

# David E Graham

## List of Publications by Year in descending order

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105  
papers

8,356  
citations

71102

41  
h-index

46799

89  
g-index

121  
all docs

121  
docs citations

121  
times ranked

9038  
citing authors

#	ARTICLE	IF	CITATIONS
1	Unravelling biogeochemical drivers of methylmercury production in an Arctic fen soil and a bog soil. <i>Environmental Pollution</i> , 2022, 299, 118878.	7.5	8
2	Quantifying pH buffering capacity in acidic, organic-rich Arctic soils: Measurable proxies and implications for soil carbon degradation. <i>Geoderma</i> , 2022, 424, 116003.	5.1	7
3	Anaerobic respiration pathways and response to increased substrate availability of Arctic wetland soils. <i>Environmental Sciences: Processes and Impacts</i> , 2020, 22, 2070-2083.	3.5	6
4	Influences of Hillslope Biogeochemistry on Anaerobic Soil Organic Matter Decomposition in a Tundra Watershed. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2020, 125, e2019JG005512.	3.0	4
5	Temporal, Spatial, and Temperature Controls on Organic Carbon Mineralization and Methanogenesis in Arctic High-Centered Polygon Soils. <i>Frontiers in Microbiology</i> , 2020, 11, 616518.	3.5	3
6	Temperature sensitivity of mineral-enzyme interactions on the hydrolysis of cellobiose and indican by $\beta$ -glucosidase. <i>Science of the Total Environment</i> , 2019, 686, 1194-1201.	8.0	20
7	Expression of benzoyl-CoA metabolism genes in the lignocellulolytic host <i>Caldicellulosiruptor bescii</i> . <i>AMB Express</i> , 2019, 9, 59.	3.0	1
8	Soil Aggregate Microbial Communities: Towards Understanding Microbiome Interactions at Biologically Relevant Scales. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	233
9	Modeling anaerobic soil organic carbon decomposition in Arctic polygon tundra: insights into soil geochemical influences on carbon mineralization. <i>Biogeosciences</i> , 2019, 16, 663-680.	3.3	21
10	Stimulation of anaerobic organic matter decomposition by subsurface organic N addition in tundra soils. <i>Soil Biology and Biochemistry</i> , 2019, 130, 195-204.	8.8	13
11	Cryomilled zinc sulfide: A prophylactic for <i>Staphylococcus aureus</i> -infected wounds. <i>Journal of Biomaterials Applications</i> , 2018, 33, 82-93.	2.4	0
12	Characterization of iron oxide nanoparticle films at the air-water interface in Arctic tundra waters. <i>Science of the Total Environment</i> , 2018, 633, 1460-1468.	8.0	8
13	Impacts of Methane on Carbon Dioxide Storage in Brine Formations. <i>Ground Water</i> , 2018, 56, 176-186.	1.3	35
14	Influence of Structural Defects on Biomineralized ZnS Nanoparticle Dissolution: An in-Situ Electron Microscopy Study. <i>Environmental Science &amp; Technology</i> , 2018, 52, 1139-1149.	10.0	42
15	Molecular Insights into Arctic Soil Organic Matter Degradation under Warming. <i>Environmental Science &amp; Technology</i> , 2018, 52, 4555-4564.	10.0	74
16	Impacts of temperature and soil characteristics on methane production and oxidation in Arctic tundra. <i>Biogeosciences</i> , 2018, 15, 6621-6635.	3.3	33
17	Improved ZnS nanoparticle properties through sequential NanoFermentation. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 8329-8339.	3.6	2
18	Transport of perfluorocarbon tracers in the Cranfield Geological Carbon Sequestration Project. , 2018, 8, 650-671.		11

