

Alexis Criscuolo

List of Publications by Year in descending order

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71
papers

5,774
citations

201674

27
h-index

88630

70
g-index

86
all docs

86
docs citations

86
times ranked

8095
citing authors

#	ARTICLE	IF	CITATIONS
1	BMGE (Block Mapping and Gathering with Entropy): a new software for selection of phylogenetic informative regions from multiple sequence alignments. <i>BMC Evolutionary Biology</i> , 2010, 10, 210.	3.2	1,153
2	Whole genome-based population biology and epidemiological surveillance of <i>Listeria monocytogenes</i> . <i>Nature Microbiology</i> , 2017, 2, 16185.	13.3	562
3	Uncovering <i>Listeria monocytogenes</i> hypervirulence by harnessing its biodiversity. <i>Nature Genetics</i> , 2016, 48, 308-313.	21.4	541
4	Emergence and clonal expansion of in vitro artemisinin-resistant <i>Plasmodium falciparum</i> kelch13 R561H mutant parasites in Rwanda. <i>Nature Medicine</i> , 2020, 26, 1602-1608.	30.7	459
5	Genomic Definition of Hypervirulent and Multidrug-Resistant <i>Klebsiella pneumoniae</i> Clonal Groups. <i>Emerging Infectious Diseases</i> , 2014, 20, 1812-1820.	4.3	409
6	Bacteriophages Can Treat and Prevent <i>Pseudomonas aeruginosa</i> Lung Infections. <i>Journal of Infectious Diseases</i> , 2010, 201, 1096-1104.	4.0	265
7	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 172-179.	21.4	264
8	AlienTrimmer: A tool to quickly and accurately trim off multiple short contaminant sequences from high-throughput sequencing reads. <i>Genomics</i> , 2013, 102, 500-506.	2.9	195
9	Real-Time Whole-Genome Sequencing for Surveillance of <i>Listeria monocytogenes</i> , France. <i>Emerging Infectious Diseases</i> , 2017, 23, 1462-1470.	4.3	154
10	Evolutionary dynamics and genomic features of the <i>Elizabethkingia anophelis</i> 2015 to 2016 Wisconsin outbreak strain. <i>Nature Communications</i> , 2017, 8, 15483.	12.8	132
11	Large-Scale Phylogenomic Analyses Indicate a Deep Origin of Primary Plastids within Cyanobacteria. <i>Molecular Biology and Evolution</i> , 2011, 28, 3019-3032.	8.9	97
12	Description of <i>Klebsiella africanensis</i> sp. nov., <i>Klebsiella variicola</i> subsp. <i>tropicalensis</i> subsp. nov. and <i>Klebsiella variicola</i> subsp. <i>variicola</i> subsp. nov.. <i>Research in Microbiology</i> , 2019, 170, 165-170.	2.1	92
13	Revisiting the taxonomy of the genus <i>Elizabethkingia</i> using whole-genome sequencing, optical mapping, and MALDI-TOF, along with proposal of three novel <i>Elizabethkingia</i> species: <i>Elizabethkingia bruuniana</i> sp. nov., <i>Elizabethkingia ursingii</i> sp. nov., and <i>Elizabethkingia occulta</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 55-72.	1.7	91
14	Multicenter Outbreak of Infections by <i>Saprochaete clavata</i> , an Unrecognized Opportunistic Fungal Pathogen. <i>MBio</i> , 2014, 5, .	4.1	75
15	SDM: A Fast Distance-Based Approach for (Super)Tree Building in Phylogenomics. <i>Systematic Biology</i> , 2006, 55, 740-755.	5.6	69
16	Phylogenomic analysis supports the ancestral presence of LPS-outer membranes in the Firmicutes. <i>ELife</i> , 2016, 5, .	6.0	69
17	Genomic epidemiology and global diversity of the emerging bacterial pathogen <i>Elizabethkingia anophelis</i> . <i>Scientific Reports</i> , 2016, 6, 30379.	3.3	65
18	morePhyML: Improving the phylogenetic tree space exploration with PhyML 3. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 944-948.	2.7	58

