

William W Metcalf

List of Publications by Year in descending order

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101
papers

7,249
citations

66343

42
h-index

64796

79
g-index

109
all docs

109
docs citations

109
times ranked

7179
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of internal loop dynamics in antibiotic permeability of outer membrane porins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	18
2	Investigating Abiotic and Biotic Mechanisms of Pyrite Reduction. Frontiers in Microbiology, 2022, 13, .	3.5	10
3	An Unusual Oxidative Rearrangement Catalyzed by a Divergent Member of the 2-oxoglutarate-Dependent Dioxygenase Superfamily during Biosynthesis of Dehydrofosmidomycin. Angewandte Chemie - International Edition, 2022, 61, .	13.8	6
4	A community resource for paired genomic and metabolomic data mining. Nature Chemical Biology, 2021, 17, 363-368.	8.0	81
5	A Phosphonate Natural Product Made by <i>Pantoea ananatis</i> is Necessary and Sufficient for the Hallmark Lesions of Onion Center Rot. MBio, 2021, 12, .	4.1	22
6	Rationalizing the generation of broad spectrum antibiotics with the addition of a positive charge. Chemical Science, 2021, 12, 15028-15044.	7.4	16
7	A computational framework to explore large-scale biosynthetic diversity. Nature Chemical Biology, 2020, 16, 60-68.	8.0	569
8	Genome Mining and Metabolomics Uncover a Rare d-Capreomycinide Containing Natural Product and Its Biosynthetic Gene Cluster. ACS Chemical Biology, 2020, 15, 3013-3020.	3.4	9
9	Functional interactions between posttranslationally modified amino acids of methyl-coenzyme M reductase in <i>Methanosarcina acetivorans</i> . PLoS Biology, 2020, 18, e3000507.	5.6	29
10	Title is missing!. , 2020, 18, e3000507.		0
11	Title is missing!. , 2020, 18, e3000507.		0
12	Title is missing!. , 2020, 18, e3000507.		0
13	Title is missing!. , 2020, 18, e3000507.		0
14	Title is missing!. , 2020, 18, e3000507.		0
15	Title is missing!. , 2020, 18, e3000507.		0
16	The streptothricin acetyltransferase (<i>sat</i>) gene as a positive selectable marker for methanogenic archaea. FEMS Microbiology Letters, 2019, 366, .	1.8	6
17	Energy Conservation and Hydrogenase Function in Methanogenic Archaea, in Particular the Genus <i>Methanosarcina</i> . Microbiology and Molecular Biology Reviews, 2019, 83, .	6.6	52
18	Fosmidomycin biosynthesis diverges from related phosphonate natural products. Nature Chemical Biology, 2019, 15, 1049-1056.	8.0	23

