

Maciej F Boni

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

8,323
citations

87401

40
h-index

66518

82
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107
all docs

107
docs citations

107
times ranked

13671
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 epidemic after social and economic reopening in three U.S. states reveals shifts in age structure and clinical characteristics. <i>Science Advances</i> , 2022, 8, eabf9868.	4.7	10
2	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 2022, 603, 679-686.	13.7	1,210
3	Long-term effects of increased adoption of artemisinin combination therapies in Burkina Faso. <i>PLOS Global Public Health</i> , 2022, 2, e0000111.	0.5	13
4	Selection Analysis Identifies Clusters of Unusual Mutational Changes in Omicron Lineage BA.1 That Likely Impact Spike Function. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	84
5	Mathematical epidemiology for a later age. <i>Theoretical Population Biology</i> , 2022, 144, 81-83.	0.5	0
6	SARS-CoV-2 Attack Rate and Population Immunity in Southern New England, March 2020 to May 2021. <i>JAMA Network Open</i> , 2022, 5, e2214171.	2.8	5
7	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	0.9	97
8	Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. <i>PLoS Biology</i> , 2021, 19, e3001115.	2.6	172
9	Optimal SARS-CoV-2 vaccine allocation using real-time attack-rate estimates in Rhode Island and Massachusetts. <i>BMC Medicine</i> , 2021, 19, 162.	2.3	25
10	An open dataset of <i>Plasmodium falciparum</i> genome variation in 7,000 worldwide samples. <i>Wellcome Open Research</i> , 2021, 6, 42.	0.9	51
11	The Role of the Gastrointestinal Tract in Toxigenic <i>Clostridium tetani</i> Infection: A Case-Control Study. <i>American Journal of Tropical Medicine and Hygiene</i> , 2021, 105, 494-497.	0.6	0
12	Generation and transmission of interlineage recombinants in the SARS-CoV-2 pandemic. <i>Cell</i> , 2021, 184, 5179-5188.e8.	13.5	182
13	The origins of SARS-CoV-2: A critical review. <i>Cell</i> , 2021, 184, 4848-4856.	13.5	330
14	Using NS1 Flavivirus Protein Microarray to Infer Past Infecting Dengue Virus Serotype and Number of Past Dengue Virus Infections in Vietnamese Individuals. <i>Journal of Infectious Diseases</i> , 2021, 223, 2053-2061.	1.9	9
15	Assessing the Effect of Climate Variables on the Incidence of Dengue Cases in the Metropolitan Region of Panama City. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 12108.	1.2	7
16	Age-seroprevalence curves for the multi-strain structure of influenza A virus. <i>Nature Communications</i> , 2021, 12, 6680.	5.8	12
17	Game theory of vaccination and depopulation for managing livestock diseases and zoonoses on small-scale farms. <i>Epidemics</i> , 2020, 30, 100370.	1.5	17
18	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2020, 37, 2706-2710.	3.5	18

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19	Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. <i>Nature Microbiology</i> , 2020, 5, 1408-1417.	5.9	772
20	Serology for SARS-CoV-2: Apprehensions, opportunities, and the path forward. <i>Science Immunology</i> , 2020, 5, .	5.6	138
21	Poultry farmer response to disease outbreaks in smallholder farming systems in southern Vietnam. <i>ELife</i> , 2020, 9, .	2.8	22
22	Serological inference of past primary and secondary dengue infection: implications for vaccination. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20190207.	1.5	12
23	Malaria eradication within a generation: ambitious, achievable, and necessary. <i>Lancet, The</i> , 2019, 394, 1056-1112.	6.3	240
24	Poultry population dynamics and mortality risks in smallholder farms of the Mekong river delta region. <i>BMC Veterinary Research</i> , 2019, 15, 205.	0.7	11
25	Sero-Prevalence Surveillance to Predict Vaccine-Preventable Disease Outbreaks; A Lesson from the 2014 Measles Epidemic in Northern Vietnam. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz030.	0.4	12
26	Multilocus sequence typing of <i>Cryptococcus neoformans</i> var. <i>grubii</i> from Laos in a regional and global context. <i>Medical Mycology</i> , 2019, 57, 557-565.	0.3	14
27	Inferring the Time of Infection from Serological Data. , 2019, , 287-303.		7
28	Improved Algorithmic Complexity for the 3SEQ Recombination Detection Algorithm. <i>Molecular Biology and Evolution</i> , 2018, 35, 247-251.	3.5	139
29	Nonannual seasonality of influenza-like illness in a tropical urban setting. <i>Influenza and Other Respiratory Viruses</i> , 2018, 12, 742-754.	1.5	13
30	Modeling tuberculosis dynamics with the presence of hyper-susceptible individuals for Ho Chi Minh City from 1996 to 2015. <i>BMC Infectious Diseases</i> , 2018, 18, 494.	1.3	3
31	The Estimates of the Health and Economic Burden of Dengue in Vietnam. <i>Trends in Parasitology</i> , 2018, 34, 904-918.	1.5	47
32	The decline of malaria in Vietnam, 1991-2014. <i>Malaria Journal</i> , 2018, 17, 226.	0.8	24
33	Projected costs associated with school-based screening to inform deployment of Dengvaxia: Vietnam as a case study. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2018, 112, 369-377.	0.7	10
34	Primary care influenza-like illness surveillance in Ho Chi Minh City, Vietnam 2013-2015. <i>Influenza and Other Respiratory Viruses</i> , 2018, 12, 623-631.	1.5	10
35	Evidence of previous but not current transmission of chikungunya virus in southern and central Vietnam: Results from a systematic review and a seroprevalence study in four locations. <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006246.	1.3	23
36	K13 Propeller Mutations in <i>Plasmodium falciparum</i> Populations in Regions of Malaria Endemicity in Vietnam from 2009 to 2016. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	41

