

# Martin G Klotz

## List of Publications by Year in descending order

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papers

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#	ARTICLE	IF	CITATIONS
1	Mutagens, Radicals, Rocket Fuel, and Laughing Gas: Stringing Metabolic Modules to Survive on Nitrogenous Poisons. <i>Advances in Environmental Microbiology</i> , 2021, , 151-159.	0.1	0
2	Comment on "A Critical Review on Nitrous Oxide Production by Ammonia-Oxidizing Archaea" by Lan Wu, Xueming Chen, Wei Wei, Yiwen Liu, Dongbo Wang, and Bing-Jie Ni. <i>Environmental Science &amp; Technology</i> , 2021, 55, 797-798.	4.6	6
3	High Synteny and Sequence Identity between Genomes of <i>Nitrosococcus oceani</i> Strains Isolated from Different Oceanic Gyres Reveals Genome Economization and Autochthonous Clonal Evolution. <i>Microorganisms</i> , 2020, 8, 693.	1.6	4
4	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
5	Consent insufficient for data release "Response". <i>Science</i> , 2019, 364, 446-446.	6.0	5
6	A Physiological and Genomic Comparison of <i>Nitrosomonas</i> Cluster 6a and 7 Ammonia-Oxidizing Bacteria. <i>Microbial Ecology</i> , 2019, 78, 985-994.	1.4	38
7	Editorial: The Responses of Marine Microorganisms, Communities and Ecofunctions to Environmental Gradients. <i>Frontiers in Microbiology</i> , 2019, 10, 115.	1.5	12
8	Evolutionary History of Copper Membrane Monooxygenases. <i>Frontiers in Microbiology</i> , 2018, 9, 2493.	1.5	50
9	Complete Genome Sequence of <i>Nitrosomonas cryotolerans</i> ATCC 49181, a Phylogenetically Distinct Ammonia-Oxidizing Bacterium Isolated from Arctic Waters. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
10	Comparative Genomic Analysis of the Class Epsilonproteobacteria and Proposed Reclassification to Epsilonbacteraeota (phyl. nov.). <i>Frontiers in Microbiology</i> , 2017, 8, 682.	1.5	409
11	Draft Genome Sequences of Two Gammaproteobacterial Methanotrophs Isolated from Rice Ecosystems. <i>Genome Announcements</i> , 2017, 5, .	0.8	8
12	Editorial: Systems Biology and Ecology of Microbial Mat Communities. <i>Frontiers in Microbiology</i> , 2016, 7, 115.	1.5	3
13	D1FHS, the Type Strain of the Ammonia-Oxidizing Bacterium <i>Nitrosococcus wardiae</i> spec. nov.: Enrichment, Isolation, Phylogenetic, and Growth Physiological Characterization. <i>Frontiers in Microbiology</i> , 2016, 7, 512.	1.5	21
14	Environmental Conditions Outweigh Geographical Contiguity in Determining the Similarity of <i>nifH</i> -Harboring Microbial Communities in Sediments of Two Disconnected Marginal Seas. <i>Frontiers in Microbiology</i> , 2016, 7, 1111.	1.5	14
15	Draft Genome Sequences of Gammaproteobacterial Methanotrophs Isolated from Marine Ecosystems. <i>Genome Announcements</i> , 2016, 4, .	0.8	23
16	Complete genome of <i>Nitrospira briensis</i> C-128, an ammonia-oxidizing bacterium from agricultural soil. <i>Standards in Genomic Sciences</i> , 2016, 11, 46.	1.5	22
17	Pathways and key intermediates required for obligate aerobic ammonia-dependent chemolithotrophy in bacteria and Thaumarchaeota. <i>ISME Journal</i> , 2016, 10, 1836-1845.	4.4	281
18	The nitrogen cycle. <i>Current Biology</i> , 2016, 26, R94-R98.	1.8	350

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19	Draft Genomes of Gammaproteobacterial Methanotrophs Isolated from Terrestrial Ecosystems. Genome Announcements, 2015, 3, .	0.8	41
20	Nitrosospira lacus sp. nov., a psychrotolerant, ammonia-oxidizing bacterium from sandy lake sediment. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 242-250.	0.8	49