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19	Taxonomic status of <i>Corynebacterium diphtheriae</i> biovar Belfanti and proposal of <i>Corynebacterium belfantii</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3826-3831.	1.7	56
20	Outbreak of Invasive Wound Mucormycosis in a Burn Unit Due to Multiple Strains of <i>Mucor circinelloides</i> f. <i>circinelloides</i> Resolved by Whole-Genome Sequencing. <i>MBio</i> , 2018, 9, .	4.1	54
21	A fast alignment-free bioinformatics procedure to infer accurate distance-based phylogenetic trees from genome assemblies. <i>Research Ideas and Outcomes</i> , 0, 5, .	1.0	53
22	S<scp>uper</scp>T<scp>riplets</scp>: a triplet-based supertree approach to phylogenomics. <i>Bioinformatics</i> , 2010, 26, i115-i123.	4.1	51
23	PhySIC: A Veto Supertree Method with Desirable Properties. <i>Systematic Biology</i> , 2007, 56, 798-817.	5.6	49
24	Development of a multiplex PCR assay for identification of <i>Klebsiella pneumoniae</i> hypervirulent clones of capsular serotype K2. <i>Journal of Medical Microbiology</i> , 2014, 63, 1608-1614.	1.8	46
25	Reclassification of <i>Haloactinobacterium glaciecola</i> as <i>Occultella glaciecola</i> gen. nov., comb. nov., of <i>Haloactinobacterium album</i> as <i>Ruania alba</i> comb. nov., with an emended description of the genus <i>Ruania</i> , recognition that the genus names <i>Haloactinobacterium</i> and <i>Ruania</i> are heterotypic synonyms and description of <i>Occultella aeris</i> sp. nov., a halotolerant isolate from surface soil sampled at an ancient copper smelter. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	44
26	Fast NJ-like algorithms to deal with incomplete distance matrices. <i>BMC Bioinformatics</i> , 2008, 9, 166.	2.6	43
27	Proteome remodelling by the stress sigma factor RpoS/ÎfS in <i>Salmonella</i> : identification of small proteins and evidence for post-transcriptional regulation. <i>Scientific Reports</i> , 2017, 7, 2127.	3.3	37
28	AlienTrimmer removes adapter oligonucleotides with high sensitivity in short-insert paired-end reads. Commentary on Turner (2014) Assessment of insert sizes and adapter content in FASTQ data from NexteraXT libraries. <i>Frontiers in Genetics</i> , 2014, 5, 130.	2.3	36
29	Genus-wide <i>Yersinia</i> core-genome multilocus sequence typing for species identification and strain characterization. <i>Microbial Genomics</i> , 2019, 5, .	2.0	31
30	A Dual Barcoding Approach to Bacterial Strain Nomenclature: Genomic Taxonomy of <i>Klebsiella pneumoniae</i> Strains. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	31
31	Genomic Sequencing of <i>Bordetella pertussis</i> for Epidemiology and Global Surveillance of Whooping Cough. <i>Emerging Infectious Diseases</i> , 2018, 24, 988-994.	4.3	29
32	Ongoing diphtheria outbreak in Yemen: a cross-sectional and genomic epidemiology study. <i>Lancet Microbe</i> , The, 2021, 2, e386-e396.	7.3	26
33	Manual and expert annotation of the nearly complete genome sequence of <i>Staphylococcus sciuri</i> strain ATCC 29059: A reference for the oxidase-positive staphylococci that supports the atypical phenotypic features of the species group. <i>Systematic and Applied Microbiology</i> , 2017, 40, 401-410.	2.8	23
34	Meat and Fish as Sources of Extended-Spectrum Î²-Lactamase-Producing <i>Escherichia coli</i>, Cambodia. <i>Emerging Infectious Diseases</i> , 2019, 25, .	4.3	23
35	<i>Peptoniphilus nemausensis</i> sp. nov. A new Gram-positive anaerobic coccus isolated from human clinical samples, an emended description of the genus <i>Peptoniphilus</i> and an evaluation of the taxonomic status of <i>Peptoniphilus</i> species with not validly published names. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126235.	2.8	21
36	Species- and Strain-Specific Adaptation of the HSP70 Super Family in Pathogenic Trypanosomatids. <i>Genome Biology and Evolution</i> , 2016, 8, 1980-1995.	2.5	20

