## Peter F Dunfield

List of Publications by Year in descending order

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57681 54771 8,610 112 46 88 citations h-index g-index papers 125 125 125 7519 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Seasonal Dynamics of Methanotrophic Bacteria in a Boreal Oil Sands End Pit Lake. Applied and Environmental Microbiology, 2022, 88, AEM0145521.	1.4	6
2	Field study on the effect of vegetation on the performance of soil methanotrophy-based engineered systems $\hat{a} \in \text{``Column experiments. Soil Biology and Biochemistry, 2022, 167, 108583.}$	4.2	3
3	Microbial Functional Diversity Correlates with Species Diversity along a Temperature Gradient. MSystems, 2022, 7, e0099121.	1.7	14
4	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. ISME Journal, 2022, 16, 1337-1347.	4.4	15
5	Genomic Analysis of the Yet-Uncultured Binatota Reveals Broad Methylotrophic, Alkane-Degradation, and Pigment Production Capacities. MBio, 2021, 12, .	1.8	13
6	Verrucomicrobial methanotrophs grow on diverse C3 compounds and use a homolog of particulate methane monooxygenase to oxidize acetone. ISME Journal, 2021, 15, 3636-3647.	4.4	29
7	GAL08, an Uncultivated Group of Acidobacteria, Is a Dominant Bacterial Clade in a Neutral Hot Spring. Frontiers in Microbiology, 2021, 12, 787651.	1.5	1
8	Phylogenetic Estimation of Community Composition and Novel Eukaryotic Lineages in Base Mine Lake: An Oil Sands Tailings Reclamation Site in Northern Alberta. Journal of Eukaryotic Microbiology, 2020, 67, 86-99.	0.8	14
9	Novel copper-containing membrane monooxygenases (CuMMOs) encoded by alkane-utilizing <i>Betaproteobacteria (i). ISME Journal, 2020, 14, 714-726.</i>	4.4	16
10	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. Frontiers in Microbiology, 2020, 11, 1848.	1.5	62
11	Ecological and genomic analyses of candidate phylum <scp>WPS</scp> â€2 bacteria in an unvegetated soil. Environmental Microbiology, 2020, 22, 3143-3157.	1.8	42
12	Methylicorpusculum oleiharenae gen. nov., sp. nov., an aerobic methanotroph isolated from an oil sands tailings pond. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2499-2508.	0.8	10
13	The origin of aerobic methanotrophy within the Proteobacteria. FEMS Microbiology Letters, 2019, 366,	0.7	14
14	Methanotrophy in Acidic Soils, Including Northern Peatlands. , 2019, , 1-25.		2
15	Methanotrophy in Acidic Soils, Including Northern Peatlands. , 2019, , 133-156.		3
16	Facultative Methane Oxidizers., 2019,, 279-297.		2
17	Evolutionary History of Copper Membrane Monooxygenases. Frontiers in Microbiology, 2018, 9, 2493.	1.5	50
18	Analysis of microbial communities in natural halite springs reveals a domainâ€dependent relationship of species diversity to osmotic stress. Environmental Microbiology Reports, 2018, 10, 695-703.	1.0	10

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19	Facultative Methane Oxidizers. , 2018, , 1-20.		3
20	Differential Transcriptional Activation of Genes Encoding Soluble Methane Monooxygenase in a Facultative Versus an Obligate Methanotroph. Microorganisms, 2018, 6, 20.	1.6	9
21	Biofiltration of methane using hybrid mixtures of biochar, lava rock and compost. Environmental Pollution, 2018, 241, 45-54.	3.7	28
22	Verrucomicrobial Methanotrophs. , 2018, , 43-55.		4
23	Stable Isotope and Metagenomic Profiling of a Methanogenic Naphthalene-Degrading Enrichment Culture. Microorganisms, 2018, 6, 65.	1.6	17
24	Biofiltration of methane. Bioresource Technology, 2018, 268, 759-772.	4.8	49
25	Investigation of Biologically Stable Biofilter Medium for Methane Mitigation by Methanotrophic Bacteria. Journal of Hazardous, Toxic, and Radioactive Waste, 2018, 22, 04018013.	1.2	6
