Lee Ann McCue

List of Publications by Year
in descending order

69 papers	3,130 citations	159585 30 h-index	168389 53 g-index
73 all docs	73 docs citations	73 times ranked	4161 citing authors

#	Article	IF	Citations
1	Phylogenetic footprinting of transcription factor binding sites in proteobacterial genomes. Nucleic Acids Research, 2001, 29, 774-782.	14.5	235
2	Transcriptomic and Proteomic Characterization of the Fur Modulon in the Metal-Reducing Bacterium Shewanella oneidensis. Journal of Bacteriology, 2004, 186, 8385-8400.	2.2	134
3	Functional Classification of cNMP-binding Proteins and Nucleotide Cyclases with Implications for Novel Regulatory Pathways in Mycobacterium tuberculosis. Genome Research, 2000, 10, 204-219.	5.5	122
4	Characterization of Mycobacterium tuberculosis Rv3676 (CRP Mt), a Cyclic AMP Receptor Protein-Like DNA Binding Protein. Journal of Bacteriology, 2005, 187, 7795-7804.	2.2	115
5	Global profiling of Shewanella oneidensis MR-1: Expression of hypothetical genes and improved functional annotations. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2099-2104.	7.1	113
6	Linking microbial community structure to β-glucosidic function in soil aggregates. ISME Journal, 2013, 7, 2044-2053.	9.8	110
7	Comparative systems biology across an evolutionary gradient within the <i>Shewanella</i> genus. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15909-15914.	7.1	96
8	Genomes and secretomes of Ascomycota fungi reveal diverse functions in plant biomass decomposition and pathogenesis. BMC Genomics, 2019, 20, 976.	2.8	96
9	Identification and Characterization of Mycobacterial Proteins Differentially Expressed under Standing and Shaking Culture Conditions, Including Rv2623 from a Novel Class of Putative ATP-Binding Proteins. Infection and Immunity, 2001, 69, 5777-5785.	2.2	95
10	Combined Statistical Analyses of Peptide Intensities and Peptide Occurrences Improves Identification of Significant Peptides from MS-Based Proteomics Data. Journal of Proteome Research, 2010, 9, 5748-5756.	3.7	93
11	ATLAS: a Snakemake workflow for assembly, annotation, and genomic binning of metagenome sequence data. BMC Bioinformatics, 2020, 21, 257.	2.6	91
12	Factors Influencing the Identification of Transcription Factor Binding Sites by Cross-Species Comparison. Genome Research, 2002, 12, 1523-1532.	5.5	90
13	Identification of co-regulated genes through Bayesian clustering of predicted regulatory binding sites. Nature Biotechnology, 2003, 21, 435-439.	17.5	89
14	A Family of acr -Coregulated Mycobacterium tuberculosis Genes Shares a Common DNA Motif and Requires Rv3133c (dos R or dev R) for Expression. Infection and Immunity, 2003, 71, 5332-5343.	2.2	88
15	Geoarchaeota: a new candidate phylum in the Archaea from high-temperature acidic iron mats in Yellowstone National Park. ISME Journal, 2013, 7, 622-634.	9.8	87
16	Identification of a novel class in the ?/? hydrolase fold superfamily: The N-myc differentiation-related proteins. Proteins: Structure, Function and Bioinformatics, 2002, 47, 163-168.	2.6	83
17	Comparative Bacterial Proteomics: Analysis of the Core Genome Concept. PLoS ONE, 2008, 3, e1542.	2.5	71
18	Identification of a Mycobacterium tuberculosis Putative Classical Nitroreductase Gene Whose Expression Is Coregulated with That of the acr Gene within Macrophages, in Standing versus Shaking Cultures, and under Low Oxygen Conditions. Infection and Immunity, 2002, 70, 1518-1529.	2.2	69

