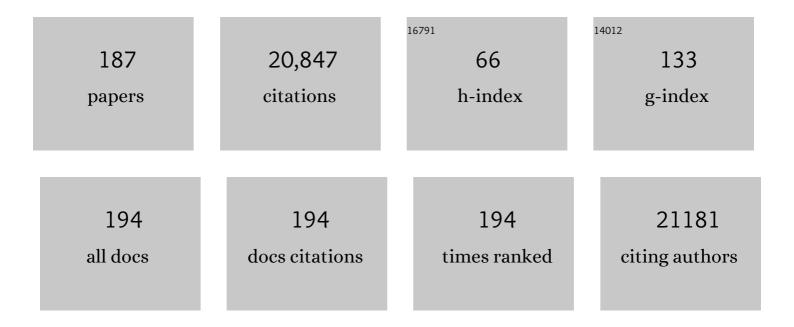
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Salt- and osmo-responsive sensor histidine kinases activate the <i>Bradyrhizobium diazoefficiens</i> general stress response to initiate functional symbiosis. Molecular Plant-Microbe Interactions, 2022, ,	1.4	1
2	Injection into and extraction from single fungal cells. Communications Biology, 2022, 5, 180.	2.0	11
3	Mitochondria transplantation between living cells. PLoS Biology, 2022, 20, e3001576.	2.6	28
4	Mapping phyllosphere microbiota interactions in planta to establish genotype–phenotype relationships. Nature Microbiology, 2022, 7, 856-867.	5.9	30
5	Dynamic character displacement among a pair of bacterial phyllosphere commensals in situ. Nature Communications, 2022, 13, .	5.8	15
6	Reciprocal growth control by competitive binding of nucleotide second messengers to a metabolic switch in Caulobacter crescentus. Nature Microbiology, 2021, 6, 59-72.	5.9	23
7	Mass spectrometry-based approaches to study lanthanides and lanthanide-dependent proteins in the phyllosphere. Methods in Enzymology, 2021, 650, 215-236.	0.4	7
8	Structural diversity of the coenzyme methylofuran and identification of enzymes for the biosynthesis of its polyglutamate side chain. Journal of Biological Chemistry, 2021, 296, 100682.	1.6	0
9	Bradyrhizobium diazoefficiens Requires Chemical Chaperones To Cope with Osmotic Stress during Soybean Infection. MBio, 2021, 12, .	1.8	8
10	A general non-self response as part of plant immunity. Nature Plants, 2021, 7, 696-705.	4.7	50
11	The plant NADPH oxidase RBOHD is required for microbiota homeostasis in leaves. Nature Microbiology, 2021, 6, 852-864.	5.9	70
12	Capacity of soil bacteria to reach the phyllosphere and convergence of floral communities despite soil microbiota variation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	38
13	Protective role of the Arabidopsis leaf microbiota against a bacterial pathogen. Nature Microbiology, 2021, 6, 1537-1548.	5.9	68
14	Consistent host and organ occupancy of phyllosphere bacteria in a community of wild herbaceous plant species. ISME Journal, 2020, 14, 245-258.	4.4	75
15	Microbiome manipulation by a soil-borne fungal plant pathogen using effector proteins. Nature Plants, 2020, 6, 1365-1374.	4.7	118
16	Methanol-dependent Escherichia coli strains with a complete ribulose monophosphate cycle. Nature Communications, 2020, 11, 5403.	5.8	31
17	Import of Aspartate and Malate by DcuABC Drives H2/Fumarate Respiration to Promote Initial Salmonella Gut-Lumen Colonization in Mice. Cell Host and Microbe, 2020, 27, 922-936.e6.	5.1	58
18	Molecular Basis of Growth Inhibition by Acetate of an Adenylate Cyclase-Deficient Mutant of Corynebacterium glutamicum. Frontiers in Microbiology, 2020, 11, 87.	1.5	11

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19	ScalaFlux: AÂscalable approach to quantify fluxes in metabolic subnetworks. PLoS Computational Biology, 2020, 16, e1007799.	1.5	12
20	Untargeted metabolomics links glutathione to bacterial cell cycle progression. Nature Metabolism, 2020, 2, 153-166.	5.1	34
21	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
22	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
23	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
24	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
25	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
26	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. , 2020, 16, e1007799.		0
27	Fluidic Force Microscopy Captures Amyloid Bonds between Microbial Cells. Trends in Microbiology, 2019, 27, 728-730.	3.5	15