26	An overview of the occurrence of ether- and ester-linked iso-diabolic acid membrane lipids in microbial cultures of the Acidobacteria: Implications for brGDGT paleoproxies for temperature and pH. Organic Geochemistry, 2018, 124, 63-76.	0.9	117
27	Oleiharenicola alkalitolerans gen. nov., sp. nov., a new member of the phylum Verrucomicrobia isolated from an oilsands tailings pond. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1078-1084.	0.8	11
28	Benzene and Naphthalene Degrading Bacterial Communities in an Oil Sands Tailings Pond. Frontiers in Microbiology, 2017, 8, 1845.	1.5	37
29	Actinocrinis puniceicyclus gen. nov., sp. nov., an actinobacterium isolated from an acidic spring. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 602-609.	0.8	10
30	Draft Genome Sequences of Two Gammaproteobacterial Methanotrophs Isolated from Rice Ecosystems. Genome Announcements, 2017, $5$ , .	0.8	8
31	Nextâ€Generation Sequencing Assessment of Eukaryotic Diversity in Oil Sands Tailings Ponds Sediments and SurfaceÂWater. Journal of Eukaryotic Microbiology, 2016, 63, 732-743.	0.8	26
32	Draft Genome Sequences of Gammaproteobacterial Methanotrophs Isolated from Marine Ecosystems. Genome Announcements, 2016, 4, .	0.8	23
33	Deep groundwater circulation and associated methane leakage in the northern Canadian Rocky Mountains. Applied Geochemistry, 2016, 68, 10-18.	1.4	21
34	The Chthonomonas calidirosea Genome Is Highly Conserved across Geographic Locations and Distinct Chemical and Microbial Environments in New Zealand's TaupŕVolcanic Zone. Applied and Environmental Microbiology, 2016, 82, 3572-3581.	1.4	9
35	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. Nature Communications, 2016, 7, 10476.	5.8	189
36	Emended description of the family Beijerinckiaceae and transfer of the genera Chelatococcus and Camelimonas to the family Chelatococcaceae fam. nov International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 3177-3182.	0.8	31

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37	Complete genome sequence of the thermophilic Acidobacteria, Pyrinomonas methylaliphatogenes type strain K22T. Standards in Genomic Sciences, 2015, 10, 101.	1.5	17
38	Anaerobic carboxydotrophic bacteria in geothermal springs identified using stable isotope probing. Frontiers in Microbiology, 2015, 6, 897.	1.5	27
39	Draft Genomes of Gammaproteobacterial Methanotrophs Isolated from Terrestrial Ecosystems. Genome Announcements, 2015, 3, .	0.8	41
40	Draft Genome Sequence of Methyloferula stellata AR4, an Obligate Methanotroph Possessing Only a Soluble Methane Monooxygenase. Genome Announcements, 2015, 3, .	0.8	28
41	Stable-Isotope Probing Identifies Uncultured Planctomycetes as Primary Degraders of a Complex Heteropolysaccharide in Soil. Applied and Environmental Microbiology, 2015, 81, 4607-4615.	1.4	88
42	Draft Genome Sequence of the Moderately Halophilic Methanotroph Methylohalobius crimeensis Strain 10Ki. Genome Announcements, 2015, 3, .	0.8	14
43	Influence of bioenergy crop Jatropha curcas amendment on soil biogeochemistry in a tropical vertisol. Mitigation and Adaptation Strategies for Global Change, 2015, 20, 1459-1470.	1.0	2
44	Cultivation of Methanotrophs. Springer Protocols, 2014, , 231-247.	0.1	28
45	Thermoflavifilum aggregans gen. nov., sp. nov., a thermophilic and slightly halophilic filamentous bacterium from the phylum Bacteroidetes. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 1264-1270.	0.8	39
46	Pyrinomonas methylaliphatogenes gen. nov., sp. nov., a novel group 4 thermophilic member of the phylum Acidobacteria from geothermal soils. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 220-227.	0.8	44
47	Distribution and diversity of <scp><i>V</i></scp> <i>errucomicrobia</i> methanotrophs in geothermal and acidic environments. Environmental Microbiology, 2014, 16, 1867-1878.	1.8	132
