

Kristen DeAngelis

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

5,213
citations

117625
34
h-index

144013
57
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70
all docs

70
docs citations

70
times ranked

7368
citing authors

#	ARTICLE	IF	CITATIONS
1	Draft Genome Sequence of <i>Leifsonia poae</i> Strain BS71, Isolated from a Drought Microcosm. Microbiology Resource Announcements, 2022, 11, e0095121.	0.6	1
2	A framework for integrating microbial dispersal modes into soil ecosystem ecology. IScience, 2022, 25, 103887.	4.1	25
3	<i>Sodalis ligni</i> Strain 159R Isolated from an Anaerobic Lignin-Degrading Consortium. Microbiology Spectrum, 2022, 10, e0234621.	3.0	1
4	Evidence for a genetic basis in functional trait tradeoffs with microbial growth rate but not growth yield. Soil Biology and Biochemistry, 2022, 172, 108765.	8.8	0
5	Soil aggregate-mediated microbial responses to long-term warming. Soil Biology and Biochemistry, 2021, 152, 108055.	8.8	30
6	Fungal community response to long-term soil warming with potential implications for soil carbon dynamics. Ecosphere, 2021, 12, e03460.	2.2	17
7	The Transcriptional Response of Soil Bacteria to Long-Term Warming and Short-Term Seasonal Fluctuations in a Terrestrial Forest. Frontiers in Microbiology, 2021, 12, 666558.	3.5	8
8	Introducing the Microbes and Social Equity Working Group: Considering the Microbial Components of Social, Environmental, and Health Justice. MSystems, 2021, 6, e0047121.	3.8	45
9	Physical protection regulates microbial thermal responses to chronic soil warming. Soil Biology and Biochemistry, 2021, 159, 108298.	8.8	5
10	Direct evidence for the role of microbial community composition in the formation of soil organic matter composition and persistence. ISME Communications, 2021, 1, .	4.2	48
11	Lignin induced iron reduction by novel sp., <i>Tolomonas lignolytic</i> BRL6-1. PLoS ONE, 2020, 15, e0233823.	2.5	8
12	Microbial diversity drives carbon use efficiency in a model soil. Nature Communications, 2020, 11, 3684.	12.8	217
13	Genome Sequences of <i>Frankineae</i> sp. Strain MT45 and <i>Jatrophihabitans</i> sp. Strain GAS493, Two Actinobacteria Isolated from Forest Soil. Microbiology Resource Announcements, 2020, 9, .	0.6	1
14	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	13.3	115
15	Carbon Use Efficiency and Its Temperature Sensitivity Covary in Soil Bacteria. MBio, 2020, 11, .	4.1	52
16	Heavy and wet: The consequences of violating assumptions of measuring soil microbial growth efficiency using the ¹⁸ O water method. Elementa, 2020, 8, .	3.2	5
17	Draft Genome Sequence of a Terrestrial Planctomycete, <i>Singulisphaera</i> sp. Strain GP187, Isolated from Forest Soil. Microbiology Resource Announcements, 2020, 9, .	0.6	2
18	Lignin induced iron reduction by novel sp., <i>Tolomonas lignolytic</i> BRL6-1. , 2020, 15, e0233823.		0

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19	Lignin induced iron reduction by novel sp., <i>Tolomonas lignolytic</i> BRL6-1. , 2020, 15, e0233823.		0
20	Lignin induced iron reduction by novel sp., <i>Tolomonas lignolytic</i> BRL6-1. , 2020, 15, e0233823.		0
21	Lignin induced iron reduction by novel sp., <i>Tolomonas lignolytic</i> BRL6-1. , 2020, 15, e0233823.		0
22	High proportions of bacteria and archaea across most biomes remain uncultured. <i>ISME Journal</i> , 2019, 13, 3126-3130.	9.8	264
23	Draft Genome Sequence of Acidobacteria Group 1 Acidipila sp. Strain EB88, Isolated from Forest Soil. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	10
24	Complete Genome Sequence of <i>Serratia quinivorans</i> Strain 124R, a Facultative Anaerobe Isolated on Organosolv Lignin as a Sole Carbon Source. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
25	Microbial responses to experimental soil warming: Five testable hypotheses. , 2019, , 141-156.		1
26	Metabolic tradeoffs and heterogeneity in microbial responses to temperature determine the fate of litter carbon in simulations of a warmer world. <i>Biogeosciences</i> , 2019, 16, 4875-4888.	3.3	4
27	Soil carbon cycling proxies: Understanding their critical role in predicting climate change feedbacks. <i>Global Change Biology</i> , 2018, 24, 895-905.	9.5	61
28	Genome Sequence of <i>Verrucomicrobium</i> sp. Strain GAS474, a Novel Bacterium Isolated from Soil. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
29	Draft Genome Sequences of Three Strains of a Novel Rhizobiales Species Isolated from Forest Soil. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
30	High-Quality Draft Genome Sequences of Four Lignocellulose-Degrading Bacteria Isolated from Puerto Rican Forest Soil: <i>Gordonia</i> sp., <i>Paenibacillus</i> sp., <i>Variovorax</i> sp., and <i>Vogesella</i> sp. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
31	Ecological Insights into the Dynamics of Plant Biomass-Degrading Microbial Consortia. <i>Trends in Microbiology</i> , 2017, 25, 788-796.	7.7	59
32	Changes in substrate availability drive carbon cycle response to chronic warming. <i>Soil Biology and Biochemistry</i> , 2017, 110, 68-78.	8.8	73
33	Long-term pattern and magnitude of soil carbon feedback to the climate system in a warming world. <i>Science</i> , 2017, 358, 101-105.	12.6	548
34	Multi-time series RNA-seq analysis of <i>Enterobacter lignolyticus</i> SCF1 during growth in lignin-amended medium. <i>PLoS ONE</i> , 2017, 12, e0186440.	2.5	20
35	Chemical communication connects soil food webs. <i>Soil Biology and Biochemistry</i> , 2016, 102, 48-51.	8.8	19
36	Long-Term Warming Alters Carbohydrate Degradation Potential in Temperate Forest Soils. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6518-6530.	3.1	68