28	Complex general stress response regulation in Sphingomonas melonis Fr1 revealed by transcriptional analyses. Scientific Reports, 2019, 9, 9404.	1.6	13
29	Synthetic microbiota reveal priority effects and keystone strains in the Arabidopsis phyllosphere. Nature Ecology and Evolution, 2019, 3, 1445-1454.	3.4	234
30	Use of rareâ€earth elements in the phyllosphere colonizer <i>Methylobacterium extorquens</i> PA1. Molecular Microbiology, 2019, 111, 1152-1166.	1.2	88
31	Fluidic Force Microscopy Demonstrates That Homophilic Adhesion by <i>Candida albicans</i> Als Proteins Is Mediated by Amyloid Bonds between Cells. Nano Letters, 2019, 19, 3846-3853.	4.5	38
32	A modular atomic force microscopy approach reveals a large range of hydrophobic adhesion forces among bacterial members of the leaf microbiota. ISME Journal, 2019, 13, 1878-1882.	4.4	32
33	Methylofuran is a prosthetic group of the formyltransferase/hydrolase complex and shuttles one-carbon units between two active sites. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25583-25590.	3.3	9
34	Escherichia coli in Auto(trophic) Mode. Cell, 2019, 179, 1244-1245.	13.5	1
35	Methanol-essential growth of Escherichia coli. Nature Communications, 2018, 9, 1508.	5.8	119

FluidFM Applications in Single-Cell Biology. , 2018, , 325-354.

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37	Genomic features of bacterial adaptation to plants. Nature Genetics, 2018, 50, 138-150.	9.4	480
38	Built to last – über die intrazellulÃæ StabilitÃævon Koenzymen. BioSpektrum, 2018, 24, 138-141.	0.0	0
39	Replacing the Ethylmalonyl-CoA Pathway with the Glyoxylate Shunt Provides Metabolic Flexibility in the Central Carbon Metabolism of <i>Methylobacterium extorquens</i> AM1. ACS Synthetic Biology, 2018, 7, 86-97.	1.9	31
40	Toblerols: Cyclopropanol ontaining Polyketide Modulators of Antibiosis in Methylobacteria. Angewandte Chemie - International Edition, 2018, 57, 977-981.	7.2	30
41	Toblerols: Cyclopropanol ontaining Polyketide Modulators of Antibiosis in Methylobacteria. Angewandte Chemie, 2018, 130, 989-993.	1.6	15
42	Genome Mining-guided and MALDI Imaging-assisted Discovery of New Antibiotics. Chimia, 2018, 72, 816-816.	0.3	2
43	Synthetic Methylotrophy: Past, Present, and Future. , 2018, , 133-151.		10
44	Bipartite interactions, antibiotic production and biosynthetic potential of the Arabidopsis leaf microbiome. Nature Microbiology, 2018, 3, 909-919.	5.9	135
45	Editorial overview: Environmental microbiology: Environmental and engineered microbiomes. Current Opinion in Microbiology, 2018, 43, v-vii.	2.3	Ο
46	Phosphorelay through the bifunctional phosphotransferase PhyT controls the general stress response in an alphaproteobacterium. PLoS Genetics, 2018, 14, e1007294.	1.5	16
47	Longevity of major coenzymes allows minimal de novo synthesis in microorganisms. Nature Microbiology, 2017, 2, 17073.	5.9	34
48	Cohesive Properties of the <i>Caulobacter crescentus</i> Holdfast Adhesin Are Regulated by a Novel c-di-GMP Effector Protein. MBio, 2017, 8, .	1.8	29
49	Single-Cell Mass Spectrometry of Metabolites Extracted from Live Cells by Fluidic Force Microscopy. Analytical Chemistry, 2017, 89, 5017-5023.	3.2	90
50	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	9.0	635
51	Transposon Sequencing Uncovers an Essential Regulatory Function of Phosphoribulokinase for Methylotrophy. Current Biology, 2017, 27, 2579-2588.e6.	1.8	34
52	Establishing Causality: Opportunities of Synthetic Communities for Plant Microbiome Research. Cell Host and Microbe, 2017, 22, 142-155.	5.1	404
53	The Arabidopsis leaf transcriptome reveals distinct but also overlapping responses to colonization by phyllosphere commensals and pathogen infection with impact on plant health. New Phytologist, 2016, 212, 192-207.	3.5	134