48	Humboldt's spa: microbial diversity is controlled by temperature in geothermal environments. ISME Journal, 2014, 8, 1166-1174.	4.4	186
49	The (d)evolution of methanotrophy in the <i>Beijerinckiaceae</i> â€"a comparative genomics analysis. ISME Journal, 2014, 8, 369-382.	4.4	91
50	Methanotrophic bacteria in warm geothermal spring sediments identified using stable-isotope probing. FEMS Microbiology Ecology, 2014, 90, 92-102.	1.3	26
51	Genomic analysis of <i>Chthonomonas calidirosea</i> , the first sequenced isolate of the phylum <i>Armatimonadetes</i> . ISME Journal, 2014, 8, 1522-1533.	4.4	39
52	Ether- and Ester-Bound <i>iso</i> -Diabolic Acid and Other Lipids in Members of Acidobacteria Subdivision 4. Applied and Environmental Microbiology, 2014, 80, 5207-5218.	1.4	112
53	Methylocella: a gourmand among methanotrophs. Trends in Microbiology, 2014, 22, 368-369.	3.5	35
54	The Phylum Armatimonadetes. , 2014, , 447-458.		24

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55	Methanotrophic bacteria in oilsands tailings ponds of northern Alberta. ISME Journal, 2013, 7, 908-921.	4.4	92
56	The Paint Pots, Kootenay National Park, Canada— a natural acid spring analogue for Mars. Canadian Journal of Earth Sciences, 2013, 50, 94-108.	0.6	36
57	Metagenomics of Hydrocarbon Resource Environments Indicates Aerobic Taxa and Genes to be Unexpectedly Common. Environmental Science & Environmental Science & 2013, 47, 10708-10717.	4.6	179
58	Draft Genome Sequence of Methylomicrobium buryatense Strain 5G, a Haloalkaline-Tolerant Methanotrophic Bacterium. Genome Announcements, 2013, $1$ , .	0.8	36
59	Phylogenetic Delineation of the Novel Phylum Armatimonadetes (Former Candidate Division OP10) and Definition of Two Novel Candidate Divisions. Applied and Environmental Microbiology, 2013, 79, 2484-2487.	1.4	21
60	Chryseolinea serpens gen. nov., sp. nov., a member of the phylum Bacteroidetes isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 654-660.	0.8	50
61	Controls on bacterial and archaeal community structure and greenhouse gas production in natural, mined, and restored Canadian peatlands. Frontiers in Microbiology, 2013, 4, 215.	1.5	42
62	Unusual Members of the PVC Superphylum: The Methanotrophic Verrucomicrobia Genus "Methylacidiphilum― , 2013, , 211-227.		17
63	Draft Genome Sequence of the Volcano-Inhabiting Thermoacidophilic Methanotroph Methylacidiphilum fumariolicum Strain SolV. Journal of Bacteriology, 2012, 194, 3729-3730.	1.0	43
64	Flavobacterium compostarboris sp. nov., isolated from leaf-and-branch compost, and emended descriptions of Flavobacterium hercynium, Flavobacterium resistens and Flavobacterium johnsoniae. International Journal of Systematic and Evolutionary Microbiology, 2012, 62, 2018-2024.	0.8	34
65	Genome Sequence of the Haloalkaliphilic Methanotrophic Bacterium Methylomicrobium alcaliphilum 20Z. Journal of Bacteriology, 2012, 194, 551-552.	1.0	72
66	Detection of autotrophic verrucomicrobial methanotrophs in a geothermal environment using stable isotope probing. Frontiers in Microbiology, 2012, 3, 303.	1.5	55
67	Electing a candidate: a speculative history of the bacterial phylum OP10. Environmental Microbiology, 2012, 14, 3069-3080.	1.8	34
68	Chthonomonas calidirosea gen. nov., sp. nov., an aerobic, pigmented, thermophilic micro-organism of a novel bacterial class, Chthonomonadetes classis nov., of the newly described phylum Armatimonadetes originally designated candidate division OP10. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 2482-2490.	0.8	75
69	Facultative and Obligate Methanotrophs. Methods in Enzymology, 2011, 495, 31-44.	0.4	61
70	Methyloferula stellata gen. nov., sp. nov., an acidophilic, obligately methanotrophic bacterium that possesses only a soluble methane monooxygenase. International Journal of Systematic and Evolutionary Microbiology, 2011, 61, 2456-2463.	0.8	233