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19	Iron-Dependent Enzyme Catalyzes the Initial Step in Biodegradation of <i>N</i> -Nitroglycine by <i>Variovorax</i> sp. Strain JS1663. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	11
20	Influence of iron redox cycling on organo-mineral associations in Arctic tundra soil. <i>Geochimica Et Cosmochimica Acta</i> , 2017, 207, 210-231.	3.9	94
21	UV-activated ZnO films on a flexible substrate for room temperature O <sub>2</sub> and H <sub>2</sub> O sensing. <i>Scientific Reports</i> , 2017, 7, 6053.	3.3	61
22	Mathematical Modelling of Arctic Polygonal Tundra with <i>Ecosys</i> : 1. Microtopography Determines How Active Layer Depths Respond to Changes in Temperature and Precipitation. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2017, 122, 3161-3173.	3.0	38
23	Microbial Community and Functional Gene Changes in Arctic Tundra Soils in a Microcosm Warming Experiment. <i>Frontiers in Microbiology</i> , 2017, 8, 1741.	3.5	26
24	Biogeochemical modeling of CO <sub>2</sub> and CH <sub>4</sub> production in anoxic Arctic soil microcosms. <i>Biogeosciences</i> , 2016, 13, 5021-5041.	3.3	27
25	Reviews and syntheses: Four decades of modeling methane cycling in terrestrial ecosystems. <i>Biogeosciences</i> , 2016, 13, 3735-3755.	3.3	102
26	Multi-spectral Infrared Computed Tomography. <i>IS&amp;T International Symposium on Electronic Imaging</i> , 2016, 28, 1-5.	0.4	1
27	Draft Genome Sequence of <i>Streptomyces vitaminophilus</i> ATCC 31673, a Producer of Pyrrolomycin Antibiotics, Some of Which Contain a Nitro Group. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
28	Manufacturing demonstration of microbially mediated zinc sulfide nanoparticles in pilot-plant scale reactors. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 7921-7931.	3.6	32
29	Simulating the Cranfield geological carbon sequestration project with high-resolution static models and an accurate equation of state. <i>International Journal of Greenhouse Gas Control</i> , 2016, 54, 282-296.	4.6	72
30	Warming increases methylmercury production in an Arctic soil. <i>Environmental Pollution</i> , 2016, 214, 504-509.	7.5	60
31	Potential carbon emissions dominated by carbon dioxide from thawed permafrost soils. <i>Nature Climate Change</i> , 2016, 6, 950-953.	18.8	288
32	Active layer hydrology in an arctic tundra ecosystem: quantifying water sources and cycling using water stable isotopes. <i>Hydrological Processes</i> , 2016, 30, 4972-4986.	2.6	68
33	Effects of warming on the degradation and production of low-molecular-weight labile organic carbon in an Arctic tundra soil. <i>Soil Biology and Biochemistry</i> , 2016, 95, 202-211.	8.8	57
34	Surface reflectance degradation by microbial communities. <i>Journal of Building Physics</i> , 2016, 40, 263-277.	2.4	3
35	Pathways of anaerobic organic matter decomposition in tundra soils from Barrow, Alaska. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2015, 120, 2345-2359.	3.0	41
36	A microbial functional group-based module for simulating methane production and consumption: Application to an incubated permafrost soil. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2015, 120, 1315-1333.	3.0	56