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19	GDGT cyclization proteins identify the dominant archaeal sources of tetraether lipids in the ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22505-22511.	7.1	66
20	Methylamine-specific methyltransferase paralogs in <i>Methanosarcina</i> are functionally distinct despite frequent gene conversion. <i>ISME Journal</i> , 2019, 13, 2173-2182.	9.8	6
21	Molecular Basis of <i>Bacillus subtilis</i> ATCC 6633 Self-Resistance to the Phosphono-oligopeptide Antibiotic Rhizocitin. <i>ACS Chemical Biology</i> , 2019, 14, 742-750.	3.4	9
22	Biochemical Characterization of the Methylmercaptopropionate:Cob(I)alamin Methyltransferase from <i>Methanosarcina acetivorans</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	5
23	Discovery of the Tyrobetaine Natural Products and Their Biosynthetic Gene Cluster <i>via</i> Metabologenomics. <i>ACS Chemical Biology</i> , 2018, 13, 1029-1037.	3.4	38
24	PcXL and HpxL are flavin-dependent, oxime-forming N-oxidases in phosphonocystoximic acid biosynthesis in <i>Streptomyces</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 6859-6868.	3.4	9
25	Genetic techniques for studies of methyl-coenzyme M reductase from <i>Methanosarcina acetivorans</i> C2A. <i>Methods in Enzymology</i> , 2018, 613, 325-347.	1.0	8
26	Genetic, Biochemical, and Molecular Characterization of <i>Methanosarcina barkeri</i> Mutants Lacking Three Distinct Classes of Hydrogenase. <i>Journal of Bacteriology</i> , 2018, 200, .	2.2	34
27	Energy Conservation via Hydrogen Cycling in the Methanogenic Archaeon <i>Methanosarcina barkeri</i> . <i>MBio</i> , 2018, 9, .	4.1	209
28	Cas9-mediated genome editing in the methanogenic archaeon <i>Methanosarcina acetivorans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2976-2981.	7.1	107
29	Classic Spotlight: Selected Highlights from the First 100 Years of the <i>Journal of Bacteriology</i> . <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	0
30	Phylogenetic relationships in the family Streptomycetaceae using multi-locus sequence analysis. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 563-583.	1.7	138
31	Draft Genome Sequence of <i>Methanobrevibacter smithii</i> Isolate WWM1085, Obtained from a Human Stool Sample. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
32	Post-translational thioamidation of methyl-coenzyme M reductase, a key enzyme in methanogenic and methanotrophic Archaea. <i>ELife</i> , 2017, 6, .	6.0	82
33	Genome-wide gene expression and RNA half-life measurements allow predictions of regulation and metabolic behavior in <i>Methanosarcina acetivorans</i> . <i>BMC Genomics</i> , 2016, 17, 924.	2.8	22
34	Classic Spotlight: Electron Bifurcation, a Unifying Concept for Energy Conservation in Anaerobes. <i>Journal of Bacteriology</i> , 2016, 198, 1358-1358.	2.2	7
35	Classic Spotlight: Metabolic Flux "Which Way To Go?". <i>Journal of Bacteriology</i> , 2016, 198, 3248-3249.	2.2	0
36	Quinovosamycins: new tunicamycin-type antibiotics in which the 1,1'-linked N-acetylglucosamine residue is replaced by N-acetylquinovosamine. <i>Journal of Antibiotics</i> , 2016, 69, 637-646.	2.0	11

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37	Classic Spotlight: What's on (in) Your Plate Today?. Journal of Bacteriology, 2016, 198, 2897-2898.	2.2	0
38	Elucidating the Rimosamide-Detoxin Natural Product Families and Their Biosynthesis Using Metabolite/Gene Cluster Correlations. ACS Chemical Biology, 2016, 11, 3452-3460.	3.4	42
39	Metabologenomics: Correlation of Microbial Gene Clusters with Metabolites Drives Discovery of a Nonribosomal Peptide with an Unusual Amino Acid Monomer. ACS Central Science, 2016, 2, 99-108.	11.3	99
40	Conserved biosynthetic pathways for phosalacine, bialaphos and newly discovered phosphonic acid natural products. Journal of Antibiotics, 2016, 69, 15-25.	2.0	20
41	Taxonomic evaluation of species in the <i>Streptomyces hirsutus</i> clade using multi-locus sequence analysis and proposals to reclassify several species in this clade. International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 2444-2450.	1.7	15
42	Metagenomic evidence for reciprocal particle exchange between the mainstem estuary and lateral bay sediments of the lower Columbia River. Frontiers in Microbiology, 2015, 6, 1074.	3.5	11
43	Genetic Basis for Metabolism of Methylated Sulfur Compounds in <i>Methanosarcina</i> Species. Journal of Bacteriology, 2015, 197, 1515-1524.	2.2	36
44	Genomic and phenotypic differentiation among <i>Methanosarcina mazei</i> populations from Columbia River sediment. ISME Journal, 2015, 9, 2191-2205.	9.8	42
45	Genetic, Genomic, and Transcriptomic Studies of Pyruvate Metabolism in <i>Methanosarcina barkeri</i> Fusaro. Journal of Bacteriology, 2015, 197, 3592-3600.	2.2	11
46	Discovery of phosphonic acid natural products by mining the genomes of 10,000 actinomycetes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12175-12180.	7.1	168
47	Towards a Computational Model of a Methane Producing Archaeum. Archaea, 2014, 2014, 1-18.	2.3	16
48	Use of a Phosphonate Methyltransferase in the Identification of the Fosfazinomycin Biosynthetic Gene Cluster. Angewandte Chemie - International Edition, 2014, 53, 1334-1337.	13.8	40
49	Purification and Characterization of Phosphonoglycans from <i>Glycomyces</i> sp. Strain NRRL B-16210 and <i>Stackebrandtia nassauensis</i> NRRL B-16338. Journal of Bacteriology, 2014, 196, 1768-1779.	2.2	27
50	Genomics-enabled discovery of phosphonate natural products and their biosynthetic pathways. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 345-356.	3.0	53
51	ITEP: An integrated toolkit for exploration of microbial pan-genomes. BMC Genomics, 2014, 15, 8.	2.8	123
52	A roadmap for natural product discovery based on large-scale genomics and metabolomics. Nature Chemical Biology, 2014, 10, 963-968.	8.0	416
53	Cyanohydrin Phosphonate Natural Product from <i>Streptomyces regensis</i> . Journal of Natural Products, 2014, 77, 243-249.	3.0	24
54	A Multienzyme Complex Channels Substrates and Electrons through Acetyl-CoA and Methane Biosynthesis Pathways in <i>Methanosarcina</i> . PLoS ONE, 2014, 9, e107563.	2.5	22