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37	On the transformation of MinHash-based uncorrected distances into proper evolutionary distances for phylogenetic inference. <i>F1000Research</i> , 2020, 9, 1309.	1.6	20
38	The population structure of <i>Clostridium tetani</i> deduced from its pan-genome. <i>Scientific Reports</i> , 2019, 9, 11220.	3.3	17
39	<i>Saprochaete clavata</i> Outbreak Infecting Cancer Center through Dishwasher. <i>Emerging Infectious Diseases</i> , 2020, 26, 2031-2038.	4.3	17
40	<i>Flavobacterium salmonis</i> sp. nov. isolated from Atlantic salmon (<i>Salmo salar</i>) and formal proposal to reclassify <i>Flavobacterium spartansii</i> as a later heterotypic synonym of <i>Flavobacterium tractae</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6147-6154.	1.7	15
41	<i>Psychrobacter pasteurii</i> and <i>Psychrobacter piechaudii</i> sp. nov., two novel species within the genus <i>Psychrobacter</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3192-3197.	1.7	13
42	The speciation and hybridization history of the genus <i>Salmonella</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	13
43	Genomic Epidemiology and Strain Taxonomy of <i>Corynebacterium diphtheriae</i> . <i>Journal of Clinical Microbiology</i> , 2021, 59, e0158121.	3.9	12
44	<i>Jeotgalicoccus meleagridis</i> sp. nov. isolated from bioaerosol from emissions of a turkey fattening plant and reclassification of <i>Jeotgalicoccus halophilus</i> Liu et al. 2011 as a later heterotypic synonym of <i>Jeotgalicoccus aerolatus</i> Martin et al. 2011. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 71, .	1.7	12
45	Characterization of <i>Clostridium Baratii</i> Type F Strains Responsible for an Outbreak of Botulism Linked to Beef Meat Consumption in France. <i>PLOS Currents</i> , 2017, 9, .	1.4	11
46	<i>Paenibacillus allorhizosphaerae</i> sp. nov., from soil of the rhizosphere of <i>Zea mays</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	11
47	<i>Arthrobacter ulcerisalmonis</i> sp. nov., isolated from an ulcer of a farmed Atlantic salmon (<i>Salmo</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T <i>Systematic and Evolutionary Microbiology</i> , 2020, 70, 1963-1968.	1.7	11
48	Molecular characterisation of <i>Chlamydia pneumoniae</i> associated to atherosclerosis. <i>Pathogens and Disease</i> , 2017, 75, .	2.0	10
49	Carriage of a Single Strain of Nontoxigenic <i>Corynebacterium diphtheriae</i> bv. Belfanti () Tj ETQq1 1 0.784314 rgBT /Overlock 10 T <i>Microbiology</i> , 2019, 57, .	3.9	10
50	<i>Xinfangfangia humi</i> sp. nov., isolated from soil amended with humic acid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 2070-2075.	1.7	10
51	<i>Pseudoneobacillus rhizosphaerae</i> gen. nov., sp. nov., isolated from maize root rhizosphere. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	1.7	10
52	<i>Campylobacter coli</i> cultured from the stools of a patient with immunoproliferative small intestinal disease. <i>Clinical Microbiology and Infection</i> , 2014, 20, 908-911.	6.0	9
53	<i>Flavobacterium bizetiae</i> sp. nov., isolated from diseased freshwater fish in Canada at the end of the 1970s. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	9
54	<i>Paracoccus haematequi</i> sp. nov., isolated from horse blood. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1682-1688.	1.7	9

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55	<i>Halomonas lysinitropha</i> sp. nov., a novel halophilic bacterium isolated from a hypersaline wetland. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 6098-6105.	1.7	9
56	<i>Devosia equisanguinis</i> sp. nov., isolated from horse blood. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	9
57	Phylogenetic Inference with Weighted Codon Evolutionary Distances. <i>Journal of Molecular Evolution</i> , 2009, 68, 377-392.	1.8	7
58	<i>Flavobacterium panici</i> sp. nov. isolated from the rhizosphere of the switchgrass <i>Panicum virgatum</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 5824-5831.	1.7	7
59	In vitro and in silico parameters for precise cgMLST typing of <i>Listeria monocytogenes</i> . <i>BMC Genomics</i> , 2022, 23, 235.	2.8	7
60	<i>Pseudomonas carbonaria</i> sp. nov., isolated from charcoal. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	6
61	<i>Filibacter tadaridae</i> sp. nov., isolated from within a guano pile from a colony of Mexican free-tailed bats <i>Tadarida brasiliensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1438-1442.	1.7	6
62	<i>Serratia vespertilionis</i> (García-Fraile et al. 2015) is a later heterotypic synonym of <i>Serratia ficaria</i> (Grimont et al. 1981). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 1961-1962.	1.7	6
63	<i>Leucobacter soli</i> sp. nov., from soil amended with humic acid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	1.7	6
64	<i>topIb</i> , a phylogenetic hallmark gene of Thaumarchaeota encodes a functional eukaryote-like topoisomerase IB. <i>Nucleic Acids Research</i> , 2016, 44, 2795-2805.	14.5	5
65	Two <i>Clostridium perfringens</i> Type E Isolates in France. <i>Toxins</i> , 2019, 11, 138.	3.4	5
66	Draft Genome Sequence of <i>Campylobacter coli</i> Strain IPSID-1 Isolated from a Patient with Immunoproliferative Small Intestinal Disease. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
67	<i>Pigmentiphaga humi</i> sp. nov., isolated from soil amended with humic acid. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1573-1578.	1.7	4
68	Draft Genome Sequence of the Fish Pathogen <i>Flavobacterium columnare</i> Genomovar III Strain PH-97028 (=CIP 109753). <i>Genome Announcements</i> , 2018, 6, .	0.8	3
69	Simulation data for the estimation of numerical constants for approximating pairwise evolutionary distances between amino acid sequences. <i>Data in Brief</i> , 2019, 25, 104212.	1.0	3
70	ROCK: digital normalization of whole genome sequencing data. <i>Journal of Open Source Software</i> , 2022, 7, 3790.	4.6	1
71	Whole-Genome Sequences of a Cluster of 14 Unidentified Related <i>Veillonella</i> sp. Strains from Human Clinical Samples and Type Strains of 3 <i>Veillonella</i> Validated Species. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0