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37	Structure of general-population antibody titer distributions to influenza A virus. <i>Scientific Reports</i> , 2017, 7, 6060.	1.6	19
38	The epidemiology and evolution of influenza A/H1N1 and A/H3N2 virus from 2010 to 2015, in Ho Chi Minh City, Vietnam. <i>Virus Evolution</i> , 2017, 3, .	2.2	1
39	Towards malaria elimination in Savannakhet, Lao PDR: mathematical modelling driven strategy design. <i>Malaria Journal</i> , 2017, 16, 483.	0.8	18
40	No Evidence of On-farm Circulation of Avian Influenza H5 Subtype in Ca Mau Province, Southern Vietnam, March 2016 – January 2017. <i>PLOS Currents</i> , 2017, 9, .	1.4	6
41	Comparative genomics of <i>Cryptococcus neoformans</i> var. <i>grubii</i> associated with meningitis in HIV infected and uninfected patients in Vietnam. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005628.	1.3	45
42	Tetanus in Southern Vietnam: Current Situation. <i>American Journal of Tropical Medicine and Hygiene</i> , 2017, 96, 93-96.	0.6	21
43	The Community As the Patient in Malaria-Endemic Areas: Preempting Drug Resistance with Multiple First-Line Therapies. <i>PLoS Medicine</i> , 2016, 13, e1001984.	3.9	49
44	Safety and Upper Respiratory Pharmacokinetics of the Hemagglutinin Stalk-Binding Antibody VIS410 Support Treatment and Prophylaxis Based on Population Modeling of Seasonal Influenza A Outbreaks. <i>EBioMedicine</i> , 2016, 5, 147-155.	2.7	48
45	Genomic analysis of local variation and recent evolution in <i>Plasmodium vivax</i> . <i>Nature Genetics</i> , 2016, 48, 959-964.	9.4	169
46	Statistical identifiability and sample size calculations for serial seroepidemiology. <i>Epidemics</i> , 2015, 12, 30-39.	1.5	14
47	Optimum population-level use of artemisinin combination therapies: a modelling study. <i>The Lancet Global Health</i> , 2015, 3, e758-e766.	2.9	62
48	Evaluating Clinical Trial Designs for Investigational Treatments of Ebola Virus Disease. <i>PLoS Medicine</i> , 2015, 12, e1001815.	3.9	45
49	Seasonality of absolute humidity explains seasonality of influenza-like illness in Vietnam. <i>Epidemics</i> , 2015, 13, 65-73.	1.5	61
50	Impact of human mobility on the emergence of dengue epidemics in Pakistan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11887-11892.	3.3	369
51	Measuring the Association Between Artemisinin-Based Case Management and Malaria Incidence in Southern Vietnam, 1991–2010. <i>American Journal of Tropical Medicine and Hygiene</i> , 2015, 92, 811-817.	0.6	9
52	Reply to Pawar et al. <i>Journal of Infectious Diseases</i> , 2014, 210, 161-163.	1.9	5
53	Reconciling Phylodynamics with Epidemiology: The Case of Dengue Virus in Southern Vietnam. <i>Molecular Biology and Evolution</i> , 2014, 31, 258-271.	3.5	42
54	The emergence and evolution of the novel epidemic norovirus GII.4 variant Sydney 2012. <i>Virology</i> , 2014, 450-451, 106-113.	1.1	111

