

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	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	5.5	573
2	A computational framework to explore large-scale biosynthetic diversity. <i>Nature Chemical Biology</i> , 2020, 16, 60-68.	8.0	569
3	A roadmap for natural product discovery based on large-scale genomics and metabolomics. <i>Nature Chemical Biology</i> , 2014, 10, 963-968.	8.0	416
4	Biosynthesis of Phosphonic and Phosphinic Acid Natural Products. <i>Annual Review of Biochemistry</i> , 2009, 78, 65-94.	11.1	303
5	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
6	Microbial Metabolism of Reduced Phosphorus Compounds. <i>Annual Review of Microbiology</i> , 2007, 61, 379-400.	7.3	246
7	Energy Conservation via Hydrogen Cycling in the Methanogenic Archaeon <i>Methanosarcina barkeri</i> . <i>MBio</i> , 2018, 9, .	4.1	209
8	Comparative genomics of actinomycetes with a focus on natural product biosynthetic genes. <i>BMC Genomics</i> , 2013, 14, 611.	2.8	175
9	Discovery of phosphonic acid natural products by mining the genomes of 10,000 actinomycetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12175-12180.	7.1	168
10	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
11	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
12	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
13	Phylogenetic relationships in the family Streptomycetaceae using multi-locus sequence analysis. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 563-583.	1.7	138
14	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
15	Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. <i>Nature Chemical Biology</i> , 2007, 3, 480-485.	8.0	126
16	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
17	IITEP: An integrated toolkit for exploration of microbial pan-genomes. <i>BMC Genomics</i> , 2014, 15, 8.	2.8	123
18	Directed Evolution of the Nonribosomal Peptide Synthetase AdmK Generates New Andrimid Derivatives In Vivo. <i>Chemistry and Biology</i> , 2011, 18, 601-607.	6.0	119

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19	Heterologous Production of Fosfomycin and Identification of the Minimal Biosynthetic Gene Cluster. <i>Chemistry and Biology</i> , 2006, 13, 1171-1182.	6.0	116
20	An unusual carbon-carbon bond cleavage reaction during phosphinothricin biosynthesis. <i>Nature</i> , 2009, 459, 871-874.	27.8	111
21	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
22	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
23	Metabologenomics: Correlation of Microbial Gene Clusters with Metabolites Drives Discovery of a Nonribosomal Peptide with an Unusual Amino Acid Monomer. <i>ACS Central Science</i> , 2016, 2, 99-108.	11.3	99
24	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
25	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
26	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
27	Post-translational thioamidation of methyl-coenzyme M reductase, a key enzyme in methanogenic and methanotrophic Archaea. <i>ELife</i> , 2017, 6, .	6.0	82
28	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
29	A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021, 17, 363-368.	8.0	81
30	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
31	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
32	Generation of Dominant Selectable Markers for Resistance to Pseudomonic Acid by Cloning and Mutagenesis of the <i>theiS</i> Gene from the Archaeon <i>Methanosarcina barkeri</i> Fusaro. <i>Journal of Bacteriology</i> , 2000, 182, 2611-2618.	2.2	73
33	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
34	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
35	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
36	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

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37	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
38	Genomics-enabled discovery of phosphonate natural products and their biosynthetic pathways. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 345-356.	3.0	53
39	Energy Conservation and Hydrogenase Function in Methanogenic Archaea, in Particular the Genus <i>Methanosarcina</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2019, 83, .	6.6	52
40	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
41	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
42	Genetic manipulation of <i>Methanosarcina</i> spp.. <i>Frontiers in Microbiology</i> , 2012, 3, 259.	3.5	45
43	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
44	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
45	Genetic and proteomic analyses of CO utilization by <i>Methanosarcina acetivorans</i> . <i>Archives of Microbiology</i> , 2007, 188, 463-472.	2.2	43
46	Molecular Cloning and Heterologous Expression of the Dehydrophos Biosynthetic Gene Cluster. <i>Chemistry and Biology</i> , 2010, 17, 402-411.	6.0	42
47	Genomic and phenotypic differentiation among <i>Methanosarcina mazei</i> populations from Columbia River sediment. <i>ISME Journal</i> , 2015, 9, 2191-2205.	9.8	42
48	Elucidating the Rimosamide-Detoxin Natural Product Families and Their Biosynthesis Using Metabolite/Gene Cluster Correlations. <i>ACS Chemical Biology</i> , 2016, 11, 3452-3460.	3.4	42
49	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
50	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
51	Use of a Phosphonate Methyltransferase in the Identification of the Fosfazinomycin Biosynthetic Gene Cluster. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 1334-1337.	13.8	40
52	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
53	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
54	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