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55	Comparative genomics of actinomycetes with a focus on natural product biosynthetic genes. <i>BMC Genomics</i> , 2013, 14, 611.	2.8	175
56	Discovery of the Antibiotic Phosacetamycin via a New Mass Spectrometry-Based Method for Phosphonic Acid Detection. <i>ACS Chemical Biology</i> , 2013, 8, 908-913.	3.4	30
57	Diversity and abundance of phosphonate biosynthetic genes in nature. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20759-20764.	7.1	148
58	Different Biosynthetic Pathways to Fosfomycin in <i>Pseudomonas syringae</i> and <i>Streptomyces</i> Species. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 4175-4183.	3.2	60
59	Genome-Scale Metabolic Reconstruction and Hypothesis Testing in the Methanogenic Archaeon <i>Methanosarcina acetivorans</i> C2A. <i>Journal of Bacteriology</i> , 2012, 194, 855-865.	2.2	79
60	Synthesis of Methylphosphonic Acid by Marine Microbes: A Source for Methane in the Aerobic Ocean. <i>Science</i> , 2012, 337, 1104-1107.	12.6	263
61	Genetic manipulation of <i>Methanosarcina</i> spp.. <i>Frontiers in Microbiology</i> , 2012, 3, 259.	3.5	45
62	Directed Evolution of the Nonribosomal Peptide Synthetase AdmK Generates New Andrimid Derivatives <i>In Vivo</i> . <i>Chemistry and Biology</i> , 2011, 18, 601-607.	6.0	119
63	The Antibiotic Dehydrophos Is Converted to a Toxic Pyruvate Analog by Peptide Bond Cleavage in <i>Salmonella enterica</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 3357-3362.	3.2	32
64	Genetic and Biochemical Characterization of a Pathway for the Degradation of 2-Aminoethylphosphonate in <i>Sinorhizobium meliloti</i> 1021. <i>Journal of Biological Chemistry</i> , 2011, 286, 22283-22290.	3.4	40
65	Genome Sequences of Three Tunicamycin-Producing <i>Streptomyces</i> Strains, <i>S. chartreusis</i> NRRL 12338, <i>S. chartreusis</i> NRRL 3882, and <i>S. lysosuperificus</i> ATCC 31396. <i>Journal of Bacteriology</i> , 2011, 193, 7021-7022.	2.2	24
66	Biosynthesis of Rhizocticins, Antifungal Phosphonate Oligopeptides Produced by <i>Bacillus subtilis</i> ATCC6633. <i>Chemistry and Biology</i> , 2010, 17, 28-37.	6.0	95
67	Deciphering the Late Biosynthetic Steps of Antimalarial Compound FR-900098. <i>Chemistry and Biology</i> , 2010, 17, 57-64.	6.0	35
68	Molecular Cloning and Heterologous Expression of the Dehydrophos Biosynthetic Gene Cluster. <i>Chemistry and Biology</i> , 2010, 17, 402-411.	6.0	42
69	Methanogenesis by <i>Methanosarcina acetivorans</i> involves two structurally and functionally distinct classes of heterodisulfide reductase. <i>Molecular Microbiology</i> , 2010, 75, 843-853.	2.5	97
70	Characterization and structure of Dhpl, a phosphonate <i>O</i> -methyltransferase involved in dehydrophos biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17557-17562.	7.1	41
71	Differences in Hydrogenase Gene Expression between <i>Methanosarcina acetivorans</i> and <i>Methanosarcina barkeri</i> . <i>Journal of Bacteriology</i> , 2009, 191, 2826-2833.	2.2	60
72	Hydrogen is a preferred intermediate in the energy-conserving electron transport chain of <i>Methanosarcina barkeri</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15915-15920.	7.1	78

