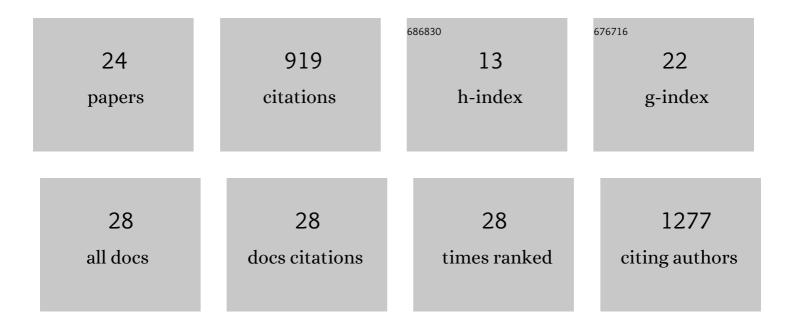
Boris V Schmid

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7397287/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Plague risk in the western United States over seven decades of environmental change. Global Change Biology, 2022, 28, 753-769.	4.2	13
2	Plague reservoir species throughout the world. Integrative Zoology, 2021, 16, 820-833.	1.3	35
3	The Genome of the Great Gerbil Reveals Species-Specific Duplication of an MHCII Gene. Genome Biology and Evolution, 2020, 12, 3832-3849.	1.1	5
4	Evolutionary selection of biofilm-mediated extended phenotypes in Yersinia pestis in response to a fluctuating environment. Nature Communications, 2020, 11, 281.	5.8	30
5	Reply to McLean et al.: Collections are critical. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14413-14413.	3.3	0
6	Human plague system associated with rodent diversity and other environmental factors. Royal Society Open Science, 2019, 6, 190216.	1.1	12
7	Living with plague: Lessons from the Soviet Union's antiplague system. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9155-9163.	3.3	31
8	Epidemiology of a bubonic plague outbreak in Glasgow, Scotland in 1900. Royal Society Open Science, 2019, 6, 181695.	1.1	19
9	Reply to Barbieri et al.: Out of the Land of Darkness: Plague on the fur trade routes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7622-7623.	3.3	4
10	Human ectoparasites and the spread of plague in Europe during the Second Pandemic. Proceedings of the National Academy of Sciences of the United States of America, 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. Proceedings of the National Academy of Sciences of the United States of America, 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. Proceedings of the National Academy of Sciences of the United States of America, 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. Sexually Transmitted Infections, 2015, 91, 423-429.	0.8	25
14	Climate-driven introduction of the Black Death and successive plague reintroductions into Europe. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3020-3025.	3.3	225
15	The trophic responses of two different rodent–vector–plague systems to climate change. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20141846.	1.2	33
16	Wet climate and transportation routes accelerate spread of human plague. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20133159.	1.2	53
17	Effects of Population Based Screening for Chlamydia Infections in The Netherlands Limited by Declining Participation Rates. PLoS ONE, 2013, 8, e58674.	1.1	10
18	Determinants of Sexual Network Structure and Their Impact on Cumulative Network Measures. PLoS Computational Biology, 2012, 8, e1002470.	1.5	13

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#	Article	IF	CITATIONS
19	Transmission of <i>Chlamydia trachomatis</i> through sexual partnerships: a comparison between three individual-based models and empirical data. Journal of the Royal Society Interface, 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. BMJ, The, 2012, 345, e4316-e4316.	3.0	119
21	Local persistence and extinction of plague in a metapopulation of great gerbil burrows, Kazakhstan. Epidemics, 2012, 4, 211-218.	1.5	11
22	Quantifying how MHC polymorphism prevents pathogens from adapting to the antigen presentation pathway. Epidemics, 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. BMC Evolutionary Biology, 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. PLoS ONE, 2008, 3, e3525.	1.1	15