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55	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
56	Genetic Basis for Metabolism of Methylated Sulfur Compounds in <i>Methanosarcina</i> Species. <i>Journal of Bacteriology</i> , 2015, 197, 1515-1524.	2.2	36
57	Deciphering the Late Biosynthetic Steps of Antimalarial Compound FR-900098. <i>Chemistry and Biology</i> , 2010, 17, 57-64.	6.0	35
58	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
59	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
60	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
61	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
62	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
63	Functional interactions between posttranslationally modified amino acids of methyl-coenzyme M reductase in <i>Methanosarcina acetivorans</i> . <i>PLoS Biology</i> , 2020, 18, e3000507.	5.6	29
64	Purification and Characterization of Phosphonoglycans from <i>Glycomyces</i> sp. Strain NRRL B-16210 and <i>Stackebrandtia nassauensis</i> NRRL B-16338. <i>Journal of Bacteriology</i> , 2014, 196, 1768-1779.	2.2	27
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	Cyanohydrin Phosphonate Natural Product from <i>Streptomyces regensis</i> . <i>Journal of Natural Products</i> , 2014, 77, 243-249.	3.0	24
67	Fosmidomycin biosynthesis diverges from related phosphonate natural products. <i>Nature Chemical Biology</i> , 2019, 15, 1049-1056.	8.0	23
68	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
69	A Phosphonate Natural Product Made by <i>Pantoea ananatis</i> is Necessary and Sufficient for the Hallmark Lesions of Onion Center Rot. <i>MBio</i> , 2021, 12, .	4.1	22
70	A Multienzyme Complex Channels Substrates and Electrons through Acetyl-CoA and Methane Biosynthesis Pathways in <i>Methanosarcina</i> . <i>PLoS ONE</i> , 2014, 9, e107563.	2.5	22
71	Regulation of putative methylsulphide methyltransferases in <i>Methanosarcina acetivorans</i> C2A. <i>Molecular Microbiology</i> , 2009, 74, 227-238.	2.5	20
72	Conserved biosynthetic pathways for phosalacine, bialaphos and newly discovered phosphonic acid natural products. <i>Journal of Antibiotics</i> , 2016, 69, 15-25.	2.0	20

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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	Role of internal loop dynamics in antibiotic permeability of outer membrane porins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	18
75	Towards a Computational Model of a Methane Producing Archaeum. <i>Archaea</i> , 2014, 2014, 1-18.	2.3	16
76	Rationalizing the generation of broad spectrum antibiotics with the addition of a positive charge. <i>Chemical Science</i> , 2021, 12, 15028-15044.	7.4	16
77	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. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2444-2450.	1.7	15
78	Metagenomic evidence for reciprocal particle exchange between the mainstem estuary and lateral bay sediments of the lower Columbia River. <i>Frontiers in Microbiology</i> , 2015, 6, 1074.	3.5	11
79	Genetic, Genomic, and Transcriptomic Studies of Pyruvate Metabolism in <i>Methanosarcina barkeri</i> Fusaro. <i>Journal of Bacteriology</i> , 2015, 197, 3592-3600.	2.2	11
80	Quinovosamycins: new tunicamycin-type antibiotics in which the β -1,6-linked N-acetylglucosamine residue is replaced by N-acetylquinovosamine. <i>Journal of Antibiotics</i> , 2016, 69, 637-646.	2.0	11
81	Investigating Abiotic and Biotic Mechanisms of Pyrite Reduction. <i>Frontiers in Microbiology</i> , 2022, 13, .	3.5	10
82	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
83	Molecular Basis of <i>Bacillus subtilis</i> ATCC 6633 Self-Resistance to the Phosphono-oligopeptide Antibiotic Rhizocticin. <i>ACS Chemical Biology</i> , 2019, 14, 742-750.	3.4	9
84	Genome Mining and Metabolomics Uncover a Rare d-Capreomycinidene Containing Natural Product and Its Biosynthetic Gene Cluster. <i>ACS Chemical Biology</i> , 2020, 15, 3013-3020.	3.4	9
85	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
86	Classic Spotlight: Electron Bifurcation, a Unifying Concept for Energy Conservation in Anaerobes. <i>Journal of Bacteriology</i> , 2016, 198, 1358-1358.	2.2	7
87	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
88	The streptothricin acetyltransferase (<i>sat</i>) gene as a positive selectable marker for methanogenic archaea. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	6
89	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
90	An Unusual Oxidative Rearrangement Catalyzed by a Divergent Member of the 2-oxoglutarate-Dependent Dioxygenase Superfamily during Biosynthesis of Dehydrofosmidomycin. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	13.8	6

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91	Biochemical Characterization of the Methylmercaptopropionate:Cob(I)alamin Methyltransferase from <i>Methanosarcina acetivorans</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	5
92	Classic Spotlight: Metabolic Fluxâ€”Which Way To Go?. <i>Journal of Bacteriology</i> , 2016, 198, 3248-3249.	2.2	0
93	Classic Spotlight: What's on (in) Your Plate Today?. <i>Journal of Bacteriology</i> , 2016, 198, 2897-2898.	2.2	0
94	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
95	Title is missing!. , 2020, 18, e3000507.		0
96	Title is missing!. , 2020, 18, e3000507.		0
97	Title is missing!. , 2020, 18, e3000507.		0
98	Title is missing!. , 2020, 18, e3000507.		0
99	Title is missing!. , 2020, 18, e3000507.		0
100	Title is missing!. , 2020, 18, e3000507.		0
101	An Unusual Oxidative Rearrangement Catalyzed by a Divergent Member of the 2â€”Oxoglutarateâ€”Dependent Dioxygenase Superfamily during Biosynthesis of Dehydrofosmidomycin. <i>Angewandte Chemie</i> , 0, , .	2.0	0