

Mark B Schultz

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

6,507
citations

185998

28
h-index

233125

45
g-index

52
all docs

52
docs citations

52
times ranked

10005
citing authors

#	ARTICLE	IF	CITATIONS
1	Bandage: interactive visualization of <i>de novo</i> genome assemblies. <i>Bioinformatics</i> , 2015, 31, 3350-3352.	1.8	1,671
2	SRST2: Rapid genomic surveillance for public health and hospital microbiology labs. <i>Genome Medicine</i> , 2014, 6, 90.	3.6	953
3	Genomic analysis of diversity, population structure, virulence, and antimicrobial resistance in <i>Klebsiella pneumoniae</i> , an urgent threat to public health. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3574-81.	3.3	942
4	GISAID's Role in Pandemic Response. <i>China CDC Weekly</i> , 2021, 3, 1049-1051.	1.0	596
5	Isolation and rapid sharing of the 2019 novel coronavirus (SARS-CoV-2) from the first patient diagnosed with COVID-19 in Australia. <i>Medical Journal of Australia</i> , 2020, 212, 459-462.	0.8	297
6	Multiple drivers of decline in the global status of freshwater crayfish (Decapoda: Astacidea). <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140060.	1.8	225
7	Microbial mercury methylation in Antarctic sea ice. <i>Nature Microbiology</i> , 2016, 1, 16127.	5.9	158
8	Five decades of genome evolution in the globally distributed, extensively antibiotic-resistant <i>Acinetobacter baumannii</i> global clone 1. <i>Microbial Genomics</i> , 2016, 2, e000052.	1.0	155
9	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , 2020, 11, 4376.	5.8	152
10	Integrated shotgun sequencing and bioinformatics pipeline allows ultra-fast mitogenome recovery and confirms substantial gene rearrangements in Australian freshwater crayfishes. <i>BMC Evolutionary Biology</i> , 2014, 14, 19.	3.2	94
11	Convergent Adaptation in the Dominant Global Hospital Clone ST239 of Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MBio</i> , 2015, 6, e00080.	1.8	81
12	Macrozooplankton community structure off East Antarctica (80°S-150°E) during the Austral summer of 1995/1996. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2000, 47, 2437-2463.	0.6	79
13	MitoPhAST, a new automated mitogenomic phylogeny tool in the post-genomic era with a case study of 89 decapod mitogenomes including eight new freshwater crayfish mitogenomes. <i>Molecular Phylogenetics and Evolution</i> , 2015, 85, 180-188.	1.2	71
14	Translating genomics into practice for real-time surveillance and response to carbapenemase-producing Enterobacteriaceae: evidence from a complex multi-institutional KPC outbreak. <i>PeerJ</i> , 2018, 6, e4210.	0.9	66
15	Repeated local emergence of carbapenem-resistant <i>Acinetobacter baumannii</i> in a single hospital ward. <i>Microbial Genomics</i> , 2016, 2, e000050.	1.0	65
16	Phylogenetic analyses reveal extensive cryptic speciation and host specialization in an economically important mite taxon. <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 928-940.	1.2	64
17	Validation of a single-step, single-tube reverse transcription loop-mediated isothermal amplification assay for rapid detection of SARS-CoV-2 RNA. <i>Journal of Medical Microbiology</i> , 2020, 69, 1169-1178.	0.7	61
18	Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing <i>Enterobacteriales</i> in Victoria, Australia, 2012 to 2016. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	1.8	56

