

# David A Coil

## List of Publications by Year in descending order

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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	A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. <i>Bioinformatics</i> , 2015, 31, 587-589.	1.8	973
2	Schrödinger's microbes: Tools for distinguishing the living from the dead in microbial ecosystems. <i>Microbiome</i> , 2017, 5, 86.	4.9	347
3	2019 Novel Coronavirus (COVID-19) Pandemic: Built Environment Considerations To Reduce Transmission. <i>MSystems</i> , 2020, 5, .	1.7	302
4	Teaching the Process of Science: Faculty Perceptions and an Effective Methodology. <i>CBE Life Sciences Education</i> , 2010, 9, 524-535.	1.1	178
5	Phosphatidylserine Is Not the Cell Surface Receptor for Vesicular Stomatitis Virus. <i>Journal of Virology</i> , 2004, 78, 10920-10926.	1.5	156
6	Host-associated microbiomes drive structure and function of marine ecosystems. <i>PLoS Biology</i> , 2019, 17, e3000533.	2.6	103
7	A microbial survey of the International Space Station (ISS). <i>PeerJ</i> , 2017, 5, e4029.	0.9	52
8	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
9	<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
10	SARS-CoV-2 detection and genomic sequencing from hospital surface samples collected at UC Davis. <i>PLoS ONE</i> , 2021, 16, e0253578.	1.1	37
11	Growth of 48 built environment bacterial isolates on board the International Space Station (ISS). <i>PeerJ</i> , 2016, 4, e1842.	0.9	37
12	Swabs to genomes: a comprehensive workflow. <i>PeerJ</i> , 2015, 3, e960.	0.9	37
13	Enhancement of Enveloped Virus Entry by Phosphatidylserine. <i>Journal of Virology</i> , 2005, 79, 11496-11500.	1.5	36
14	Gut Check: The evolution of an educational board game. <i>PLoS Biology</i> , 2017, 15, e2001984.	2.6	31
15	Intragenic tandem repeat variation between <i>Legionella pneumophila</i> strains. <i>BMC Microbiology</i> , 2008, 8, 218.	1.3	28
16	Whole genome sequencing of extended-spectrum $\beta$ -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
17	Genome Analysis of <i>Streptococcus pyogenes</i> Associated with Pharyngitis and Skin Infections. <i>PLoS ONE</i> , 2016, 11, e0168177.	1.1	20
18	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

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19	Twitching motility in <i>Legionella pneumophila</i> . FEMS Microbiology Letters, 2009, 293, 271-277.	0.7	17
20	<i>Porphyrobacter mercurialis</i> sp. nov., isolated from a stadium seat and emended description of the genus <i>Porphyrobacter</i> . PeerJ, 2015, 3, e1400.	0.9	16
21	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
22	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. MSphere, 2019, 4, .	1.3	14
23	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> . Archives of Microbiology, 2010, 192, 625-631.	1.0	13
24	A faster and more accurate assay for intracellular replication of <i>Legionella pneumophila</i> in amoebae hosts. Journal of Microbiological Methods, 2008, 72, 214-216.	0.7	12
25	Bacteria isolated from Bengal cat ( <i>Felis catus</i> Æ— <i>Prionailurus bengalensis</i> ) anal sac secretions produce volatile compounds potentially associated with animal signaling. PLoS ONE, 2019, 14, e0216846.	1.1	11
26	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
27	Genomic attributes of extended-spectrum ð²-lactamase-producing <i>Escherichia coli</i> isolated from patients in Lebanon. Future Microbiology, 2017, 12, 213-226.	1.0	10
28	Network analysis to evaluate the impact of research funding on research community consolidation. PLoS ONE, 2019, 14, e0218273.	1.1	10
29	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. Genome Announcements, 2017, 5, .	0.8	10
30	Draft Genome Sequence of an Actinobacterium, <i>Brachybacterium muris</i> Strain UCD-AY4. Genome Announcements, 2013, 1, e0008613.	0.8	9
31	Draft Genome Sequences of 26 <i>Porphyromonas</i> Strains Isolated from the Canine Oral Microbiome. Genome Announcements, 2015, 3, .	0.8	9
32	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 oryzihabitans</i> strain H72. Standards in Genomic Sciences, 2017, 12, 17.	1.5	9
33	Phosphatidylserine treatment relieves the block to retrovirus infection of cells expressing glycosylated virus receptors. Retrovirology, 2005, 2, 49.	0.9	7
34	Draft Genome Sequence of <i>Curtobacterium flaccumfaciens</i> Strain UCD-AKU (Phylum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td (<i>A	0.8	7
35	Genomes from bacteria associated with the canine oral cavity: A test case for automated genome-based taxonomic assignment. PLoS ONE, 2019, 14, e0214354.	1.1	7
36	Bacterial communities associated with cell phones and shoes. PeerJ, 2020, 8, e9235.	0.9	6

