

# Emma B Hodcroft

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2431803/publications.pdf>

Version: 2024-02-01

18  
papers

2,243  
citations

687363

13  
h-index

839539

18  
g-index

24  
all docs

24  
docs citations

24  
times ranked

4607  
citing authors

#	ARTICLE	IF	CITATIONS
1	Nextclade: clade assignment, mutation calling and quality control for viral genomes. <i>Journal of Open Source Software</i> , 2021, 6, 3773.	4.6	496
2	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712.	27.8	363
3	Cryptic transmission of SARS-CoV-2 in Washington state. <i>Science</i> , 2020, 370, 571-575.	12.6	217
4	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
5	Public health actions to control new SARS-CoV-2 variants. <i>Cell</i> , 2021, 184, 1127-1132.	28.9	149
6	Augur: a bioinformatics toolkit for phylogenetic analyses of human pathogens. <i>Journal of Open Source Software</i> , 2021, 6, 2906.	4.6	129
7	Transmission of SARS-CoV-2 in domestic cats imposes a narrow bottleneck. <i>PLoS Pathogens</i> , 2021, 17, e1009373.	4.7	84
8	Identification of resident memory CD8 <sup>+</sup> T cells with functional specificity for SARS-CoV-2 in unexposed oropharyngeal lymphoid tissue. <i>Science Immunology</i> , 2021, 6, eabk0894.	11.9	71
9	Non-disclosed men who have sex with men in UK HIV transmission networks: phylogenetic analysis of surveillance data. <i>Lancet HIV</i> , 2018, 5, e309-e316.	4.7	38
10	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
11	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
12	Intra- and interpatient evolution of enterovirus D68 analyzed by whole-genome deep sequencing. <i>Virus Evolution</i> , 2019, 5, vez007.	4.9	20
13	Evolution, geographic spreading, and demographic distribution of Enterovirus D68. <i>PLoS Pathogens</i> , 2022, 18, e1010515.	4.7	19
14	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	6.4	18
15	Understanding disclosed and cryptic HIV transmission risk via genetic analysis. <i>Current Opinion in HIV and AIDS</i> , 2019, 14, 205-212.	3.8	11
16	Pervasive and non-random recombination in near full-length HIV genomes from Uganda. <i>Virus Evolution</i> , 2020, 6, veaa004.	4.9	9
17	Clonality, genetic variation, and the origin of isolated western populations of the carnivorous plant, <i>Sarracenia alata</i> . <i>Journal of the Torrey Botanical Society</i> , 2014, 141, 326-337.	0.3	3
18	The International Virus Bioinformatics Meeting 2022. <i>Viruses</i> , 2022, 14, 973.	3.3	3