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37	Geochemical drivers of organic matter decomposition in arctic tundra soils. <i>Biogeochemistry</i> , 2015, 126, 397-414.	3.5	53
38	Microtopographic and depth controls on active layer chemistry in Arctic polygonal ground. <i>Geophysical Research Letters</i> , 2015, 42, 1808-1817.	4.0	44
39	Isotopic identification of soil and permafrost nitrate sources in an Arctic tundra ecosystem. <i>Journal of Geophysical Research G: Biogeosciences</i> , 2015, 120, 1000-1017.	3.0	22
40	Stoichiometry and temperature sensitivity of methanogenesis and $\text{CO}_2$ production from saturated polygonal tundra in Barrow, Alaska. <i>Global Change Biology</i> , 2015, 21, 722-737.	9.5	68
41	Size tunable elemental copper nanoparticles: extracellular synthesis by thermoanaerobic bacteria and capping molecules. <i>Journal of Materials Chemistry C</i> , 2015, 3, 644-650.	5.5	39
42	<i>In situ</i> capping for size control of monochalcogenide (ZnS, CdS and SnS) nanocrystals produced by anaerobic metal-reducing bacteria. <i>Nanotechnology</i> , 2015, 26, 325602.	2.6	13
43	Direct determination of protonation states and visualization of hydrogen bonding in a glycoside hydrolase with neutron crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12384-12389.	7.1	35
44	Indexing Permafrost Soil Organic Matter Degradation Using High-Resolution Mass Spectrometry. <i>PLoS ONE</i> , 2015, 10, e0130557.	2.5	78
45	L-Arabinose Binding, Isomerization, and Epimerization by D-Xylose Isomerase: X-Ray/Neutron Crystallographic and Molecular Simulation Study. <i>Structure</i> , 2014, 22, 1287-1300.	3.3	22
46	Engineering acidic <i>Streptomyces rubiginosus</i> D-xylose isomerase by rational enzyme design. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 59-64.	2.1	19
47	Improvement of cellulose catabolism in <i>Clostridium cellulolyticum</i> by sporulation abolishment and carbon alleviation. <i>Biotechnology for Biofuels</i> , 2014, 7, 25.	6.2	25
48	X-ray crystallographic studies of family 11 xylanase Michaelis and product complexes: implications for the catalytic mechanism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 11-23.	2.5	34
49	Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. <i>Biology Direct</i> , 2013, 8, 9.	4.6	102
50	Nitrogen and sulfur requirements for <i>Clostridium thermocellum</i> and <i>Caldicellulosiruptor bescii</i> on cellulosic substrates in minimal nutrient media. <i>Bioresource Technology</i> , 2013, 130, 125-135.	9.6	33
51	Heterologous expression, purification, crystallization and preliminary X-ray analysis of <i>Trichoderma reesei</i> xylanase II and four variants. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 320-323.	0.7	2
52	Microbes in thawing permafrost: the unknown variable in the climate change equation. <i>ISME Journal</i> , 2012, 6, 709-712.	9.8	153
53	Combined inactivation of the <i>Clostridium cellulolyticum</i> lactate and malate dehydrogenase genes substantially increases ethanol yield from cellulose and switchgrass fermentations. <i>Biotechnology for Biofuels</i> , 2012, 5, 2.	6.2	125
54	Label-free Quantitative Proteomics for the Extremely Thermophilic Bacterium <i>Caldicellulosiruptor obsidiansis</i> Reveal Distinct Abundance Patterns upon Growth on Cellobiose, Crystalline Cellulose, and Switchgrass. <i>Journal of Proteome Research</i> , 2011, 10, 5302-5314.	3.7	33