21	Methane oxidation coupled to nitrate reduction under hypoxia by the <i>Gammaproteobacterium</i> <i>Methylobacterium denitrificans</i> , sp. nov. type strain FJG1. Environmental Microbiology, 2015, 17, 3219-3232.	1.8	258
22	Distribution of ether lipids and composition of the archaeal community in terrestrial geothermal springs: impact of environmental variables. Environmental Microbiology, 2015, 17, 1600-1614.	1.8	29
23	Draft Genome Sequence of the Moderately Halophilic Methanotroph <i>Methylohalobius crimeensis</i> Strain 10Ki. Genome Announcements, 2015, 3, .	0.8	14
24	Deep-sea methane seep sediments in the Okhotsk Sea sustain diverse and abundant anammox bacteria. FEMS Microbiology Ecology, 2014, 87, 503-516.	1.3	44
25	Production of branched tetraether lipids in Tibetan hot springs: A possible linkage to nitrite reduction by thermotolerant or thermophilic bacteria?. Chemical Geology, 2014, 386, 209-217.	1.4	12
26	The environmental controls that govern the end product of bacterial nitrate respiration. Science, 2014, 345, 676-679.	6.0	391
27	Metabolic Environments and Genomic Features Associated with Pathogenic and Mutualistic Interactions Between Bacteria and Plants. Molecular Plant-Microbe Interactions, 2014, 27, 664-677.	1.4	16
28	Soil Nitrifiers and Nitrification. , 2014, , 347-383.		28
29	Nitrification in Inland Waters. , 2014, , 385-403.		3
30	Diversity and evolution of bioenergetic systems involved in microbial nitrogen compound transformations. Biochimica Et Biophysica Acta - Bioenergetics, 2013, 1827, 114-135.	0.5	300
31	Draft Genome Sequence of <i>Methylomicrobium buryatense</i> Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. Genome Announcements, 2013, 1, .	0.8	36
32	Genome Sequence of the Obligate Gammaproteobacterial Methanotroph <i>Methylomicrobium album</i> Strain BG8. Genome Announcements, 2013, 1, e0017013.	0.8	23
33	Draft Genome Sequence of <i>Nitrosospira</i> sp. Strain APG3, a Psychrotolerant Ammonia-Oxidizing Bacterium Isolated from Sandy Lake Sediment. Genome Announcements, 2013, 1, .	0.8	12
34	Environment-Dependent Distribution of the Sediment <i>nifH</i> -Harboring Microbiota in the Northern South China Sea. Applied and Environmental Microbiology, 2013, 79, 121-132.	1.4	39
35	Thaumarchaeotal Signature Gene Distribution in Sediments of the Northern South China Sea: an Indicator of the Metabolic Intersection of the Marine Carbon, Nitrogen, and Phosphorus Cycles?. Applied and Environmental Microbiology, 2013, 79, 2137-2147.	1.4	58
36	Abundance and distribution of diverse membrane-bound monooxygenase ( <i>CMMO</i> ) genes within the <i>Costa Rica</i> oxygen minimum zone. Environmental Microbiology Reports, 2013, 5, 414-423.	1.0	42

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37	Diversity, abundance, and distribution of <i>NO</i> -forming nitrite reductase-encoding genes in deep-sea subsurface sediments of the South China Sea. <i>Geobiology</i> , 2013, 11, 170-179.	1.1	25
38	Nitrate ammonification by <i>Nautilia profundicola</i> AmH: experimental evidence consistent with a free hydroxylamine intermediate. <i>Frontiers in Microbiology</i> , 2013, 4, 180.	1.5	45
39	Energy-mediated vs. ammonium-regulated gene expression in the obligate ammonia-oxidizing bacterium, <i>Nitrosococcus oceani</i> . <i>Frontiers in Microbiology</i> , 2013, 4, 277.	1.5	24
40	Complete genome sequence of <i>Nitrosomonas</i> sp. Is79, an ammonia oxidizing bacterium adapted to low ammonium concentrations. <i>Standards in Genomic Sciences</i> , 2013, 7, 469-482.	1.5	43
41	Draft Genome Sequence of the Volcano-Inhabiting Thermoacidophilic Methanotroph <i>Methylacidiphilum fumarolicum</i> Strain SolV. <i>Journal of Bacteriology</i> , 2012, 194, 3729-3730.	1.0	43
