

David A Coil

List of Publications by Year in descending order

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Version: 2024-02-01

59
papers

2,760
citations

430754

18
h-index

189801

50
g-index

66
all docs

66
docs citations

66
times ranked

4579
citing authors

#	ARTICLE	IF	CITATIONS
1	The challenge of SARS-CoV-2 environmental monitoring in schools using floors and portable HEPA filtration units: Fresh or relic RNA?. PLoS ONE, 2022, 17, e0267212.	1.1	11
2	Air versus Water Chilling of Chicken: a Pilot Study of Quality, Shelf-Life, Microbial Ecology, and Economics. MSystems, 2021, 6, .	1.7	4
3	SARS-CoV-2 detection and genomic sequencing from hospital surface samples collected at UC Davis. PLoS ONE, 2021, 16, e0253578.	1.1	37
4	Reconstruction of Metagenome-Assembled Genomes from Aquaria. Microbiology Resource Announcements, 2021, 10, e0055721.	0.3	1
5	Inoculation With <i>Desulfovibrio</i> sp. Does Not Enhance Chalk Formation in the Pacific Oyster. Frontiers in Marine Science, 2020, 7, .	1.2	3
6	Draft Genome Analysis of <i>Christensenella minuta</i> DSM 22607, exhibiting an unusual expansion of transporter homologs of unknown function. Journal of Genomics, 2020, 8, 25-29.	0.6	5
7	Draft Genome Sequences of <i>Bacillus glennii</i> V44-8, <i>Bacillus saganii</i> V47-23a, <i>Bacillus</i> sp. Strain V59.32b, <i>Bacillus</i> sp. Strain MER_TA_151, and <i>Paenibacillus</i> sp. Strain MER_111, Isolated from Cleanrooms Where the Viking and Mars Exploration Rover Spacecraft Were Assembled. Microbiology Resource Announcements, 2020, 9, .	0.3	0
8	Reply to McDonald, "Protections against the Risk of Airborne SARS-CoV-2 Infection". MSystems, 2020, 5, .	1.7	0
9	Whole genome sequence analysis reveals the broad distribution of the RtxA type 1 secretion system and four novel putative type 1 secretion systems throughout the <i>Legionella</i> genus. PLoS ONE, 2020, 15, e0223033.	1.1	5
10	2019 Novel Coronavirus (COVID-19) Pandemic: Built Environment Considerations To Reduce Transmission. MSystems, 2020, 5, .	1.7	302
11	Bacterial communities associated with cell phones and shoes. PeerJ, 2020, 8, e9235.	0.9	6
12	Isolation and sequence-based characterization of a koala symbiont: <i>Lonepinella koalarum</i> . PeerJ, 2020, 8, e10177.	0.9	5
13	Title is missing!. , 2020, 15, e0223033.		0
14	Title is missing!. , 2020, 15, e0223033.		0
15	Title is missing!. , 2020, 15, e0223033.		0
16	Title is missing!. , 2020, 15, e0223033.		0
17	Network analysis to evaluate the impact of research funding on research community consolidation. PLoS ONE, 2019, 14, e0218273.	1.1	10
18	Comparison of Whole-Genome Sequences of <i>Legionella pneumophila</i> in Tap Water and in Clinical Strains, Flint, Michigan, USA, 2016. Emerging Infectious Diseases, 2019, 25, 2013-2020.	2.0	14

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19	Host-associated microbiomes drive structure and function of marine ecosystems. <i>PLoS Biology</i> , 2019, 17, e3000533.	2.6	103
20	Bacteria isolated from Bengal cat (<i>Felis catus</i> – <i>Prionailurus bengalensis</i>) anal sac secretions produce volatile compounds potentially associated with animal signaling. <i>PLoS ONE</i> , 2019, 14, e0216846.	1.1	11
21	Genomes from bacteria associated with the canine oral cavity: A test case for automated genome-based taxonomic assignment. <i>PLoS ONE</i> , 2019, 14, e0214354.	1.1	7
22	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. <i>MSphere</i> , 2019, 4, .	1.3	14
23	Genomic attributes of extended-spectrum β -lactamase-producing <i>Escherichia coli</i> isolated from patients in Lebanon. <i>Future Microbiology</i> , 2017, 12, 213-226.	1.0	10
24	Draft genome sequences of eight bacteria isolated from the indoor environment: <i>Staphylococcus capitis</i> strain H36, <i>S. capitis</i> strain H65, <i>S. cohnii</i> strain H62, <i>S. hominis</i> strain H69, <i>Microbacterium</i> sp. strain H83, <i>Mycobacterium iranicum</i> strain H39, <i>Plantibacter</i> sp. strain H53, and <i>Pseudomonas oryzae</i> strain H72. <i>Standards in Genomic Sciences</i> , 2017, 12, 17.	1.5	9
25	Schrödinger's microbes: Tools for distinguishing the living from the dead in microbial ecosystems. <i>Microbiome</i> , 2017, 5, 86.	4.9	347
26	Draft Genome Sequences of <i>Pseudomonas moraviensis</i> UCD-KL30, <i>Vibrio ostreicida</i> UCD-KL16, <i>Colwellia</i> sp. Strain UCD-KL20, <i>Shewanella</i> sp. Strain UCD-KL12, and <i>Shewanella</i> sp. Strain UCD-KL21, Isolated from Seagrass. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
27	Gut Check: The evolution of an educational board game. <i>PLoS Biology</i> , 2017, 15, e2001984.	2.6	31
28	A microbial survey of the International Space Station (ISS). <i>PeerJ</i> , 2017, 5, e4029.	0.9	52
29	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> UCD-JA29 Isolated from a Patient with Sepsis. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
30	Draft Genome Sequences of Two <i>Pseudoalteromonas porphyrae</i> Strains Isolated from Seagrass Sediment. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
31	Draft Genome Sequences of Two <i>Vibrio splendidus</i> Strains, Isolated from Seagrass Sediment. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
32	Genome Analysis of <i>Streptococcus pyogenes</i> Associated with Pharyngitis and Skin Infections. <i>PLoS ONE</i> , 2016, 11, e0168177.	1.1	20
33	Growth of 48 built environment bacterial isolates on board the International Space Station (ISS). <i>PeerJ</i> , 2016, 4, e1842.	0.9	37
34	Draft Genome Sequence of <i>Pseudoalteromonas tetraodonis</i> Strain UCD-SED8 (Phylum Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50,142 Td (<i	0.8	4
35	Draft Genome Sequence of <i>Bacillus vietnamensis</i> Strain UCD-SED5 (Phylum Firmicutes). <i>Genome Announcements</i> , 2015, 3, .	0.8	4
36	Whole genome sequencing of extended-spectrum β -lactamase producing <i>Klebsiella pneumoniae</i> isolated from a patient in Lebanon. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 32.	1.8	20