54	The One-carbon Carrier Methylofuran from Methylobacterium extorquens AM1 Contains a Large Number of α- and γ-Linked Glutamic Acid Residues. Journal of Biological Chemistry, 2016, 291, 9042-9051.	1.6	8

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55	Systems-level Proteomics of Two Ubiquitous Leaf Commensals Reveals Complementary Adaptive Traits for Phyllosphere Colonization. Molecular and Cellular Proteomics, 2016, 15, 3256-3269.	2.5	48
56	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. Nature Biotechnology, 2016, 34, 828-837.	9.4	2,802
57	The Plant Microbiota: Systems-Level Insights and Perspectives. Annual Review of Genetics, 2016, 50, 211-234.	3.2	627
58	Tunable Single-Cell Extraction for Molecular Analyses. Cell, 2016, 166, 506-516.	13.5	155
59	Role of the PFXFATG[G/Y] Motif in the Activation of SdrG, a Response Regulator Involved in the Alphaproteobacterial General Stress Response. Structure, 2016, 24, 1237-1247.	1.6	14
60	Metabolic footprint of epiphytic bacteria on <i>Arabidopsis thaliana</i> leaves. ISME Journal, 2016, 10, 632-643.	4.4	113
61	Multiple σEcfG and NepR Proteins Are Involved in the General Stress Response in Methylobacterium extorquens. PLoS ONE, 2016, 11, e0152519.	1.1	12
62	Screening and Engineering the Synthetic Potential of Carboxylating Reductases from Central Metabolism and Polyketide Biosynthesis. Angewandte Chemie - International Edition, 2015, 54, 13457-13461.	7.2	48
63	Core pathways operating during methylotrophy of <scp><i>B</i></scp> <i>acillus methanolicus</i> â€ <scp>MGA</scp> 3 and induction of a bacillithiolâ€dependent detoxification pathway upon formaldehyde stress. Molecular Microbiology, 2015, 98, 1089-1100.	1.2	42
64	The branched <scp>CcsA</scp> / <scp>CckA</scp> â€ <scp>ChpT</scp> â€ <scp>CtrA</scp> phosphorelay of <scp><i>S</i></scp> <i>phingomonas melonis</i> controls motility and biofilm formation. Molecular Microbiology, 2015, 97, 47-63.	1.2	18
65	Stable Fluorescent and Enzymatic Tagging of <i>Bradyrhizobium diazoefficiens</i> to Analyze Host-Plant Infection and Colonization. Molecular Plant-Microbe Interactions, 2015, 28, 959-967.	1.4	38
66	Methylotrophy in the thermophilic Bacillus methanolicus, basic insights and application for commodity production from methanol. Applied Microbiology and Biotechnology, 2015, 99, 535-551.	1.7	63
67	Extra Cytoplasmic Function sigma factors, recent structural insights into promoter recognition and regulation. Current Opinion in Structural Biology, 2015, 30, 71-78.	2.6	52
68	Engineering Escherichia coli for methanol conversion. Metabolic Engineering, 2015, 28, 190-201.	3.6	166
69	High-level production of ethylmalonyl-CoA pathway-derived dicarboxylic acids by Methylobacterium extorquens under cobalt-deficient conditions and by polyhydroxybutyrate negative strains. Applied Microbiology and Biotechnology, 2015, 99, 3407-3419.	1.7	44
70	Bacterial adhesion force quantification by fluidic force microscopy. Nanoscale, 2015, 7, 4070-4079.	2.8	72
71	The general stress response in Alphaproteobacteria. Trends in Microbiology, 2015, 23, 164-171.	3.5	65
72	4-[2-O-11Z-Octadecenoyl-β-glucopyranosyl]-4,4′-diapolycopene-4,4′-dioic acid and 4-[2-O-9Z-hexadecenoyl-β-glucopyranosyl]-4,4′-diapolycopene-4,4′-dioic acid: new C30-carotenoids produced by Methylobacterium. Tetrahedron Letters, 2015, 56, 2791-2794.	0.7	10

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73	The use of ene adducts to study and engineer enoyl-thioester reductases. Nature Chemical Biology, 2015, 11, 398-400.	3.9	27
