | 2.9 | 79 |
| 33 | Genetic Draft and Quasi-Neutrality in Large Facultatively Sexual Populations. Genetics, 2011, 188, 975-996. | 2.9 | 78 |
| 34 | Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523. | 7.1 | 68 |
| 35 | Applying spectral fingerprinting to the analysis of FRET images. Microscopy Research and Technique, 2004, 64, 185-195. | 2.2 | 64 |
| 36 | Fluctuations of Fitness Distributions and the Rate of Mullerâ€™s Ratchet. Genetics, 2012, 191, 1283-1293. | 2.9 | 63 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 37 | HIV Cell-to-Cell Spread Results in Earlier Onset of Viral Gene Expression by Multiple Infections per Cell. PLoS Pathogens, 2016, 12, e1005964. | 4.7 | 62 |
| 38 | 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 |
| 39 | Rapid and Consistent Evolution of Colistin Resistance in Extensively Drug-Resistant Pseudomonas aeruginosa during Morbidostat Culture. Antimicrobial Agents and Chemotherapy, 2017, 61, . | 3.2 | 57 |
| 40 | FFPopSim: an efficient forward simulation package for the evolution of large populations. Bioinformatics, 2012, 28, 3332-3333. | 4.1 | 52 |
| 41 | Topological estimation of percolation thresholds. Journal of Statistical Mechanics: Theory and Experiment, 2008, 2008, P01011. | 2.3 | 50 |
| 42 | Correlated Evolution of Nearby Residues in Drosophilid Proteins. PLoS Genetics, 2011, 7, e1001315. | 3.5 | 48 |
| 43 | Estimating the Strength of Selective Sweeps from Deep Population Diversity Data. Genetics, 2012, 191, 593-605. | 2.9 | 46 |
| 44 | Quantifying Selection against Synonymous Mutations in HIV-1 env Evolution. Journal of Virology, 2013, 87, 11843-11850. | 3.4 | 45 |
| 45 | Estimating time of HIV-1 infection from next-generation sequence diversity. PLoS Computational Biology, 2017, 13, e1005775. | 3.2 | 45 |
| 46 | Force-Induced DNA Slippage. Biophysical Journal, 2007, 92, 2491-2497. | 0.5 | 44 |
| 47 | Error rates, PCR recombination, and sampling depth in HIV-1 whole genome deep sequencing. Virus Research, 2017, 239, 106-114. | 2.2 | 42 |
| 48 | Mathematical modeling of escape of HIV from cytotoxic T lymphocyte responses. Journal of Statistical Mechanics: Theory and Experiment, 2013, 2013, P01010. | 2.3 | 38 |
| 49 | Quantitative contribution of efflux to multi-drug resistance of clinical Escherichia coli and Pseudomonas aeruginosa strains. EBioMedicine, 2019, 41, 479-487. | 6.1 | 37 |
| 50 | Inferring HIV Escape Rates from Multi-Locus Genotype Data. Frontiers in Immunology, 2013, 4, 252. | 4.8 | 35 |
| 51 | Integrating genotypes and phenotypes improves long-term forecasts of seasonal influenza A/H3N2 evolution. ELife, 2020, 9, . | 6.0 | 35 |
| 52 | Kinetic Accessibility of Buried DNA Sites in Nucleosomes. Physical Review Letters, 2006, 97, 208102. | 7.8 | 33 |
| 53 | SARS-CoV-2 N501Y Introductions and Transmissions in Switzerland from Beginning of October 2020 to February 2021â€"Implementation of Swiss-Wide Diagnostic Screening and Whole Genome Sequencing. Microorganisms, 2021, 9, 677. | 3.6 | 32 |
| 54 | Phylodynamic theory of persistence, extinction and speciation of rapidly adapting pathogens. ELife, 2019, 8, . | 6.0 | 30 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 55 | Improving the quality and workflow of bacterial genome sequencing and analysis: paving the way for a Switzerland-wide molecular epidemiological surveillance platform. Swiss Medical Weekly, 2018, 148, w14693. | 1.6 | 28 |
| 56 | Challenges with Using Primer IDs to Improve Accuracy of Next Generation Sequencing. PLoS ONE, 2015, 10, e0119123. | 2.5 | 27 |
| 57 | Real-Time Analysis and Visualization of Pathogen Sequence Data. Journal of Clinical Microbiology, 2018, 56, . | 3.9 | 25 |
| 58 | Interactions between seasonal human coronaviruses and implications for the SARS-CoV-2 pandemic: A retrospective study in Stockholm, Sweden, 2009-2020. Journal of Clinical Virology, 2021, 136, 104754. | 3.1 | 25 |
| 59 | Asynchrony between virus diversity and antibody selection limits influenza virus evolution. ELife, 2020, 9, . | 6.0 | 25 |
| 60 | Intra- and interpatient evolution of enterovirus D68 analyzed by whole-genome deep sequencing. Virus Evolution, 2019, 5, vez007. | 4.9 | 20 |
| 61 | Intermediate phase in DNA melting. Physical Review E, 2006, 73, 030902. | 2.1 | 19 |
| 62 | Evolution and rapid spread of a reassortant A(H3N2) virus that predominated the 2017–2018 influenza season. Virus Evolution, 2019, 5, vez046. | 4.9 | 19 |
| 63 | Evolution, geographic spreading, and demographic distribution of Enterovirus D68. PLoS Pathogens, 2022, 18, e1010515. | 4.7 | 19 |
| 64 | Dynamics of Force-Induced DNA Slippage. Physical Review Letters, 2004, 93, 198102. | 7.8 | 18 |
| 65 | Molecular Epidemiology and Evolutionary Trajectory of Emerging Echovirus 30, Europe. Emerging Infectious Diseases, 2021, 27, 1616-1626. | 4.3 | 18 |
| 66 | Characterising the epidemic spread of influenza A/H3N2 within a city through phylogenetics. PLoS Pathogens, 2020, 16, e1008984. | 4.7 | 17 |
| 67 | Emergence of clones in sexual populations. Journal of Statistical Mechanics: Theory and Experiment, 2013, 2013, P01008. | 2.3 | 16 |
| 68 | Target search on a dynamic DNA molecule. Physical Review E, 2011, 84, 051911. | 2.1 | 14 |
| 69 | Incomplete inhibition of HIV infection results in more HIV infected lymph node cells by reducing cell death. ELife, 2018, 7, . | 6.0 | 12 |
| 70 | Limited Predictability of Amino Acid Substitutions in Seasonal Influenza Viruses. Molecular Biology and Evolution, 2021, 38, 2767-2777. | 8.9 | 12 |
| 71 | DNA as a Programmable Viscoelastic Nanoelement. Biophysical Journal, 2005, 89, 3846-3855. | 0.5 | 10 |
| 72 | Colistin susceptibility test evaluation of multiple-resistance-level Pseudomonas aeruginosa isolates generated in a morbidostat device. Journal of Antimicrobial Chemotherapy, 2018, 73, 3368-3374. | 3.0 | 10 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 73 | Quantifying the range of a lipid phosphate signal in vivo. Journal of Cell Science, 2013, 126, 5453-64. | 2.0 | 9 |
| 74 | Evaluation of two workflows for whole genome sequencing-based typing of influenza A viruses. Journal of Virological Methods, 2019, 266, 30-33. | 2.1 | 9 |
| 75 | Efficient inference, potential, and limitations of site-specific substitution models. Virus Evolution, 2020, 6, veaa066. | 4.9 | 3 |
| 76 | Optimal Flexibility for Conformational Transitions in Macromolecules. Physical Review Letters, 2007, 99, 178101. | 7.8 | 1 |