42	Effects of Nitrogen Dioxide and Anoxia on Global Gene and Protein Expression in Long-Term Continuous Cultures of <i>Nitrosomonas eutropha</i> C91. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4788-4794.	1.4	15
43	Genome Sequence of the Haloalkaliphilic Methanotrophic Bacterium <i>Methylomicrobium alcaliphilum</i> 20Z. <i>Journal of Bacteriology</i> , 2012, 194, 551-552.	1.0	72
44	Nitrous oxide production by lithotrophic ammonia-oxidizing bacteria and implications for engineered nitrogen-removal systems. <i>Biochemical Society Transactions</i> , 2011, 39, 1832-1837.	1.6	160
45	The Microbial Sulfur Cycle. <i>Frontiers in Microbiology</i> , 2011, 2, 241.	1.5	39
46	A novel family of functional operons encoding methane/ammonia monooxygenase-related proteins in gammaproteobacterial methanotrophs. <i>Environmental Microbiology Reports</i> , 2011, 3, 91-100.	1.0	149
47	Molecular characterization of putative biocorroding microbiota with a novel niche detection of <i>Epsilon</i> - and <i>Zetaproteobacteria</i> in Pacific Ocean coastal seawaters. <i>Environmental Microbiology</i> , 2011, 13, 3059-3074.	1.8	124
48	The <i>Wolinella succinogenes</i> <i>mcc</i> gene cluster encodes an unconventional respiratory sulphite reduction system. <i>Molecular Microbiology</i> , 2011, 82, 1515-1530.	1.2	63
49	Model of the molecular basis for hydroxylamine oxidation and nitrous oxide production in methanotrophic bacteria. <i>FEMS Microbiology Letters</i> , 2011, 322, 82-89.	0.7	97
50	<i>Nitrosococcus watsonii</i> sp. nov., a new species of marine obligate ammonia-oxidizing bacteria that is not omnipresent in the world's oceans: calls to validate the names <i>Nitrosococcus halophilus</i> ™ and <i>Nitrosomonas mobilis</i> ™. <i>FEMS Microbiology Ecology</i> , 2011, 76, 39-48.	1.3	74
51	Characterizing Bacterial Gene Expression in Nitrogen Cycle Metabolism with RT-qPCR. <i>Methods in Enzymology</i> , 2011, 496, 345-372.	0.4	15
52	Preface. <i>Methods in Enzymology</i> , 2011, 496, xix-xx.	0.4	2
53	Preface. <i>Methods in Enzymology</i> , 2011, 486, xix-xx.	0.4	1
54	Genome Sequence of the Arctic Methanotroph <i>Methylobacter tundripaludum</i> SV96. <i>Journal of Bacteriology</i> , 2011, 193, 6418-6419.	1.0	78

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55	Genome Sequence of <i>Nitrosomonas</i> sp. Strain AL212, an Ammonia-Oxidizing Bacterium Sensitive to High Levels of Ammonia. <i>Journal of Bacteriology</i> , 2011, 193, 6112-6112.	1.0	10
56	Genome Sequence of <i>Nitrosomonas</i> sp. Strain AL212, an Ammonia-Oxidizing Bacterium Sensitive to High Levels of Ammonia. <i>Journal of Bacteriology</i> , 2011, 193, 5047-5048.	1.0	35
57	Complete Genome Sequence of the Aerobic Marine Methanotroph <i>Methylomonas methanica</i> MC09. <i>Journal of Bacteriology</i> , 2011, 193, 7001-7002.	1.0	72
58	Genome Sequence of the Methanotrophic Alphaproteobacterium <i>Methylocystis</i> sp. Strain Rockwell (ATCC 49242). <i>Journal of Bacteriology</i> , 2011, 193, 2668-2669.	1.0	55
59	Nitrifying and denitrifying pathways of methanotrophic bacteria. <i>Biochemical Society Transactions</i> , 2011, 39, 1826-1831.	1.6	155
60	<i>Nitrosopumilus maritimus</i> genome reveals unique mechanisms for nitrification and autotrophy in globally distributed marine crenarchaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8818-8823.	3.3	853
61	A comparison of primer sets for detecting 16S rRNA and hydrazine oxidoreductase genes of anaerobic ammonium-oxidizing bacteria in marine sediments. <i>Applied Microbiology and Biotechnology</i> , 2010, 86, 781-790.	1.7	117