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19	DNA evidence of whale sharks (<i>Rhincodon typus</i>) feeding on red crab (<i>Gecarcoidea natalis</i>) larvae at Christmas Island, Australia. <i>Marine and Freshwater Research</i> , 2009, 60, 607.	0.7	49
20	Nuclear and Mitochondrial Patterns of Population Structure in North Pacific False Killer Whales (<i>Pseudorca crassidens</i>). <i>Journal of Heredity</i> , 2014, 105, 611-626.	1.0	49
21	Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent <i>Staphylococcus aureus</i> bacteraemia. <i>Genome Medicine</i> , 2018, 10, 65.	3.6	49
22	Fossil evidence in Australia for oldest known freshwater crayfish of Gondwana. <i>Gondwana Research</i> , 2008, 14, 287-296.	3.0	46
23	Distribution and Diversity of Soil Microfauna from East Antarctica: Assessing the Link between Biotic and Abiotic Factors. <i>PLoS ONE</i> , 2014, 9, e87529.	1.1	46
24	Phylogeography of the freshwater crayfish <i>Cherax destructor</i> Clark (Parastacidae) in inland Australia: historical fragmentation and recent range expansion. <i>Biological Journal of the Linnean Society</i> , 2004, 83, 539-550.	0.7	45
25	Phylogeography of <i>var</i> gene repertoires reveals fine-scale geospatial clustering of <i>Plasmodium falciparum</i> populations in a highly endemic area. <i>Molecular Ecology</i> , 2015, 24, 484-497.	2.0	39
26	Evolution underground: A molecular phylogenetic investigation of Australian burrowing freshwater crayfish (Decapoda: Parastacidae) with particular focus on <i>Engaeus</i> Erichson. <i>Molecular Phylogenetics and Evolution</i> , 2009, 50, 580-598.	1.2	38
27	Donor-Derived <i>Mycoplasma hominis</i> and an Apparent Cluster of <i>M. hominis</i> Cases in Solid Organ Transplant Recipients. <i>Clinical Infectious Diseases</i> , 2017, 65, 1504-1508.	2.9	34
28	Mitochondrial DNA analyses reveal widespread tardigrade diversity in Antarctica. <i>Invertebrate Systematics</i> , 2015, 29, 578.	0.5	33
29	Genomic insights into a sustained national outbreak of <i>Yersinia pseudotuberculosis</i> . <i>Genome Biology and Evolution</i> , 2016, 8, evw285.	1.1	31
30	Topical Antibiotic Use Coselects for the Carriage of Mobile Genetic Elements Conferring Resistance to Unrelated Antimicrobials in <i>Staphylococcus aureus</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	28
31	The changing landscape of vancomycin-resistant <i>Enterococcus faecium</i> in Australia: a population-level genomic study. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 3268-3278.	1.3	27
32	Cryptic diversity in <i>Engaeus</i> Erichson, <i>Geocharax</i> Clark and <i>Gramastacus Riek</i> (Decapoda : Parastacidae) revealed by mitochondrial 16S rDNA sequences. <i>Invertebrate Systematics</i> , 2007, 21, 569.	0.5	26
33	Comprehensive antibiotic-linked mutation assessment by resistance mutation sequencing (RM-seq). <i>Genome Medicine</i> , 2018, 10, 63.	3.6	26
34	Sea-level changes and palaeo-ranges: reconstruction of ancient shorelines and river drainages and the phylogeography of the Australian land crayfish <i>Engaeus sericatus</i> Clark (Decapoda: Tj ETQq0 0 0 rgBT /Overlap 10 Tf 56 137 Td	1.0	26
35	Mobile phones and computer keyboards: unlikely reservoirs of multidrug-resistant organisms in the tertiary intensive care unit. <i>Journal of Hospital Infection</i> , 2018, 99, 295-298.	1.4	21
36	More evolution underground: Accelerated mitochondrial substitution rate in Australian burrowing freshwater crayfishes (Decapoda: Parastacidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 118, 88-98.	1.2	19

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37	First comprehensive multi-tissue transcriptome of <i>Cherax quadricarinatus</i> (Decapoda: Parastacidae) reveals unexpected diversity of endogenous cellulase. <i>Organisms Diversity and Evolution</i> , 2016, 16, 185-200.	0.7	18
38	Target-Specific Assay for Rapid and Quantitative Detection of <i>Mycobacterium chimaera</i> DNA. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1847-1856.	1.8	17
39	Reconstruction of the Genomes of Drug-Resistant Pathogens for Outbreak Investigation through Metagenomic Sequencing. <i>MSphere</i> , 2019, 4, .	1.3	15
40	A Supervised Statistical Learning Approach for Accurate <i>Legionella pneumophila</i> Source Attribution during Outbreaks. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	8
41	The complete mitogenome of the Australian land crayfish <i>Engaeus lyelli</i> (Clark 1936) (Crustacea: Tj ETQq1 1.0, 784314 rgBT / Overlock 10	0.6	5
42	Genomic investigation of <i>Staphylococcus aureus</i> recovered from Gambian women and newborns following an oral dose of intra-partum azithromycin. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3170-3178.	1.3	5
43	The complete mitogenome of the Australian crayfish <i>Geocharax gracilis</i> Clark 1936 (Crustacea: Tj ETQq1 1.0, 784314 rgBT / Overlock 10	0.6	4
44	Development of twenty-four novel microsatellite markers for the freshwater crayfish, <i>Geocharax gracilis</i> , using next generation sequencing. <i>Conservation Genetics Resources</i> , 2012, 4, 555-558.	0.4	3
45	Comment on: Benchmarking of methods for identification of antimicrobial resistance genes in bacterial whole genome data. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 635.2-636.	1.3	0