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73	Physiology and Posttranscriptional Regulation of Methanol:Coenzyme M Methyltransferase Isozymes in <i>Methanosarcina acetivorans</i> C2A. <i>Journal of Bacteriology</i> , 2009, 191, 6928-6935.	2.2	19
74	Regulation of putative methylsulphide methyltransferases in <i>Methanosarcina acetivorans</i> C2A. <i>Molecular Microbiology</i> , 2009, 74, 227-238.	2.5	20
75	An unusual carbon-carbon bond cleavage reaction during phosphinothricin biosynthesis. <i>Nature</i> , 2009, 459, 871-874.	27.8	111
76	Biosynthesis of Phosphonic and Phosphinic Acid Natural Products. <i>Annual Review of Biochemistry</i> , 2009, 78, 65-94.	11.1	303
77	Cloning, Expression, and Biochemical Characterization of <i>Streptomyces rubellomurinus</i> Genes Required for Biosynthesis of Antimalarial Compound FR900098. <i>Chemistry and Biology</i> , 2008, 15, 765-770.	6.0	88
78	Distinct regulators control the expression of methanol methyltransferase isozymes in <i>Methanosarcina acetivorans</i> C2A. <i>Molecular Microbiology</i> , 2008, 67, 649-661.	2.5	37
79	Genetic Analysis of the Methanol- and Methylamine-Specific Methyltransferase 2 Genes of <i>Methanosarcina acetivorans</i> C2A. <i>Journal of Bacteriology</i> , 2008, 190, 4017-4026.	2.2	39
80	Biosynthesis of 2-Hydroxyethylphosphonate, an Unexpected Intermediate Common to Multiple Phosphonate Biosynthetic Pathways. <i>Journal of Biological Chemistry</i> , 2008, 283, 23161-23168.	3.4	45
81	New methods for tightly regulated gene expression and highly efficient chromosomal integration of cloned genes for <i>Methanosarcina</i> species. <i>Archaea</i> , 2008, 2, 193-203.	2.3	109
82	Microbial Metabolism of Reduced Phosphorus Compounds. <i>Annual Review of Microbiology</i> , 2007, 61, 379-400.	7.3	246
83	Reassignment of the Structure of the Antibiotic A53868 Reveals an Unusual Amino Dehydrophosphonic Acid. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 9089-9092.	13.8	38
84	Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. <i>Nature Chemical Biology</i> , 2007, 3, 480-485.	8.0	126
85	Genetic and proteomic analyses of CO utilization by <i>Methanosarcina acetivorans</i> . <i>Archives of Microbiology</i> , 2007, 188, 463-472.	2.2	43
86	The <i>Methanosarcina barkeri</i> Genome: Comparative Analysis with <i>Methanosarcina acetivorans</i> and <i>Methanosarcina mazei</i> Reveals Extensive Rearrangement within Methanosarcinal Genomes. <i>Journal of Bacteriology</i> , 2006, 188, 7922-7931.	2.2	158
87	Heterologous Production of Fosfomycin and Identification of the Minimal Biosynthetic Gene Cluster. <i>Chemistry and Biology</i> , 2006, 13, 1171-1182.	6.0	116
88	Differential Regulation of the Three Methanol Methyltransferase Isozymes in <i>Methanosarcina acetivorans</i> C2A. <i>Journal of Bacteriology</i> , 2006, 188, 7274-7283.	2.2	29
89	Genetic analysis of <i>mch</i> mutants in two <i>Methanosarcina</i> species demonstrates multiple roles for the methanopterin-dependent C-1 oxidation/reduction pathway and differences in H ₂ metabolism between closely related species. <i>Molecular Microbiology</i> , 2005, 55, 1671-1680.	2.5	59
90	Genetic, physiological and biochemical characterization of multiple methanol methyltransferase isozymes in <i>Methanosarcina acetivorans</i> C2A. <i>Molecular Microbiology</i> , 2005, 56, 1183-1194.	2.5	44