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37	Drivers and patterns of iron redox cycling from surface to bedrock in a deep tropical forest soil: a new conceptual model. <i>Biogeochemistry</i> , 2016, 130, 177-190.	3.5	48
38	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolumonas lignolytica</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 106.	1.5	43
39	Long-term forest soil warming alters microbial communities in temperate forest soils. <i>Frontiers in Microbiology</i> , 2015, 6, 104.	3.5	270
40	Two decades of warming increases diversity of a potentially lignolytic bacterial community. <i>Frontiers in Microbiology</i> , 2015, 6, 480.	3.5	73
41	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , 2014, 9, 19.	1.5	40
42	Draft Genome Sequence of the Lignin-Degrading <i>Burkholderia</i> sp. Strain LIG30, Isolated from Wet Tropical Forest Soil. <i>Genome Announcements</i> , 2014, 2, .	0.8	26
43	Enzyme activities of aerobic lignocellulolytic bacteria isolated from wet tropical forest soils. <i>Systematic and Applied Microbiology</i> , 2014, 37, 60-67.	2.8	103
44	Changes in microbial dynamics during long-term decomposition in tropical forests. <i>Soil Biology and Biochemistry</i> , 2013, 66, 60-68.	8.8	47
45	Up Against The Wall: The Effects of Climate Warming on Soil Microbial Diversity and The Potential for Feedbacks to The Carbon Cycle. <i>Diversity</i> , 2013, 5, 409-425.	1.7	31
46	Evidence supporting dissimilatory and assimilatory lignin degradation in <i>Enterobacter lignolyticus</i> SCF1. <i>Frontiers in Microbiology</i> , 2013, 4, 280.	3.5	92
47	Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. <i>Standards in Genomic Sciences</i> , 2013, 7, 382-398.	1.5	12
48	Global transcriptome response to ionic liquid by a tropical rain forest soil bacterium, <i>Enterobacter lignolyticus</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2173-82.	7.1	85
49	Anaerobic Decomposition of Switchgrass by Tropical Soil-Derived Feedstock-Adapted Consortia. <i>MBio</i> , 2012, 3, .	4.1	19
50	Phylogenetic Clustering of Soil Microbial Communities by 16S rRNA but Not 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2459-2461.	3.1	28
51	Application of phenotypic microarrays to environmental microbiology. <i>Current Opinion in Biotechnology</i> , 2012, 23, 41-48.	6.6	45
52	PCR Amplification-Independent Methods for Detection of Microbial Communities by the High-Density Microarray PhyloChip. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6313-6322.	3.1	74
53	Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. <i>Nature</i> , 2011, 480, 368-371.	27.8	601
54	Characterization of Trapped Lignin-Degrading Microbes in Tropical Forest Soil. <i>PLoS ONE</i> , 2011, 6, e19306.	2.5	178

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55	Complete genome sequence of <i>Enterobacter lignolyticus</i> SCF1. Standards in Genomic Sciences, 2011, 5, 69-85.	1.5	76
56	Effects of selected root exudate components on soil bacterial communities. FEMS Microbiology Ecology, 2011, 77, 600-610.	2.7	316
57	Strategies for Enhancing the Effectiveness of Metagenomic-based Enzyme Discovery in Lignocellulolytic Microbial Communities. Bioenergy Research, 2010, 3, 146-158.	3.9	100
58	Microbial communities acclimate to recurring changes in soil redox potential status. Environmental Microbiology, 2010, 12, 3137-3149.	3.8	294
59	Selective progressive response of soil microbial community to wild oat roots. ISME Journal, 2009, 3, 168-178.	9.8	306
60	Bacterial Diversity Analysis of Huanglongbing Pathogen-Infected Citrus, Using PhyloChip Arrays and 16S rRNA Gene Clone Library Sequencing. Applied and Environmental Microbiology, 2009, 75, 1566-1574.	3.1	125
61	Bacterial quorum sensing and nitrogen cycling in rhizosphere soil. FEMS Microbiology Ecology, 2008, 66, 197-207.	2.7	126
62	PLANT AND MICROBIAL CONTROLS ON NITROGEN RETENTION AND LOSS IN A HUMID TROPICAL FOREST. Ecology, 2008, 89, 3030-3040.	3.2	146
63	Sensitive Whole-Cell Biosensor Suitable for Detecting a Variety of N -Acyl Homoserine Lactones in Intact Rhizosphere Microbial Communities. Applied and Environmental Microbiology, 2007, 73, 3724-3727.	3.1	37
64	Root Interactions with Soil Microbial Communities and Processes. , 2007, , 1-29.		43
65	Two Novel Bacterial Biosensors for Detection of Nitrate Availability in the Rhizosphere. Applied and Environmental Microbiology, 2005, 71, 8537-8547.	3.1	89