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55	Use of Label-Free Quantitative Proteomics To Distinguish the Secreted Cellulolytic Systems of <i>Caldicellulosiruptor bescii</i> and <i>Caldicellulosiruptor obsidiansis</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 4042-4054.	3.1	71
56	2-Oxoacid Metabolism in Methanogenic CoM and CoB Biosynthesis. <i>Methods in Enzymology</i> , 2011, 494, 301-326.	1.0	10
57	A new role for coenzyme F <sub>420</sub> in aflatoxin reduction by soil mycobacteria. <i>Molecular Microbiology</i> , 2010, 78, 533-536.	2.5	9
58	Complete Genome Sequence of the Cellulolytic Thermophile <i>Caldicellulosiruptor obsidiansis</i> OB47. <i>Journal of Bacteriology</i> , 2010, 192, 6099-6100.	2.2	39
59	Substrate Specificity Determinants of the Methanogen Hemoacnitase Enzyme: Structure and Function of the Small Subunit. <i>Biochemistry</i> , 2010, 49, 2687-2696.	2.5	18
60	Archaeal ApbC/Nbp35 Homologs Function as Iron-Sulfur Cluster Carrier Proteins. <i>Journal of Bacteriology</i> , 2009, 191, 1490-1497.	2.2	52
61	Transcriptional Regulation of the <i>Escherichia coli</i> Gene <i>rraB</i> , Encoding a Protein Inhibitor of RNase E. <i>Journal of Bacteriology</i> , 2009, 191, 6665-6674.	2.2	12
62	Independent inactivation of arginine decarboxylase genes by nonsense and missense mutations led to pseudogene formation in <i>Chlamydia trachomatis</i> serovar L2 and D strains. <i>BMC Evolutionary Biology</i> , 2009, 9, 166.	3.2	13
63	Convergent evolution of coenzyme M biosynthesis in the Methanosarcinales: cysteate synthase evolved from an ancestral threonine synthase. <i>Biochemical Journal</i> , 2009, 424, 467-478.	3.7	43
64	Enzymatic analysis of uridine diphosphate N-acetyl-d -glucosamine. <i>Analytical Biochemistry</i> , 2008, 381, 94-100.	2.4	27
65	Methanogens with pseudomurein use diaminopimelate aminotransferase in lysine biosynthesis. <i>FEBS Letters</i> , 2008, 582, 1369-1374.	2.8	9
66	Crenarchaeal Arginine Decarboxylase Evolved from an S-Adenosylmethionine Decarboxylase Enzyme. <i>Journal of Biological Chemistry</i> , 2008, 283, 25829-25838.	3.4	42
67	Acetamido Sugar Biosynthesis in the Euryarchaea. <i>Journal of Bacteriology</i> , 2008, 190, 2987-2996.	2.2	46
68	A korarchaeal genome reveals insights into the evolution of the Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8102-8107.	7.1	253
69	Outer and Inner Membrane Proteins Compose an Arginine-Agmatine Exchange System in <i>Chlamydomonas pneumoniae</i> . <i>Journal of Bacteriology</i> , 2008, 190, 7431-7440.	2.2	11
70	Methanogen Hemoacnitase Catalyzes Both Hydrolyase Reactions in Coenzyme B Biosynthesis. <i>Journal of Biological Chemistry</i> , 2008, 283, 28888-28896.	3.4	31
71	Identification and Characterization of Archaeal and Fungal tRNA Methyltransferases. <i>Methods in Enzymology</i> , 2007, 425, 185-209.	1.0	1
72	Characterization of an Acid-Dependent Arginine Decarboxylase Enzyme from <i>Chlamydomonas pneumoniae</i> . <i>Journal of Bacteriology</i> , 2007, 189, 7376-7383.	2.2	16

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73	Yeast Mitochondrial Initiator tRNA Is Methylated at Guanosine 37 by the Trm5-encoded tRNA (Guanine-N1-)-methyltransferase. <i>Journal of Biological Chemistry</i> , 2007, 282, 27744-27753.	3.4	52
74	Biosynthesis of Phosphoserine in the Methanococcales. <i>Journal of Bacteriology</i> , 2007, 189, 575-582.	2.2	43
75	Enzymology and Evolution of the Pyruvate Pathway to 2-Oxobutyrate in <i>Methanocaldococcus jannaschii</i> . <i>Journal of Bacteriology</i> , 2007, 189, 4391-4400.	2.2	55
76	Acetyl-coenzyme A Synthases and Nickel-Containing Carbon Monoxide Dehydrogenases. , 2007, , 357-415.		13
77	Identification and characterization of a $\gamma$ -tyrosine decarboxylase in. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2005, 1722, 175-182.	2.4	36
78	Complete Genome Sequence of the Genetically Tractable Hydrogenotrophic Methanogen <i>Methanococcus maripaludis</i> . <i>Journal of Bacteriology</i> , 2004, 186, 6956-6969.	2.2	208
79	Identification of the 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase required for coenzyme F 420 biosynthesis. <i>Archives of Microbiology</i> , 2003, 180, 455-464.	2.2	66
80	Pyruvoyl-Dependent Arginine Decarboxylase from <i>Methanococcus jannaschii</i> . <i>Structure</i> , 2003, 11, 285-294.	3.3	34
81	Reductive dehalogenation of monobromobimane by tris(2-carboxyethyl)phosphine. <i>Analytical Biochemistry</i> , 2003, 318, 325-328.	2.4	11
82	The <i>Methanococcus jannaschii</i> CTP Deaminase Is a Bifunctional Deaminase and Diphosphatase. <i>Journal of Biological Chemistry</i> , 2003, 278, 11100-11106.	3.4	26
83	Glutathione synthetase homologs encode $\Delta$ -L-glutamate ligases for methanogenic coenzyme F420 and tetrahydrosarcinapterin biosyntheses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 9785-9790.	7.1	52
84	Phosphoprotein with Phosphoglycerate Mutase Activity from the Archaeon <i>Sulfolobus solfataricus</i> . <i>Journal of Bacteriology</i> , 2003, 185, 2112-2121.	2.2	24
85	The genome of <i>Nanoarchaeum equitans</i> : Insights into early archaeal evolution and derived parasitism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12984-12988.	7.1	488
86	The Structural Determination of Phosphosulfolactate Synthase from <i>Methanococcus jannaschii</i> at 1.7-Å... Resolution. <i>Journal of Biological Chemistry</i> , 2003, 278, 45858-45863.	3.4	16
87	Transfer RNA-dependent amino acid biosynthesis: An essential route to asparagine formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2678-2683.	7.1	91
88	Identification of Coenzyme M Biosynthetic Phosphosulfolactate Synthase. <i>Journal of Biological Chemistry</i> , 2002, 277, 13421-13429.	3.4	79
89	<i>Methanococcus jannaschii</i> Uses a Pyruvoyl-dependent Arginine Decarboxylase in Polyamine Biosynthesis. <i>Journal of Biological Chemistry</i> , 2002, 277, 23500-23507.	3.4	46
90	Orthologs of a novel archaeal and of the bacterial peptidyl-tRNA hydrolase are nonessential in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16707-16712.	7.1	64