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91	Assignment of the [4Fe-4S] clusters of Ech hydrogenase from <i>Methanosarcina barkeri</i> to individual subunits via the characterization of site-directed mutants. <i>FEBS Journal</i> , 2005, 272, 4741-4753.	4.7	33
92	Molecular Cloning, Sequence Analysis, and Heterologous Expression of the Phosphinothricin Tripeptide Biosynthetic Gene Cluster from <i>Streptomyces viridochromogenes</i> DSM 40736. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 230-240.	3.2	81
93	Development of a Markerless Genetic Exchange Method for <i>Methanosarcina acetivorans</i> C2A and Its Use in Construction of New Genetic Tools for Methanogenic Archaea. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1425-1433.	3.1	125
94	Directed Mutagenesis and Plasmid-Based Complementation in the Methanogenic Archaeon <i>Methanosarcina acetivorans</i> C2A Demonstrated by Genetic Analysis of Proline Biosynthesis. <i>Journal of Bacteriology</i> , 2002, 184, 1449-1454.	2.2	43
95	Genetic analysis of the archaeon <i>Methanosarcina barkeri</i> Fusaro reveals a central role for Ech hydrogenase and ferredoxin in methanogenesis and carbon fixation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 5632-5637.	7.1	160
96	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	5.5	573
97	Generation of Dominant Selectable Markers for Resistance to Pseudomonic Acid by Cloning and Mutagenesis of the <i>theilS</i> Gene from the Archaeon <i>Methanosarcina barkeri</i> Fusaro. <i>Journal of Bacteriology</i> , 2000, 182, 2611-2618.	2.2	73
98	Molecular Genetic Analysis of Phosphite and Hypophosphite Oxidation by <i>Pseudomonas stutzeri</i> WM88. <i>Journal of Bacteriology</i> , 1998, 180, 5547-5558.	2.2	136
99	An Anaerobic, Intrachamber Incubator for Growth of <i>Methanosarcina</i> spp. on Methanol-Containing Solid Media. <i>Applied and Environmental Microbiology</i> , 1998, 64, 768-770.	3.1	52
100	Molecular genetic studies of a 10.9-kb operon in <i>Escherichia coli</i> for phosphonate uptake and biodegradation. <i>FEMS Microbiology Letters</i> , 1992, 100, 133-139.	1.8	62
101	An Unusual Oxidative Rearrangement Catalyzed by a Divergent Member of the 2-oxoglutarate-Dependent Dioxygenase Superfamily during Biosynthesis of Dehydrofosmidomycin. <i>Angewandte Chemie</i> , 0, , .	2.0	0