74	Two-Tiered Histidine Kinase Pathway Involved in Heat Shock and Salt Sensing in the General Stress Response of Sphingomonas melonis Fr1. Journal of Bacteriology, 2015, 197, 1466-1477.	1.0	30
75	Bacterial Networks in Cells and Communities. Journal of Molecular Biology, 2015, 427, 3785-3792.	2.0	9
76	DynaMet: A Fully Automated Pipeline for Dynamic LC–MS Data. Analytical Chemistry, 2015, 87, 9679-9686.	3.2	17
77	Functional overlap of the Arabidopsis leaf and root microbiota. Nature, 2015, 528, 364-369.	13.7	1,062
78	Fast sampling method for mammalian cell metabolic analyses using liquid chromatography–mass spectrometry. Nature Protocols, 2015, 10, 1-11.	5.5	51
79	Methylobacterium extorquens: methylotrophy and biotechnological applications. Applied Microbiology and Biotechnology, 2015, 99, 517-534.	1.7	116
80	A Set of Versatile Brick Vectors and Promoters for the Assembly, Expression, and Integration of Synthetic Operons in <i>Methylobacterium extorquens</i> AM1 and Other Alphaproteobacteria. ACS Synthetic Biology, 2015, 4, 430-443.	1.9	55
81	Direct evidence for a covalent ene adduct intermediate in NAD(P)H-dependent enzymes. Nature Chemical Biology, 2014, 10, 50-55.	3.9	65
82	A Synthetic Community Approach Reveals Plant Genotypes Affecting the Phyllosphere Microbiota. PLoS Genetics, 2014, 10, e1004283.	1.5	369
83	A Proteomic Approach of Bradyrhizobium/Aeschynomene Root and Stem Symbioses Reveals the Importance of the fixA Locus for Symbiosis. International Journal of Molecular Sciences, 2014, 15, 3660-3670.	1.8	34
84	Complex two-component signaling regulates the general stress response in Alphaproteobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5196-204.	3.3	47
85	A Link between Arabinose Utilization and Oxalotrophy in Bradyrhizobium japonicum. Applied and Environmental Microbiology, 2014, 80, 2094-2101.	1.4	28
86	Structural basis for â^'10 promoter element melting by environmentally induced sigma factors. Nature Structural and Molecular Biology, 2014, 21, 269-276.	3.6	82
87	Spatial distribution analyses of natural phyllosphereâ€colonizing bacteria on <scp><i>A</i></scp> <i>rabidopsis thaliana</i> revealed by fluorescence <i>in situ</i> hybridization. Environmental Microbiology, 2014, 16, 2329-2340.	1.8	125
88	Proteomic analysis of the thermophilic methylotroph <i><scp>B</scp>acillus methanolicus</i> <scp>MGA</scp> 3. Proteomics, 2014, 14, 725-737.	1.3	47
89	Isolation of single mammalian cells from adherent cultures by fluidic force microscopy. Lab on A Chip, 2014, 14, 402-414.	3.1	45
90	<i>Shigella</i> reroutes host cell central metabolism to obtain high-flux nutrient supply for vigorous intracellular growth. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 9929-9934.	3.3	71

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91	Toward a Rational Design of Surface Textures Promoting Endothelialization. Nano Letters, 2014, 14, 1069-1079.	4.5	61
92	<i>In vitro</i> activation of NADâ€dependent alcohol dehydrogenases by Nudix hydrolases is more widespread than assumed. FEBS Letters, 2014, 588, 2993-2999.	1.3	25
93	Force-controlled manipulation of single cells: from AFM to FluidFM. Trends in Biotechnology, 2014, 32, 381-388.	4.9	190
94	Synthetic vanillate-regulated promoter for graded gene expression in Sphingomonas. Scientific Reports, 2014, 4, 6453.	1.6	10
95	Microfluidics: Forceâ€Controlled Fluidic Injection into Single Cell Nuclei (Small 11/2013). Small, 2013, 9, 1870-1870.	5.2	1
96	Forceâ€Controlled Fluidic Injection into Single Cell Nuclei. Small, 2013, 9, 1904-1907.	5.2	70
97	Isolation of Optically Targeted Single Bacteria by Application of Fluidic Force Microscopy to Aerobic Anoxygenic Phototrophs from the Phyllosphere. Applied and Environmental Microbiology, 2013, 79, 4895-4905.	1.4	44
