

Mathias C Walter

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,638
citations

516710

16
h-index

377865

34
g-index

41
all docs

41
docs citations

41
times ranked

8082
citing authors

#	ARTICLE	IF	CITATIONS
1	In vitro evaluation of the effect of mutations in primer binding sites on detection of SARS-CoV-2 by RT-qPCR. <i>Journal of Virological Methods</i> , 2022, 299, 114352.	2.1	11
2	<i>Coxiella burnetii</i> . , 2022, , 247-262.		2
3	In-Depth Analysis of <i>Bacillus anthracis</i> 16S rRNA Genes and Transcripts Reveals Intra- and Intergenomic Diversity and Facilitates Anthrax Detection. <i>MSystems</i> , 2022, 7, e0136121.	3.8	2
4	Molecular and genomic characterization of a novel equine molluscum contagiosum-like virus. <i>Journal of General Virology</i> , 2021, 102, .	2.9	7
5	Catching SARS-CoV-2 by Sequence Hybridization: a Comparative Analysis. <i>MSystems</i> , 2021, 6, e0039221.	3.8	11
6	FlexTaxD: flexible modification of taxonomy databases for improved sequence classification. <i>Bioinformatics</i> , 2021, 37, 3932-3933.	4.1	2
7	Ultrasensitive Detection of <i>Bacillus anthracis</i> by Real-Time PCR Targeting a Polymorphism in Multi-Copy 16S rRNA Genes and Their Transcripts. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12224.	4.1	8
8	CoxBase: an Online Platform for Epidemiological Surveillance, Visualization, Analysis, and Typing of <i>Coxiella burnetii</i> Genomic Sequences. <i>MSystems</i> , 2021, 6, e0040321.	3.8	5
9	Whole genome sequencing and phylogenetic classification of Tunisian SARS-CoV-2 strains from patients of the Military Hospital in Tunis. <i>Virus Genes</i> , 2020, 56, 767-771.	1.6	10
10	First Phylogenetic Analysis of Malian SARS-CoV-2 Sequences Provides Molecular Insights into the Genomic Diversity of the Sahel Region. <i>Viruses</i> , 2020, 12, 1251.	3.3	7
11	Comparison of <i>Coxiella burnetii</i> Excretion between Sheep and Goats Naturally Infected with One Cattle-Associated Genotype. <i>Pathogens</i> , 2020, 9, 652.	2.8	20
12	Investigation of a COVID-19 outbreak in Germany resulting from a single travel-associated primary case: a case series. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 920-928.	9.1	383
13	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
14	A headache with surprising outcome: first case of brucellosis caused by <i>Brucella suis</i> biovar 1 in Germany. <i>Infection</i> , 2019, 47, 863-868.	4.7	11
15	MinION as part of a biomedical rapidly deployable laboratory. <i>Journal of Biotechnology</i> , 2017, 250, 16-22.	3.8	44
16	Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi <i>Armillaria</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1931-1941.	7.8	145
17	Genome Sequence of <i>Bacillus safensis</i> Strain Ingolstadt Isolated from the Pectoralis Pouch of a Patient with Defibrillator-Related Surgery. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
18	Complete Circular Genome Sequence and Temperature Independent Adaptation to Anaerobiosis of <i>Listeria weihenstephanensis</i> DSM 24698. <i>Frontiers in Microbiology</i> , 2017, 8, 1672.	3.5	1

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19	Whole genome sequencing of <i>Brucella melitensis</i> isolated from 57 patients in Germany reveals high diversity in strains from Middle East. <i>PLoS ONE</i> , 2017, 12, e0175425.	2.5	72
20	A complete toolset for the study of <i>Ustilago bromivora</i> and <i>Brachypodium</i> sp. as a fungal-temperate grass pathosystem. <i>ELife</i> , 2016, 5, .	6.0	49
21	The Intervening Sequence of <i>Coxiella burnetii</i> : Characterization and Evolution. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 83.	3.9	6
22	Unexpected genomic relationships between <i>Bacillus anthracis</i> strains from Bangladesh and Central Europe. <i>Infection, Genetics and Evolution</i> , 2016, 45, 66-74.	2.3	5
23	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016, 44, D286-D293.	14.5	1,937
24	<i>Coxiella</i> -like endosymbiont in argasid ticks (<i>Ornithodoros muesebecki</i>) from a Socotra Cormorant colony in Umm Al Quwain, United Arab Emirates. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 166-171.	2.7	25
25	HoPaCI-DB: host- <i>Pseudomonas</i> and <i>Coxiella</i> interaction database. <i>Nucleic Acids Research</i> , 2014, 42, D671-D676.	14.5	21
26	Molecular analysis of <i>Coxiella burnetii</i> in Germany reveals evolution of unique clonal clusters. <i>International Journal of Medical Microbiology</i> , 2014, 304, 868-876.	3.6	36
27	Genome sequence of <i>Coxiella burnetii</i> strain Namibia. <i>Standards in Genomic Sciences</i> , 2014, 9, 22.	1.5	12
28	Genome Sequence of <i>Coxiella burnetii</i> Strain AuQ01 (Arandale) from an Australian Patient with Acute Q Fever. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
29	Microevolution of the Chromosomal Region of Acute Disease Antigen A (<i>adaA</i>) in the Query (Q) Fever Agent <i>Coxiella burnetii</i> . <i>PLoS ONE</i> , 2013, 8, e53440.	2.5	17
30	Sequence-structure relationships in yeast mRNAs. <i>Nucleic Acids Research</i> , 2012, 40, 956-962.	14.5	12
31	FGDB: revisiting the genome annotation of the plant pathogen <i>Fusarium graminearum</i> . <i>Nucleic Acids Research</i> , 2011, 39, D637-D639.	14.5	81
32	MIPS: curated databases and comprehensive secondary data resources in 2010. <i>Nucleic Acids Research</i> , 2011, 39, D220-D224.	14.5	77
33	Pathogenicity Determinants in Smut Fungi Revealed by Genome Comparison. <i>Science</i> , 2010, 330, 1546-1548.	12.6	301
34	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411.	14.5	97
35	Beyond the "best" match: machine learning annotation of protein sequences by integration of different sources of information. <i>Bioinformatics</i> , 2008, 24, 621-628.	4.1	12