71	Hell's Gate globin I: An acid and thermostable bacterial hemoglobin resembling mammalian neuroglobin. FEBS Letters, 2011, 585, 3250-3258.	1.3	29
72	Methylocapsa aurea sp. nov., a facultative methanotroph possessing a particulate methane monooxygenase, and emended description of the genus Methylocapsa. International Journal of Systematic and Evolutionary Microbiology, 2010, 60, 2659-2664.	0.8	120

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73	Complete Genome Sequence of the Aerobic Facultative Methanotroph <i>Methylocella silvestris</i> BL2. Journal of Bacteriology, 2010, 192, 3840-3841.	1.0	79
74	Complete Genome Sequence of <i>Beijerinckia indica</i> subsp. <i>indica</i> . Journal of Bacteriology, 2010, 192, 4532-4533.	1.0	19
75	A reanalysis of phospholipid fatty acids as ecological biomarkers for methanotrophic bacteria. ISME Journal, 2009, 3, 606-617.	4.4	110
76	Environmental, genomic and taxonomic perspectives on methanotrophic <i>Verrucomicrobia</i> Environmental Microbiology Reports, 2009, 1, 293-306.	1.0	431
77	Isolation of novel bacteria, including a candidate division, from geothermal soils in New Zealand. Environmental Microbiology, 2008, 10, 2030-2041.	1.8	169
78	Complete genome sequence of the extremely acidophilic methanotroph isolate V4, Methylacidiphilum infernorum, a representative of the bacterial phylum Verrucomicrobia. Biology Direct, 2008, 3, 26.	1.9	216
79	Cultureâ€independent characterization of a novel microbial community at a hydrothermal vent at Brothers volcano, Kermadec arc, New Zealand. Journal of Geophysical Research, 2008, 113, .	3.3	23
80	Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium Anoxybacillus flavithermus WK1. Genome Biology, 2008, 9, R161.	13.9	71
81	Edaphobacter modestus gen. nov., sp. nov., and Edaphobacter aggregans sp. nov., acidobacteria isolated from alpine and forest soils. International Journal of Systematic and Evolutionary Microbiology, 2008, 58, 1114-1122.	0.8	123
82	Methylocystis heyeri sp. nov., a novel type II methanotrophic bacterium possessing  signature' fatty acids of type I methanotrophs. International Journal of Systematic and Evolutionary Microbiology, 2007, 57, 472-479.	0.8	123
83	Methane oxidation by an extremely acidophilic bacterium of the phylum Verrucomicrobia. Nature, 2007, 450, 879-882.	13.7	526
84	The active methanotrophic community in hydromorphic soils changes in response to changing methane concentration. Environmental Microbiology, 2006, 8, 321-333.	1.8	115
85	Abundance and activity of uncultured methanotrophic bacteria involved in the consumption of atmospheric methane in two forest soils. Environmental Microbiology, 2005, 7, 1150-1161.	1.8	177
86	Response and adaptation of different methanotrophic bacteria to low methane mixing ratios. Environmental Microbiology, 2005, 7, 1307-1317.	1.8	163
87	Regulation of methane oxidation in the facultative methanotrophMethylocella silvestrisBL2. Molecular Microbiology, 2005, 58, 682-692.	1.2	126
88	Methylocella Species Are Facultatively Methanotrophic. Journal of Bacteriology, 2005, 187, 4665-4670.	1.0	265
89	Diversity of Methanotrophic Bacteria in Tropical Upland Soils under Different Land Uses. Applied and Environmental Microbiology, 2005, 71, 3826-3831.	1.4	74
90	Methylohalobius crimeensis gen. nov., sp. nov., a moderately halophilic, methanotrophic bacterium isolated from hypersaline lakes of Crimea. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 1817-1826.	0.8	134

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91	Methane utilization by Methylobacterium species: new evidence but still no proof for an old controversy. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 1919-1920.	0.8	25