98	Single-domain response regulator involved in the general stress response of Methylobacterium extorquens. Microbiology (United Kingdom), 2013, 159, 1067-1076.	0.7	18
99	eMZed: an open source framework in Python for rapid and interactive development of LC/MS data analysis workflows. Bioinformatics, 2013, 29, 963-964.	1.8	45
100	Cumate-Inducible Gene Expression System for Sphingomonads and Other Alphaproteobacteria. Applied and Environmental Microbiology, 2013, 79, 6795-6802.	1.4	72
101	Mutation in the C-Di-AMP Cyclase dacA Affects Fitness and Resistance of Methicillin Resistant Staphylococcus aureus. PLoS ONE, 2013, 8, e73512.	1.1	74
102	Methylotrophic Bacillus methanolicus Encodes Two Chromosomal and One Plasmid Born NAD+ Dependent Methanol Dehydrogenase Paralogs with Different Catalytic and Biochemical Properties. PLoS ONE, 2013, 8, e59188.	1.1	73
103	Oxalyl-Coenzyme A Reduction to Glyoxylate Is the Preferred Route of Oxalate Assimilation in Methylobacterium extorquens AM1. Journal of Bacteriology, 2012, 194, 3144-3155.	1.0	41
104	Complete Genome Sequences of Six Strains of the Genus Methylobacterium. Journal of Bacteriology, 2012, 194, 4746-4748.	1.0	99
105	Microbial life in the phyllosphere. Nature Reviews Microbiology, 2012, 10, 828-840.	13.6	1,600
106	Markerless Gene Deletion System for Sphingomonads. Applied and Environmental Microbiology, 2012, 78, 3774-3777.	1.4	62
107	Forward Genetic <i>In Planta</i> Screen for Identification of Plant-Protective Traits of Sphingomonas sp. Strain Fr1 against Pseudomonas syringae DC3000. Applied and Environmental Microbiology, 2012, 78, 5529-5535.	1.4	54
108	Cooperative Vaccinia Infection Demonstrated at the Single-Cell Level Using FluidFM. Nano Letters, 2012, 12, 4219-4227.	4.5	57

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109	The Ethylmalonyl-CoA Pathway Is Used in Place of the Glyoxylate Cycle by Methylobacterium extorquens AM1 during Growth on Acetate. Journal of Biological Chemistry, 2012, 287, 757-766.	1.6	77
110	Complete genome sequence and metabolic potential of the quinaldine-degrading bacterium Arthrobacter sp. Rue61a. BMC Genomics, 2012, 13, 534.	1.2	72
111	The molecular basis of phosphate discrimination in arsenate-rich environments. Nature, 2012, 491, 134-137.	13.7	209
112	Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. ISME Journal, 2012, 6, 1378-1390.	4.4	635
113	Rapid and Serial Quantification of Adhesion Forces of Yeast and Mammalian Cells. PLoS ONE, 2012, 7, e52712.	1.1	106
114	Structural basis for sigma factor mimicry in the general stress response of Alphaproteobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1405-14.	3.3	49
115	GFAJ-1 Is an Arsenate-Resistant, Phosphate-Dependent Organism. Science, 2012, 337, 467-470.	6.0	104
116	Microbial rhodopsins on leaf surfaces of terrestrial plants. Environmental Microbiology, 2012, 14, 140-146.	1.8	78
117	Bacterial anoxygenic photosynthesis on plant leaf surfaces. Environmental Microbiology Reports, 2012, 4, 209-216.	1.0	94
118	Characterization of Methylobacterium strains isolated from the phyllosphere and description of Methylobacterium longum sp. nov. Antonie Van Leeuwenhoek, 2012, 101, 169-183.	0.7	35
119	Co-Consumption of Methanol and Succinate by Methylobacterium extorquens AM1. PLoS ONE, 2012, 7, e48271.	1.1	31
120	Nanoscale Ion-Pair Reversed-Phase HPLCâ^'MS for Sensitive Metabolome Analysis. Analytical Chemistry, 2011, 83, 850-855.	3.2	83
121	Protection of Arabidopsis thaliana against Leaf-Pathogenic Pseudomonas syringae by Sphingomonas Strains in a Controlled Model System. Applied and Environmental Microbiology, 2011, 77, 3202-3210.	1.4	480
