Cyril Savin

List of Publications by Year in descending order

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840776 1058476 15 529 11 14 citations h-index g-index papers 16 16 16 763 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	First Description of a Yersinia pseudotuberculosis Clonal Outbreak in France, Confirmed Using a New Core Genome Multilocus Sequence Typing Method. Microbiology Spectrum, 2022, 10, .	3.0	0
2	Yersinia artesiana sp. nov., Yersinia proxima sp. nov., Yersinia alsatica sp. nov., Yersina vastinensis sp. nov., Yersinia thracica sp. nov. and Yersinia occitanica sp. nov., isolated from humans and animals. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 5363-5372.	1.7	36
3	Yersinia pestis and plague: an updated view on evolution, virulence determinants, immune subversion, vaccination and diagnostics. Microbes and Infection, 2019, 21, 202-212.	1.9	29
4	Genus-wide Yersinia core-genome multilocus sequence typing for species identification and strain characterization. Microbial Genomics, 2019, 5 , .	2.0	31
5	Isolation of a <i>Yersinia enterocolitica</i> biotype 1B strain in France, and evaluation of its genetic relatedness to other European and North American biotype 1B strains. Emerging Microbes and Infections, 2018, 7, 1-3.	6.5	7
6	Yersinia enterocolitica, a Neglected Cause of Human Enteric Infections in Côte d'Ivoire. PLoS Neglected Tropical Diseases, 2017, 11, e0005216.	3.0	30
7	The Asian house shrew Suncus murinus as a reservoir and source of human outbreaks of plague in Madagascar. PLoS Neglected Tropical Diseases, 2017, 11, e0006072.	3.0	24
8	Yersiniosis in France: overview and potential sources of infection. International Journal of Infectious Diseases, 2016, 46, 1-7.	3.3	76
9	Fast and Sensitive Detection of Enteropathogenic Yersinia by Immunoassays. Journal of Clinical Microbiology, 2015, 53, 146-159.	3.9	16
10	Use of Whole-Genus Genome Sequence Data To Develop a Multilocus Sequence Typing Tool That Accurately Identifies Yersinia Isolates to the Species and Subspecies Levels. Journal of Clinical Microbiology, 2015, 53, 35-42.	3.9	45
11	The Yersinia pseudotuberculosis complex: Characterization and delineation of a new species, Yersinia wautersii. International Journal of Medical Microbiology, 2014, 304, 452-463.	3.6	54
12	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i>). Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6768-6773.	7.1	154
13	Draft Genome Sequence of a Clinical Strain of Yersinia enterocolitica (IP10393) of Bioserotype $4/0:3$ from France. Genome Announcements, 2013, 1, .	0.8	3
14	Evaluation of a Single Procedure Allowing the Isolation of Enteropathogenic Yersinia along with Other Bacterial Enteropathogens from Human Stools. PLoS ONE, 2012, 7, e41176.	2.5	13
15	Characterization of Atypical Isolates of <i>Yersinia intermedia</i> and Definition of Two New Biotypes. Journal of Clinical Microbiology, 2009, 47, 2377-2380.	3.9	11