#	ARTICLE	IF	CITATIONS
19	Modeling Microbial Dynamics in Heterogeneous Environments: Growth on Soil Carbon Sources. Microbial Ecology, 2012, 63, 883-897.	2.8	66
20	Identification of Mobile Elements and Pseudogenes in the *Shewanella oneidensis* MR-1 Genome. Applied and Environmental Microbiology, 2008, 74, 3257-3265.	3.1	63
21	Soil Respiration and Bacterial Structure and Function after 17 Years of a Reciprocal Soil Transplant Experiment. PLoS ONE, 2016, 11, e0150599.	2.5	60
22	Metaphenomic Responses of a Native Prairie Soil Microbiome to Moisture Perturbations. MSystems, 2019, 4, .	3.8	56
23	Micrometer-scale physical structure and microbial composition of soil macroaggregates. Soil Biology and Biochemistry, 2013, 65, 60-68.	8.8	54
24	The Gibbs Centroid Sampler. Nucleic Acids Research, 2007, 35, W232-W237.	14.5	52
25	Making connections between novel transcription factors and their DNA motifs. Genome Research, 2005, 15, 312-320.	5.5	49
26	Myrionecta rubra population genetic diversity and its cryptophyte chloroplast specificity in recurrent red tides in the Columbia River estuary. Aquatic Microbial Ecology, 2011, 62, 85-97.	1.8	44
27	Measurements of microbial community activities in individual soil macroaggregates. Soil Biology and Biochemistry, 2012, 48, 192-195.	8.8	43
28	The Human Cytomegalovirus Genes and Proteins Required for DNA Synthesis. Intervirology, 1996, 39, 378-388.	2.8	42
29	The National Microbiome Data Collaborative: enabling microbiome science. Nature Reviews Microbiology, 2020, 18, 313-314.	28.6	42
30	*pmartR*: Quality Control and Statistics for Mass Spectrometry-Based Biological Data. Journal of Proteome Research, 2019, 18, 1418-1425.	3.7	39
31	Red Waters of Myrionecta rubra are Biogeochemical Hotspots for the Columbia River Estuary with Impacts on Primary/Secondary Productions and Nutrient Cycles. Estuaries and Coasts, 2012, 35, 878-891.	2.2	36
32	Soil texture and environmental conditions influence the biogeochemical responses of soils to drought and flooding. Communications Earth & Environment, 2021, 2, .	6.8	35
33	Molecular analysis of sporulation in Streptomyces griseus. Gene, 1992, 115, 173-179.	2.2	32
34	ftmsRanalysis: An R package for exploratory data analysis and interactive visualization of FT-MS data. PLoS Computational Biology, 2020, 16, e1007654.	3.2	32
35	VESPA: software to facilitate genomic annotation of prokaryotic organisms through integration of proteomic and transcriptomic data. BMC Genomics, 2012, 13, 131.	2.8	31
36	A phylogenetic Gibbs sampler that yields centroid solutions for cis-regulatory site prediction. Bioinformatics, 2007, 23, 1718-1727.	4.1	30