92	Methanotrophic bacteria in boreal forest soil after fire. FEMS Microbiology Ecology, 2004, 50, 195-202.	1.3	53
93	Differential detection of type II methanotrophic bacteria in acidic peatlands using newly developed 16S rRNA-targeted fluorescent oligonucleotide probes. FEMS Microbiology Ecology, 2003, 43, 299-308.	1.3	80
94	Methylocella silvestris sp. nov., a novel methanotroph isolated from an acidic forest cambisol. International Journal of Systematic and Evolutionary Microbiology, 2003, 53, 1231-1239.	0.8	211
95	Wide Distribution of a Novel pmoA -Like Gene Copy among Type II Methanotrophs, and Its Expression in Methylocystis Strain SC2. Applied and Environmental Microbiology, 2003, 69, 5593-5602.	1.4	94
96	Diversity and Activity of Methanotrophic Bacteria in Different Upland Soils. Applied and Environmental Microbiology, 2003, 69, 6703-6714.	1.4	294
97	Isolation of a Methylocystis strain containing a novel pmoA-like gene. FEMS Microbiology Ecology, 2002, 41, 17-26.	1.3	56
98	Activity and community structure of methane-oxidising bacteria in a wet meadow soil. FEMS Microbiology Ecology, 2002, 41, 247-257.	1.3	73
99	GenBank accession numbers for the nearly complete 16S rRNA gene sequences for the isolates are AJ458466 to AJ458510. Partial sequences of the pmoA, mxaF and mmoX genes have been deposited under the accession numbers AJ458994à€"AJ459052, AJ459053à€"AJ459100 and AJ458511à€"AJ458535, respectively. Where multiple strains contained identical sequences, only one has been deposited. Microbiology	0.7	123
100	(United Kingdom), 2002, 148, 2831-2846. A novel pmoA lineage represented by the acidophilic methanotrophic bacterium Methylocapsa acidophila B2. Archives of Microbiology, 2001, 177, 117-121.	1.0	34
101	Archaeal community structures in rice soils from different geographical regions before and after initiation of methane production. FEMS Microbiology Ecology, 2001, 37, 175-186.	1.3	108
102	Use of the T-RFLP technique to assess spatial and temporal changes in the bacterial community structure within an agricultural soil planted with transgenic and non-transgenic potato plants. FEMS Microbiology Ecology, 2000, 32, 241-247.	1.3	261
103	Starvation Alters the Apparent Half-Saturation Constant for Methane in the Type II Methanotroph Methylocystis Strain LR1. Applied and Environmental Microbiology, 2000, 66, 4136-4138.	1.4	65
104	Nitrogen monoxide production and consumption in an organic soil. Biology and Fertility of Soils, 1999, 30, 153-159.	2.3	22
105	High-Affinity Methane Oxidation by a Soil Enrichment Culture Containing a Type II Methanotroph. Applied and Environmental Microbiology, 1999, 65, 1009-1014.	1.4	167
106	Organic matter, heterotrophic activity, and NO· consumption in soils. Global Change Biology, 1998, 4, 199-207.	4.2	29
107	Biological oxidation of nitric oxide in a humisol. Biology and Fertility of Soils, 1997, 24, 294-300.	2.3	23
108	Effect of nitrogen fertilizers and moisture content on CH4 and N2O fluxes in a humisol: Measurements in the field and intact soil cores. Biogeochemistry, 1995, 29, 199-222.	1.7	108

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109	Methane production and consumption in temperate and subarctic peat soils: Response to temperature and pH. Soil Biology and Biochemistry, 1993, 25, 321-326.	4.2	624
110	Use of the T-RFLP technique to assess spatial and temporal changes in the bacterial community structure within an agricultural soil planted with transgenic and non-transgenic potato plants. , 0, .		13
111	Archaeal community structures in rice soils from different geographical regions before and after initiation of methane production., 0,.		5
112	Isolation of a Methylocystis strain containing a novel pmo A-like gene. , 0, .		2