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55	Economic epidemiology of avian influenza on smallholder poultry farms. <i>Theoretical Population Biology</i> , 2013, 90, 135-144.	0.5	39
56	Impact of treatment heterogeneity on drug resistance and supply chain costs. <i>Socio-Economic Planning Sciences</i> , 2013, 47, 158-171.	2.5	5
57	The dynamics of GII.4 Norovirus in Ho Chi Minh City, Vietnam. <i>Infection, Genetics and Evolution</i> , 2013, 18, 335-343.	1.0	10
58	Multiple populations of artemisinin-resistant <i>Plasmodium falciparum</i> in Cambodia. <i>Nature Genetics</i> , 2013, 45, 648-655.	9.4	424
59	Spatiotemporal Dynamics of Dengue Epidemics, Southern Vietnam. <i>Emerging Infectious Diseases</i> , 2013, 19, 945-953.	2.0	83
60	Migration and Persistence of Human Influenza A Viruses, Vietnam, 2001–2008. <i>Emerging Infectious Diseases</i> , 2013, 19, 1756-1765.	2.0	16
61	Virulence attenuation during an influenza A/H5N1 pandemic. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120207.	1.8	17
62	Population-Level Antibody Estimates to Novel Influenza A/H7N9. <i>Journal of Infectious Diseases</i> , 2013, 208, 554-558.	1.9	51
63	Recombination within the Pandemic Norovirus GII.4 Lineage. <i>Journal of Virology</i> , 2013, 87, 6270-6282.	1.5	239
64	Fitness benefits in fluoroquinolone-resistant <i>Salmonella Typhi</i> in the absence of antimicrobial pressure. <i>ELife</i> , 2013, 2, e01229.	2.8	103
65	No evidence for intra-segment recombination of 2009 H1N1 influenza virus in swine. <i>Gene</i> , 2012, 494, 242-245.	1.0	16
66	In vivo susceptibility of <i>Plasmodium falciparum</i> to artesunate in Binh Phuoc Province, Vietnam. <i>Malaria Journal</i> , 2012, 11, 355.	0.8	115
67	Assessing the Potential of a Candidate Dengue Vaccine with Mathematical Modeling. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1450.	1.3	31
68	Most Cases of Cryptococcal Meningitis in HIV-Uninfected Patients in Vietnam Are Due to a Distinct Amplified Fragment Length Polymorphism-Defined Cluster of <i>Cryptococcus neoformans</i> var. <i>grubii</i> VN1. <i>Journal of Clinical Microbiology</i> , 2011, 49, 658-664.	1.8	40
69	Dengue Dynamics in Binh Thuan Province, Southern Vietnam: Periodicity, Synchronicity and Climate Variability. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e747.	1.3	88
70	Guidelines for Identifying Homologous Recombination Events in Influenza A Virus. <i>PLoS ONE</i> , 2010, 5, e10434.	1.1	72
71	The Burden and Characteristics of Enteric Fever at a Healthcare Facility in a Densely Populated Area of Kathmandu. <i>PLoS ONE</i> , 2010, 5, e13988.	1.1	58
72	Early Pandemic Influenza (2009 H1N1) in Ho Chi Minh City, Vietnam: A Clinical Virological and Epidemiological Analysis. <i>PLoS Medicine</i> , 2010, 7, e1000277.	3.9	53

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73	No observed effect of homologous recombination on influenza C virus evolution. <i>Virology Journal</i> , 2010, 7, 227.	1.4	9
74	Modelling the progression of pandemic influenza A (H1N1) in Vietnam and the opportunities for reassortment with other influenza viruses. <i>BMC Medicine</i> , 2009, 7, 43.	2.3	26
75	ORIGINAL ARTICLE: Probability of emergence of antimalarial resistance in different stages of the parasite life cycle. <i>Evolutionary Applications</i> , 2009, 2, 52-61.	1.5	40
76	A changing picture of shigellosis in southern Vietnam: shifting species dominance, antimicrobial susceptibility and clinical presentation. <i>BMC Infectious Diseases</i> , 2009, 9, 204.	1.3	111
77	Traits, Habitats, and Clades: Identifying Traits of Potential Importance to Environmental Filtering. <i>American Naturalist</i> , 2009, 174, E1-E22.	1.0	45
78	Clinically immune hosts as a refuge for drug-sensitive malaria parasites. <i>Malaria Journal</i> , 2008, 7, 67.	0.8	63
79	Vaccination and antigenic drift in influenza. <i>Vaccine</i> , 2008, 26, C8-C14.	1.7	146
80	Homologous Recombination Is Very Rare or Absent in Human Influenza A Virus. <i>Journal of Virology</i> , 2008, 82, 4807-4811.	1.5	111
81	Benefits of using multiple first-line therapies against malaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14216-14221.	3.3	122
82	Mathematical Models for a New Era of Malaria Eradication. <i>PLoS Medicine</i> , 2008, 5, e231.	3.9	11
83	An Exact Nonparametric Method for Inferring Mosaic Structure in Sequence Triplets. <i>Genetics</i> , 2007, 176, 1035-1047.	1.2	687
84	Epidemic dynamics and antigenic evolution in a single season of influenza A. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 1307-1316.	1.2	85
85	EVOLUTION OF ANTIBIOTIC RESISTANCE BY HUMAN AND BACTERIAL NICHE CONSTRUCTION. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 477-491.	1.1	48
86	SPECIES AND FUNCTIONAL DIVERSITY OF NATIVE AND HUMAN-DOMINATED PLANT COMMUNITIES. <i>Ecology</i> , 2005, 86, 2365-2372.	1.5	111
87	Evolution of antibiotic resistance by human and bacterial niche construction. <i>Evolution; International Journal of Organic Evolution</i> , 2005, 59, 477-91.	1.1	41
88	Influenza drift and epidemic size: the race between generating and escaping immunity. <i>Theoretical Population Biology</i> , 2004, 65, 179-191.	0.5	68
89	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa. <i>Nature</i> , 0, , .	13.7	61