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37	Draft Genome Sequences of 26 <i>Porphyromonas</i> Strains Isolated from the Canine Oral Microbiome. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
38	A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. <i>Bioinformatics</i> , 2015, 31, 587-589.	1.8	973
39	<i>Porphyrobacter mercurialis</i> sp. nov., isolated from a stadium seat and emended description of the genus <i>Porphyrobacter</i> . <i>PeerJ</i> , 2015, 3, e1400.	0.9	16
40	Swabs to genomes: a comprehensive workflow. <i>PeerJ</i> , 2015, 3, e960.	0.9	37
41	microBEnet: Lessons Learned from Building an Interdisciplinary Scientific Community in the Online Sphere. <i>PLoS Biology</i> , 2014, 12, e1001884.	2.6	4
42	Draft Genome Sequence of <i>Tatumella</i> sp. Strain UCD-D_suzukii (Phylum <i>Proteobacteria</i>) Isolated from <i>Drosophila suzukii</i> Larvae. <i>Genome Announcements</i> , 2014, 2, .	0.8	4
43	Draft Genome Sequence of an Actinobacterium, <i>Brachybacterium muris</i> Strain UCD-AY4. <i>Genome Announcements</i> , 2013, 1, e0008613.	0.8	9
44	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain UCD-TDU (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, e0012013.	0.8	5
45	Draft Genome Sequence of <i>Kocuria</i> sp. Strain UCD-OTCP (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
46	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td</i>) (<i>Actinobacteria</i>)	0.8	7
47	Draft Genome Sequence of <i>Leucobacter</i> sp. Strain UCD-THU (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
48	Draft Genome Sequence of <i>Dietzia</i> sp. Strain UCD-THP (Phylum <i>Actinobacteria</i>). <i>Genome Announcements</i> , 2013, 1, .	0.8	5
49	The role of fimV and the importance of its tandem repeat copy number in twitching motility, pigment production, and morphology in <i>Legionella pneumophila</i> . <i>Archives of Microbiology</i> , 2010, 192, 625-631.	1.0	13
50	A <i>Legionella pneumophila</i> collagen-like protein encoded by a gene with a variable number of tandem repeats is involved in the adherence and invasion of host cells. <i>FEMS Microbiology Letters</i> , 2010, 306, 168-176.	0.7	44
51	Teaching the Process of Science: Faculty Perceptions and an Effective Methodology. <i>CBE Life Sciences Education</i> , 2010, 9, 524-535.	1.1	178
52	Twitching motility in <i>Legionella pneumophila</i> . <i>FEMS Microbiology Letters</i> , 2009, 293, 271-277.	0.7	17
53	Intragenic tandem repeat variation between <i>Legionella pneumophila</i> strains. <i>BMC Microbiology</i> , 2008, 8, 218.	1.3	28
54	A faster and more accurate assay for intracellular replication of <i>Legionella pneumophila</i> in amoebae hosts. <i>Journal of Microbiological Methods</i> , 2008, 72, 214-216.	0.7	12

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55	Enhancement of Enveloped Virus Entry by Phosphatidylserine. <i>Journal of Virology</i> , 2005, 79, 11496-11500.	1.5	36
56	Phosphatidylserine treatment relieves the block to retrovirus infection of cells expressing glycosylated virus receptors. <i>Retrovirology</i> , 2005, 2, 49.	0.9	7
57	Phosphatidylserine Is Not the Cell Surface Receptor for Vesicular Stomatitis Virus. <i>Journal of Virology</i> , 2004, 78, 10920-10926.	1.5	156
58	Comparative sequencing of a multicopy subtelomeric region containing olfactory receptor genes reveals multiple interactions between non-homologous chromosomes. <i>Human Molecular Genetics</i> , 2001, 10, 2363-2372.	1.4	51
59	Jaagsiekte Sheep Retrovirus Env Protein Stabilizes Retrovirus Vectors against Inactivation by Lung Surfactant, Centrifugation, and Freeze-Thaw Cycling. <i>Journal of Virology</i> , 2001, 75, 8864-8867.	1.5	17