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91	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	5.5	573
92	Elucidation of methanogenic coenzyme biosyntheses: from spectroscopy to genomics. <i>Natural Product Reports</i> , 2002, 19, 133-147.	10.3	109
93	A Member of a New Class of GTP Cyclohydrolases Produces Formylaminopyrimidine Nucleotide Monophosphates. <i>Biochemistry</i> , 2002, 41, 15074-15084.	2.5	40
94	A divergent archaeal member of the alkaline phosphatase binuclear metalloenzyme superfamily has phosphoglycerate mutase activity. <i>FEBS Letters</i> , 2002, 517, 190-194.	2.8	27
95	Identification of coenzyme M biosynthetic 2-phosphosulfolactate phosphatase. <i>FEBS Journal</i> , 2001, 268, 5176-5188.	0.2	32
96	Transfer Region of a <i>Bacteroides</i> Conjugative Transposon, CTnDOT. <i>Plasmid</i> , 2001, 45, 41-51.	1.4	39
97	Genome of <i>Methanocaldococcus (methanococcus) jannaschii</i> . <i>Methods in Enzymology</i> , 2001, 330, 40-123.	1.0	18
98	Post-transcriptional modification in archaeal tRNAs: identities and phylogenetic relations of nucleotides from mesophilic and hyperthermophilic <i>Methanococcales</i> . <i>Nucleic Acids Research</i> , 2001, 29, 4699-4706.	14.5	114
99	A dual-specificity aminoacyl-tRNA synthetase in the deep-rooted eukaryote <i>Giardia lamblia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 12997-13002.	7.1	43
100	Identification of a Highly Diverged Class of S-Adenosylmethionine Synthetases in the Archaea. <i>Journal of Biological Chemistry</i> , 2000, 275, 4055-4059.	3.4	47
101	S-Adenosylmethionine Decarboxylase from the Archaeon <i>Methanococcus jannaschii</i> : Identification of a Novel Family of Pyruvoyl Enzymes. <i>Journal of Bacteriology</i> , 2000, 182, 6667-6672.	2.2	25
102	An archaeal genomic signature. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 3304-3308.	7.1	74
103	Cysteinylyl-tRNA formation: the last puzzle of aminoacyl-tRNA synthesis. <i>FEBS Letters</i> , 1999, 462, 302-306.	2.8	27
104	The complete genome of the hyperthermophilic bacterium <i>Aquifex aeolicus</i> . <i>Nature</i> , 1998, 392, 353-358.	27.8	1,120
105	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon <i>Archaeoglobus fulgidus</i> . <i>Nature</i> , 1997, 390, 364-370.	27.8	1,460