

Boris V Schmid

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

919
citations

686830

13
h-index

676716

22
g-index

28
all docs

28
docs citations

28
times ranked

1277
citing authors

#	ARTICLE	IF	CITATIONS
1	Plague risk in the western United States over seven decades of environmental change. <i>Global Change Biology</i> , 2022, 28, 753-769.	4.2	13
2	Plague reservoir species throughout the world. <i>Integrative Zoology</i> , 2021, 16, 820-833.	1.3	35
3	The Genome of the Great Gerbil Reveals Species-Specific Duplication of an MHCII Gene. <i>Genome Biology and Evolution</i> , 2020, 12, 3832-3849.	1.1	5
4	Evolutionary selection of biofilm-mediated extended phenotypes in <i>Yersinia pestis</i> in response to a fluctuating environment. <i>Nature Communications</i> , 2020, 11, 281.	5.8	30
5	Reply to McLean et al.: Collections are critical. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14413-14413.	3.3	0
6	Human plague system associated with rodent diversity and other environmental factors. <i>Royal Society Open Science</i> , 2019, 6, 190216.	1.1	12
7	Living with plague: Lessons from the Soviet Union's antiplague system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9155-9163.	3.3	31
8	Epidemiology of a bubonic plague outbreak in Glasgow, Scotland in 1900. <i>Royal Society Open Science</i> , 2019, 6, 181695.	1.1	19
9	Reply to Barbieri et al.: Out of the Land of Darkness: Plague on the fur trade routes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7622-7623.	3.3	4
10	Human ectoparasites and the spread of plague in Europe during the Second Pandemic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1304-1309.	3.3	110
11	Integrative approach using <i>Yersinia pestis</i> genomes to revisit the historical landscape of plague during the Medieval Period. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11790-E11797.	3.3	68
12	Reply to Park et al.: Human ectoparasite transmission of plague during the Second Pandemic is still plausible. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7894-E7895.	3.3	0
13	Chlamydia screening is not cost-effective at low participation rates: evidence from a repeated register-based implementation study in the Netherlands. <i>Sexually Transmitted Infections</i> , 2015, 91, 423-429.	0.8	25
14	Climate-driven introduction of the Black Death and successive plague reintroductions into Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3020-3025.	3.3	225
15	The trophic responses of two different rodent "vector" plague systems to climate change. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20141846.	1.2	33
16	Wet climate and transportation routes accelerate spread of human plague. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20133159.	1.2	53
17	Effects of Population Based Screening for Chlamydia Infections in The Netherlands Limited by Declining Participation Rates. <i>PLoS ONE</i> , 2013, 8, e58674.	1.1	10
18	Determinants of Sexual Network Structure and Their Impact on Cumulative Network Measures. <i>PLoS Computational Biology</i> , 2012, 8, e1002470.	1.5	13

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19	Transmission of <i>Chlamydia trachomatis</i> through sexual partnerships: a comparison between three individual-based models and empirical data. <i>Journal of the Royal Society Interface</i> , 2012, 9, 136-146.	1.5	63
20	Effectiveness of yearly, register based screening for chlamydia in the Netherlands: controlled trial with randomised stepped wedge implementation. <i>BMJ</i> , The, 2012, 345, e4316-e4316.	3.0	119
21	Local persistence and extinction of plague in a metapopulation of great gerbil burrows, Kazakhstan. <i>Epidemics</i> , 2012, 4, 211-218.	1.5	11
22	Quantifying how MHC polymorphism prevents pathogens from adapting to the antigen presentation pathway. <i>Epidemics</i> , 2010, 2, 99-108.	1.5	6
23	The distribution of CTL epitopes in HIV-1 appears to be random, and similar to that of other proteomes. <i>BMC Evolutionary Biology</i> , 2009, 9, 184.	3.2	11
24	The Specificity and Polymorphism of the MHC Class I Prevents the Global Adaptation of HIV-1 to the Monomorphic Proteasome and TAP. <i>PLoS ONE</i> , 2008, 3, e3525.	1.1	15