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37	Fnr (EtrA) acts as a fine-tuning regulator of anaerobic metabolism in Shewanella oneidensisMR-1. BMC Microbiology, 2011, 11, 64.	3.3	30
38	PhyloScan: identification of transcription factor binding sites using cross-species evidence. Algorithms for Molecular Biology, 2007, 2, 1.	1.2	28
39	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborativeâ€™s Workshop and Follow-On Activities. MSystems, 2021, 6, .	3.8	28
40	Niche differentiation of bacteria and fungi in carbon and nitrogen cycling of different habitats in a temperate coniferous forest: A metaproteomic approach. Soil Biology and Biochemistry, 2021, 155, 108170.	8.8	28
41	Network analysis of transcriptomics expands regulatory landscapes in<i>Synechococcus</i>sp. PCC 7002. Nucleic Acids Research, 2016, 44, 8810-8825.	14.5	26
42	Identification and Characterization of a Developmentally Regulated Protein, EshA, Required for Sporogenic Hyphal Branches in Streptomyces griseus. Journal of Bacteriology, 2001, 183, 3004-3015.	2.2	23
43	A model of cyclic transcriptomic behavior in the cyanobacterium Cyanothece sp. ATCC 51142. Molecular BioSystems, 2011, 7, 2407.	2.9	23
44	Fluctuations in Species-Level Protein Expression Occur during Element and Nutrient Cycling in the Subsurface. PLoS ONE, 2013, 8, e57819.	2.5	21
45	Identification of bldA mutants of Streptomyces griseus. Gene, 1996, 171, 75-78.	2.2	19
46	Measuring Global Credibility with Application to Local Sequence Alignment. PLoS Computational Biology, 2008, 4, e1000077.	3.2	19
47	Factors affecting the bacterial community composition and heterotrophic production of Columbia River estuarine turbidity maxima. MicrobiologyOpen, 2017, 6, e00522.	3.0	19
48	The tricarboxylic acid cycle in Shewanella oneidensis is independent of Fur and RyhB control. BMC Microbiology, 2010, 10, 264.	3.3	18
49	Using the Gibbs Motif Sampler to Find Conserved Domains in DNA and Protein Sequences. Current Protocols in Bioinformatics, 2005, 10, Unit 2.8.	25.8	17
50	Rhodopseudomonas palustris Regulons Detected by Cross-Species Analysis of Alphaproteobacterial Genomes. Applied and Environmental Microbiology, 2005, 71, 7442-7452.	3.1	17
51	Protist 18S rRNA gene sequence analysis reveals multiple sources of organic matter contributing to turbidity maxima of the Columbia River estuary. Marine Ecology - Progress Series, 2011, 438, 19-31.	1.9	16
52	SPOCS: software for predicting and visualizing orthology/paralogy relationships among genomes. Bioinformatics, 2013, 29, 2641-2642.	4.1	14
53	Temporal dynamics of CO2 and CH4 loss potentials in response to rapid hydrological shifts in tidal freshwater wetland soils. Ecological Engineering, 2018, 114, 104-114.	3.6	13
54	Quantum Mechanical Methods Predict Accurate Thermodynamics of Biochemical Reactions. ACS Omega, 2021, 6, 9948-9959.	3.5	12

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55	Proteomic Profiles of Five Strains of Oxygenic Photosynthetic Cyanobacteria of the Genus *Cyanothece*. Journal of Proteome Research, 2014, 13, 3262-3276.	3.7	11
56	A Bayesian integration model of high-throughput proteomics and metabolomics data for improved early detection of microbial infections. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 451-63.	0.7	10
57	Using the Gibbs Motif Sampler for Phylogenetic Footprinting. Methods in Molecular Biology, 2007, 395, 403-423.	0.9	8
58	A BAYESIAN INTEGRATION MODEL OF HIGH-THROUGHPUT PROTEOMICS AND METABOLOMICS DATA FOR IMPROVED EARLY DETECTION OF MICROBIAL INFECTIONS. , 2008, , .		6
59	Fusion of laboratory and textual data for investigative bioforensics. Forensic Science International, 2013, 226, 118-124.	2.2	6
60	Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. Frontiers in Bioinformatics, 2022, 1, .	2.1	6
61	The Relative Inefficiency of Sequence Weights Approaches in Determining a Nucleotide Position Weight Matrix. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article13.	0.6	5
62	PSpecteR: A User-Friendly and Interactive Application for Visualizing Top-Down and Bottom-Up Proteomics Data in R. Journal of Proteome Research, 2021, 20, 2014-2020.	3.7	4
63	Fourier transform ion cyclotron resonance mass spectrometry (FTâ€ICRâ€MS) peak intensity normalization for complex mixture analyses. Rapid Communications in Mass Spectrometry, 2021, 35, e9068.	1.5	4
64	Soluble Expression and Complex Formation of Proteins Required for HCMV DNA Replication Using the SFV Expression System. Protein Expression and Purification, 1998, 13, 301-312.	1.3	3
65	Software to perform automated comparisons of pair-wise percent identities for microbial species. BioTechniques, 2006, 40, 578-582.	1.8	0
66	Let the Data Do the Talking: Hypothesis Discovery from Large-Scale Data Sets in Real Time. , 0, , 235-257.		0
67	Identification of metabolite and protein explanatory variables governing microbiome establishment and re-establishment within a cellulose-degrading anaerobic bioreactor. PLoS ONE, 2018, 13, e0204831.	2.5	0
68	Analytics challenge---High-throughput visual analytics biological sciences. , 2006, , .		0
69	Using the Gibbs Motif Sampler for Phylogenetic Footprinting. , 0, , 403-424.		0