62	Diversity, abundance and distribution of amoA-encoding archaea in deep-sea methane seep sediments of the Okhotsk Sea. <i>FEMS Microbiology Ecology</i> , 2010, 72, 370-385.	1.3	68
63	The Grand Challenge of Microbiology: To Know Better, Protect, Utilize and Celebrate the Unseen Majority on Our Planet. <i>Frontiers in Microbiology</i> , 2010, 1, 1.	1.5	42
64	Genome Sequence of the Obligate Methanotroph <i>Methylosinus trichosporium</i> Strain OB3b. <i>Journal of Bacteriology</i> , 2010, 192, 6497-6498.	1.0	98
65	Diversity, Abundance, and Spatial Distribution of Sediment Ammonia-Oxidizing <i>Betaproteobacteria</i> in Response to Environmental Gradients and Coastal Eutrophication in Jiaozhou Bay, China. <i>Applied and Environmental Microbiology</i> , 2010, 76, 4691-4702.	1.4	155
66	Environmental Factors Shape Sediment Anammox Bacterial Communities in Hypernutriented Jiaozhou Bay, China. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7036-7047.	1.4	140
67	Harnessing the Power of Microbial Genomics for Exploring Exceptions and Shifting Perceptions. <i>Frontiers in Microbiology</i> , 2010, 1, 146.	1.5	2
68	Adaptations to Submarine Hydrothermal Environments Exemplified by the Genome of <i>Nautilia profundicola</i> . <i>PLoS Genetics</i> , 2009, 5, e1000362.	1.5	126
69	Nitrifier genomics and evolution of the nitrogen cycle. <i>FEMS Microbiology Letters</i> , 2008, 278, 146-156.	0.7	185
70	Transcription of nitrification genes by the methane-oxidizing bacterium, <i>Methylococcus capsulatus</i> strain Bath. <i>ISME Journal</i> , 2008, 2, 1213-1220.	4.4	57
71	Environmental detection of octahaem cytochrome <i>c</i> hydroxylamine/hydrazine oxidoreductase genes of aerobic and anaerobic ammonium-oxidizing bacteria. <i>Environmental Microbiology</i> , 2008, 10, 3140-3149.	1.8	175
72	Evolution of an octahaem cytochrome <i>c</i> protein family that is key to aerobic and anaerobic ammonia oxidation by bacteria. <i>Environmental Microbiology</i> , 2008, 10, 3150-3163.	1.8	147

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73	Ammonia-dependent differential regulation of the gene cluster that encodes ammonia monooxygenase in <i>Nitrosococcus oceani</i> ATCC 19707. <i>Environmental Microbiology</i> , 2008, 10, 3026-3035.	1.8	18
74	Complete Genome Sequence of <i>Nitrobacter hamburgensis</i> X14 and Comparative Genomic Analysis of Species within the Genus <i>Nitrobacter</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 2852-2863.	1.4	115
75	Characterization of Two New Genes, <i>amoR</i> and <i>amoD</i> , in the <i>amo</i> Operon of the Marine Ammonia Oxidizer <i>Nitrosococcus oceani</i> ATCC 19707. <i>Applied and Environmental Microbiology</i> , 2008, 74, 312-318.	1.4	31
76	Genome of the Epsilonproteobacterial Chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 1145-1156.	1.4	228
77	Complete Genome Sequence of <i>Nitrospira multiformis</i> , an Ammonia-Oxidizing Bacterium from the Soil Environment. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3559-3572.	1.4	212
78	Cytochromes P460 and $\beta$ ; A new family of high-spin cytochromes. <i>FEBS Letters</i> , 2007, 581, 911-916.	1.3	53
79	The Impact of Genome Analyses on Our Understanding of Ammonia-Oxidizing Bacteria. <i>Annual Review of Microbiology</i> , 2007, 61, 503-528.	2.9	165
80	Whole-genome analysis of the ammonia-oxidizing bacterium, <i>Nitrosomonas eutropha</i> C91: implications for niche adaptation. <i>Environmental Microbiology</i> , 2007, 9, 2993-3007.	1.8	150