122	Enzymes involved in the anaerobic degradation of <i>meta</i> â€substituted halobenzoates. Molecular Microbiology, 2011, 82, 758-769.	1.2	39
123	Genome-scale reconstruction and system level investigation of the metabolic network of Methylobacterium extorquensAM1. BMC Systems Biology, 2011, 5, 189.	3.0	111
124	Bacterial adaptation to life in association with plants $\hat{a} \in A$ proteomic perspective from culture to in situ conditions. Proteomics, 2011, 11, 3086-3105.	1.3	62
125	Role of Sphingomonas sp. Strain Fr1 PhyR-NepR-σ ^{EcfG} Cascade in General Stress Response and Identification of a Negative Regulator of PhyR. Journal of Bacteriology, 2011, 193, 6629-6638.	1.0	60
126	Bacterial RuBisCO Is Required for Efficient Bradyrhizobium/Aeschynomene Symbiosis. PLoS ONE, 2011, 6, e21900.	1.1	34

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127	Rhizobial Adaptation to Hosts, a New Facet in the Legume Root-Nodule Symbiosis. Molecular Plant-Microbe Interactions, 2010, 23, 784-790.	1.4	68
128	Competitiveness of Diverse Methylobacterium Strains in the Phyllosphere of Arabidopsis thaliana and Identification of Representative Models, Including M. extorquens PA1. Microbial Ecology, 2010, 60, 440-452.	1.4	102
129	An integrated proteomics and transcriptomics reference data set provides new insights into the <i>Bradyrhizobium japonicum</i> bacteroid metabolism in soybean root nodules. Proteomics, 2010, 10, 1391-1400.	1.3	111
130	Site and plant species are important determinants of the <i>Methylobacterium</i> community composition in the plant phyllosphere. ISME Journal, 2010, 4, 719-728.	4.4	297
131	Functional investigation of methanol dehydrogenase-like protein XoxF in Methylobacterium extorquens AM1. Microbiology (United Kingdom), 2010, 156, 2575-2586.	0.7	108
132	Force-controlled spatial manipulation of viable mammalian cells and micro-organisms by means of FluidFM technology. Applied Physics Letters, 2010, 97, .	1.5	80
133	Methylobacterium Genome Sequences: A Reference Blueprint to Investigate Microbial Metabolism of C1 Compounds from Natural and Industrial Sources. PLoS ONE, 2009, 4, e5584.	1.1	204
134	Metabolite Profiling Uncovers Plasmid-Induced Cobalt Limitation under Methylotrophic Growth Conditions. PLoS ONE, 2009, 4, e7831.	1.1	36
135	Demonstration of the ethylmalonyl-CoA pathway by using ¹³ C metabolomics. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4846-4851.	3.3	232
136	Small RNA-dependent Expression of Secondary Metabolism Is Controlled by Krebs Cycle Function in Pseudomonas fluorescens. Journal of Biological Chemistry, 2009, 284, 34976-34985.	1.6	82
137	Methanol-based industrial biotechnology: current status and future perspectives of methylotrophic bacteria. Trends in Biotechnology, 2009, 27, 107-115.	4.9	245
138	The PhyRâ€if ^{EcfG} signalling cascade is involved in stress response and symbiotic efficiency in <i>Bradyrhizobium japonicum</i> . Molecular Microbiology, 2009, 73, 291-305.	1.2	103
139	Sigma factor mimicry involved in regulation of general stress response. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3467-3472.	3.3	121
140	Community proteogenomics reveals insights into the physiology of phyllosphere bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16428-16433.	3.3	774
141	Quantitative metabolome analysis using liquid chromatography–high-resolution mass spectrometry. Analytical Biochemistry, 2008, 382, 94-100.	1.1	91
142	Cultivation-Independent Characterization of <i>Methylobacterium</i> Populations in the Plant Phyllosphere by Automated Ribosomal Intergenic Spacer Analysis. Applied and Environmental Microbiology, 2008, 74, 2218-2228.	1.4	57