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37	Draft Genome Sequence of <i>Microbacterium</i> sp. Strain UCD-TDU (Phylum <i>Actinobacteria</i> ). Genome Announcements, 2013, 1, e0012013.	0.8	5
38	Draft Genome Sequence of <i>Kocuria</i> sp. Strain UCD-OTCP (Phylum <i>Actinobacteria</i> ). Genome Announcements, 2013, 1, .	0.8	5
39	Draft Genome Sequence of <i>Leucobacter</i> sp. Strain UCD-THU (Phylum <i>Actinobacteria</i> ). Genome Announcements, 2013, 1, .	0.8	5
40	Draft Genome Sequence of <i>Dietzia</i> sp. Strain UCD-THP (Phylum <i>Actinobacteria</i> ). Genome Announcements, 2013, 1, .	0.8	5
41	Draft Genome Sequences of Two <i>Pseudoalteromonas porphyrae</i> Strains Isolated from Seagrass Sediment. Genome Announcements, 2016, 4, .	0.8	5
42	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
43	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
44	Isolation and sequence-based characterization of a koala symbiont: <i>Lonepinella koalarum</i> . PeerJ, 2020, 8, e10177.	0.9	5
45	microBEnet: Lessons Learned from Building an Interdisciplinary Scientific Community in the Online Sphere. PLoS Biology, 2014, 12, e1001884.	2.6	4
46	Draft Genome Sequence of <i>Tatumella</i> sp. Strain UCD-D_suzukii (Phylum <i>Proteobacteria</i> ) Isolated from <i>Drosophila suzukii</i> Larvae. Genome Announcements, 2014, 2, .	0.8	4
47	Draft Genome Sequence of <i>Pseudoalteromonas tetraodonis</i> Strain UCD-SED8 (Phylum Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5038)	0.8	4
48	Draft Genome Sequence of <i>Bacillus vietnamensis</i> Strain UCD-SED5 (Phylum Firmicutes). Genome Announcements, 2015, 3, .	0.8	4
49	Air versus Water Chilling of Chicken: a Pilot Study of Quality, Shelf-Life, Microbial Ecology, and Economics. MSysystems, 2021, 6, .	1.7	4
50	Inoculation With <i>Desulfovibrio</i> sp. Does Not Enhance Chalk Formation in the Pacific Oyster. Frontiers in Marine Science, 2020, 7, .	1.2	3
51	Draft Genome Sequences of Two <i>Vibrio splendidus</i> Strains, Isolated from Seagrass Sediment. Genome Announcements, 2016, 4, .	0.8	2
52	Reconstruction of Metagenome-Assembled Genomes from Aquaria. Microbiology Resource Announcements, 2021, 10, e0055721.	0.3	1
53	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> UCD-JA29 Isolated from a Patient with Sepsis. Genome Announcements, 2016, 4, .	0.8	0
54	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

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55	Reply to McDonald, "Protections against the Risk of Airborne SARS-CoV-2 Infection", MSystems, 2020, 5, .	1.7	0
56	Title is missing!. , 2020, 15, e0223033.		0
57	Title is missing!. , 2020, 15, e0223033.		0
58	Title is missing!. , 2020, 15, e0223033.		0
59	Title is missing!. , 2020, 15, e0223033.		0