81	A gene encoding a membrane protein exists upstream of the <i>amoA/amoB</i> genes in ammonia oxidizing bacteria: a third member of the <i>amo</i> operon?. <i>FEMS Microbiology Letters</i> , 2006, 150, 65-73.	0.7	37
82	Transcript profiles of <i>Nitrosomonas europaea</i> during growth and upon deprivation of ammonia and carbonate. <i>FEMS Microbiology Letters</i> , 2006, 257, 76-83.	0.7	56
83	The Genome of Deep-Sea Vent Chemolithoautotroph <i>Thiomicrospira crunogena</i> XCL-2. <i>PLoS Biology</i> , 2006, 4, e383.	2.6	144
84	Complete Genome Sequence of the Marine, Chemolithoautotrophic, Ammonia-Oxidizing Bacterium <i>Nitrosococcus oceani</i> ATCC 19707. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6299-6315.	1.4	139
85	Genome Sequence of the Chemolithoautotrophic Nitrite-Oxidizing Bacterium <i>Nitrobacter winogradskyi</i> Nb-255. <i>Applied and Environmental Microbiology</i> , 2006, 72, 2050-2063.	1.4	169
86	Structure and Sequence Conservation of <i>hao</i> Cluster Genes of Autotrophic Ammonia-Oxidizing Bacteria: Evidence for Their Evolutionary History. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5371-5382.	1.4	67
87	Urease-Encoding Genes in Ammonia-Oxidizing Bacteria. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2342-2348.	1.4	99
88	Structure of the Clade 1 catalase, CatF of <i>Pseudomonas syringae</i> , at 1.8 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 50, 423-436.	1.5	45
89	The Molecular Evolution of Catalatic Hydroperoxidases: Evidence for Multiple Lateral Transfer of Genes Between Prokaryota and from Bacteria into Eukaryota. <i>Molecular Biology and Evolution</i> , 2003, 20, 1098-1112.	3.5	143
90	Complete Genome Sequence of the Ammonia-Oxidizing Bacterium and Obligate Chemolithoautotroph <i>Nitrosomonas europaea</i> . <i>Journal of Bacteriology</i> , 2003, 185, 2759-2773.	1.0	510

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91	Redundancy, phylogeny and differential expression of <i>Histoplasma capsulatum</i> catalases The GenBank accession numbers for the cDNA sequences reported in this paper are AF139985 (CATB), AF189368 (CATA) and AF189369 (CATP).. <i>Microbiology</i> (United Kingdom), 2002, 148, 1129-1142.	0.7	66
92	Diversity of ammonia monooxygenase operon in autotrophic ammonia-oxidizing bacteria. <i>Archives of Microbiology</i> , 2002, 177, 139-149.	1.0	291
93	Crystallization and preliminary X-ray analysis of clade I catalases from <i>Pseudomonas syringae</i> and <i>Listeria seeligeri</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1184-1186.	2.5	6
94	AnkB, a Periplasmic Ankyrin-Like Protein in <i>Pseudomonas aeruginosa</i> , Is Required for Optimal Catalase B (KatB) Activity and Resistance to Hydrogen Peroxide. <i>Journal of Bacteriology</i> , 2000, 182, 4545-4556.	1.0	54
95	The amo operon in marine, ammonia-oxidizing $\alpha$ -proteobacteria. <i>FEMS Microbiology Letters</i> , 1999, 180, 21-29.	0.7	45
96	The amo operon in marine, ammonia-oxidizing $\beta$ -proteobacteria. <i>FEMS Microbiology Letters</i> , 1999, 180, 21-29.	0.7	40
97	Bacterioferritin A Modulates Catalase A (KatA) Activity and Resistance to Hydrogen Peroxide in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 1999, 181, 3730-3742.	1.0	138
98	Transcription of the amoC, amoA and amoB genes in <i>Nitrosomonas europaea</i> and <i>Nitrosospira</i> sp. NpAV. <i>FEMS Microbiology Letters</i> , 1998, 167, 81-88.	0.7	62
99	Multiple copies of ammonia monooxygenase (amo) operons have evolved under biased AT/GC mutational pressure in ammonia-oxidizing autotrophic bacteria. <i>FEMS Microbiology Letters</i> , 1998, 168, 303-311.	0.7	75