143	PhyR Is Involved in the General Stress Response of <i>Methylobacterium extorquens</i> AM1. Journal of Bacteriology, 2008, 190, 1027-1035.	1.0	94
144	The Legionella Autoinducer Synthase LqsA Produces an α-Hydroxyketone Signaling Molecule. Journal of Biological Chemistry, 2008, 283, 18113-18123.	1.6	101

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145	The Ralstonia solanacearum pathogenicity regulator HrpB induces 3-hydroxy-oxindole synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15870-15875.	3.3	28
146	Identification of a Fourth Formate Dehydrogenase in <i>Methylobacterium extorquens</i> AM1 and Confirmation of the Essential Role of Formate Oxidation in Methylotrophy. Journal of Bacteriology, 2007, 189, 9076-9081.	1.0	64
147	Methylobacterium extorquensAM1 produces a novel type of acyl-homoserine lactone with a double unsaturated side chain under methylotrophic growth conditions. FEBS Letters, 2006, 580, 561-567.	1.3	36
148	A Plasmid-Borne Truncated luxI Homolog Controls Quorum-Sensing Systems and Extracellular Carbohydrate Production in Methylobacterium extorquens AM1. Journal of Bacteriology, 2006, 188, 7321-7324.	1.0	18
149	A proteomic study of Methylobacterium extorquens reveals a response regulator essential for epiphytic growth. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13186-13191.	3.3	142
150	Methylotrophic Metabolism Is Advantageous for Methylobacterium extorquens during Colonization of Medicago truncatula under Competitive Conditions. Applied and Environmental Microbiology, 2005, 71, 7245-7252.	1.4	189
151	How an Enzyme Binds the C1 Carrier Tetrahydromethanopterin. Journal of Biological Chemistry, 2005, 280, 13712-13719.	1.6	18
152	MtdC, a Novel Class of Methylene Tetrahydromethanopterin Dehydrogenases. Journal of Bacteriology, 2005, 187, 6069-6074.	1.0	17
153	A Dynamic Zinc Redox Switch. Journal of Biological Chemistry, 2005, 280, 2826-2830.	1.6	16
154	A genomic view of methane oxidation by aerobic bacteria and anaerobic archaea. Genome Biology, 2005, 6, 208.	13.9	103
155	The Enigmatic Planctomycetes May Hold a Key to the Origins of Methanogenesis and Methylotrophy. Molecular Biology and Evolution, 2004, 21, 1234-1241.	3.5	123
156	Multiple Formate Dehydrogenase Enzymes in the Facultative Methylotroph Methylobacterium extorquens AM1 Are Dispensable for Growth on Methanol. Journal of Bacteriology, 2004, 186, 22-28.	1.0	90
157	Comparison of the proteome ofMethylobacterium extorquens AM1 grown under methylotrophic and nonmethylotrophic conditions. Proteomics, 2004, 4, 1247-1264.	1.3	54
158	The tungsten-containing formate dehydrogenase from Methylobacterium extorquens AM1: Purification and properties. FEBS Journal, 2003, 270, 325-333.	0.2	89
159	Purification of the Formate-Tetrahydrofolate Ligasefrom Methylobacterium extorquens AM1 and Demonstrationof Its Requirement for MethylotrophicGrowth. Journal of Bacteriology, 2003, 185, 7169-7175.	1.0	73
160	A Glutathione-dependent Formaldehyde-activating Enzyme (Gfa) from Paracoccus denitrificans Detected and Purified via Two-dimensional Proton Exchange NMR Spectroscopy. Journal of Biological Chemistry, 2002, 277, 3069-3072.	1.6	76
161	Generation of formate by the formyltransferase/hydrolase complex (Fhc) fromMethylobacterium extorquensAM1. FEBS Letters, 2002, 523, 133-137.	1.3	54
162	Structure of Methylene-Tetrahydromethanopterin Dehydrogenase from Methylobacterium extorquens AM1. Structure, 2002, 10, 1127-1137.	1.6	21

#	Article	IF	CITATIONS
163	Cofactor-dependent pathways of formaldehyde oxidation in methylotrophic bacteria. Archives of Microbiology, 2002, 178, 239-249.	1.0	194
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