100	Phylogenetic relationships among prokaryotic and eukaryotic catalases. <i>Molecular Biology and Evolution</i> , 1997, 14, 951-958.	3.5	171
101	A gene encoding a membrane protein exists upstream of the genes in ammonia oxidizing bacteria: a third member of the operon?. <i>FEMS Microbiology Letters</i> , 1997, 150, 65-73.	0.7	62
102	The gene encoding ammonia monooxygenase subunit A exists in three nearly identical copies in <i>Nitrosospira</i> sp. NpAV. <i>FEMS Microbiology Letters</i> , 1996, 139, 181-188.	0.7	24
103	The gene encoding ammonia monooxygenase subunit A exists in three nearly identical copies in <i>Nitrosospira</i> sp. NpAV. <i>FEMS Microbiology Letters</i> , 1996, 139, 181-188.	0.7	83
104	Sequence of an ammonia monooxygenase subunit A-encoding gene from <i>Nitrosospira</i> sp. NpAV. <i>Gene</i> , 1995, 163, 159-160.	1.0	42
105	Sequence of a gene encoding periplasmic <i>Pseudomonas syringae</i> ankyrin. <i>Gene</i> , 1995, 164, 187-188.	1.0	4
106	Cloning, characterization and phenotypic expression in <i>Escherichia coli</i> of catF, which encodes the catalytic subunit of catalase isozyme CatF of <i>Pseudomonas syringae</i> . <i>Applied Microbiology and Biotechnology</i> , 1995, 43, 656-666.	1.7	22
107	The role of catalase isozymes in the culturability of the root colonizer <i>Pseudomonas putida</i> after exposure to hydrogen peroxide and antibiotics. <i>Canadian Journal of Microbiology</i> , 1994, 40, 382-387.	0.8	9
108	The importance of bacterial growth phase for in planta virulence and pathogenicity testing: coordinated stress response regulation in fluorescent pseudomonads?. <i>Canadian Journal of Microbiology</i> , 1993, 39, 948-957.	0.8	10

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109	Picomolar concentrations of tentoxin affect Mg <sup>2+</sup> - and Ca <sup>2+</sup> -ATPase activities of plasma membrane vesicles from roots of winter wheat seedlings. <i>Physiologia Plantarum</i> , 1989, 75, 405-410.	2.6	3
110	Growth and internal ion concentrations in seedlings of winter wheat are affected by 1 pM tentoxin. <i>Physiologia Plantarum</i> , 1988, 73, 295-298.	2.6	7
111	The action of tentoxin on membrane processes in plants. <i>Physiologia Plantarum</i> , 1988, 74, 575-582.	2.6	24
112	Effect of tentoxin on K <sup>+</sup> -transport in winter wheat seedlings of different K <sup>+</sup> -status. <i>Physiologia Plantarum</i> , 1988, 72, 298-304.	2.6	14
113	Potassium transport through lipid bilayer membranes facilitated by tentoxin dimers. <i>Biophysical Chemistry</i> , 1987, 27, 183-189.	1.5	6
114	Delayed Fluorescence as Evidence for a Tentoxin Action on the Photosynthetic Electron Flow in <i>Chlorella</i> . <i>Biochemie Und Physiologie Der Pflanzen</i> , 1984, 179, 707-709.	0.5	7
115	Physiology and Genomics of Ammonia-Oxidizing <i>Archaea</i> . , 0, , 115-155.		25
116	Metabolism and Genomics of Nitrite-Oxidizing Bacteria: Emphasis on Studies of Pure Cultures and of <i>Nitrobacter</i> Species. , 0, , 265-293.		7
117	Diversity, Environmental Genomics, and Ecophysiology of Nitrite-Oxidizing Bacteria. , 0, , 295-322.		20
118	Nitrification in the Ocean. , 0, , 323-345.		32
119	Nitrification in Wastewater Treatment. , 0, , 405-433.		7
120	Nitrification: An Introduction and Overview of the State of the Field. , 0, , 1-8.		12
121	Ammonia-Oxidizing Bacteria: Their Biochemistry and Molecular Biology. , 0, , 9-37.		22
122	Diversity and Environmental Distribution of Ammonia-Oxidizing Bacteria. , 0, , 39-55.		25
123	Genomics of Ammonia-Oxidizing Bacteria and Insights into Their Evolution. , 0, , 57-94.		26
124	Heterotrophic Nitrification and Nitrifier Denitrification. , 0, , 95-114.		58