

# Brian P Hedlund

## List of Publications by Citations

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121  
papers

5,108  
citations

30  
h-index

71  
g-index

152  
ext. papers

7,725  
ext. citations

7.3  
avg, IF

5.04  
L-index

#	Paper	IF	Citations
121	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , <b>2013</b> , 499, 431-7	50.4	1484
120	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 725-731	44.5	648
119	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> , <b>2008</b> , 105, 8102-7	11.5	214
118	Global occurrence of archaeal amoA genes in terrestrial hot springs. <i>Applied and Environmental Microbiology</i> , <b>2008</b> , 74, 6417-26	4.8	156
117	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. <i>Nature Communications</i> , <b>2013</b> , 4, 1854	17.4	143
116	A comprehensive census of microbial diversity in hot springs of Tengchong, Yunnan Province China using 16S rRNA gene pyrosequencing. <i>PLoS ONE</i> , <b>2013</b> , 8, e53350	3.7	140
115	Microbiology and geochemistry of great boiling and mud hot springs in the United States Great Basin. <i>Extremophiles</i> , <b>2009</b> , 13, 447-59	3	131
114	Verrucomicrobia div. nov., a new division of the bacteria containing three new species of Prostheco bacter. <i>Antonie Van Leeuwenhoek</i> , <b>1997</b> , 72, 29-38	2.1	127
113	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 499-509	44.5	120
112	Phylogeny and physiology of candidate phylum 'Atribacteria' (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , <b>2016</b> , 10, 273-86	11.9	118
111	Sediment microbial communities in Great Boiling Spring are controlled by temperature and distinct from water communities. <i>ISME Journal</i> , <b>2013</b> , 7, 718-29	11.9	106
110	Moderately thermophilic magnetotactic bacteria from hot springs in Nevada. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 3740-3	4.8	103
109	Impact of single-cell genomics and metagenomics on the emerging view of extremophile "microbial dark matter". <i>Extremophiles</i> , <b>2014</b> , 18, 865-75	3	96
108	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , <b>2016</b> , 7, 10476	17.4	90
107	Ammonia oxidation, denitrification and dissimilatory nitrate reduction to ammonium in two US Great Basin hot springs with abundant ammonia-oxidizing archaea. <i>Environmental Microbiology</i> , <b>2011</b> , 13, 2371-86	5.2	83
106	Evaluation of the Antimicrobial Activity of Endophytic Bacterial Populations From Chinese Traditional Medicinal Plant Licorice and Characterization of the Bioactive Secondary Metabolites Produced by Against. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 924	5.7	68
105	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , <b>2020</b> , 5, 987-994	26.6	64

104	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <i>Nature Communications</i> , <b>2018</b> , 9, 2832	17.4	50
103	Seasonal patterns in microbial communities inhabiting the hot springs of Tengchong, Yunnan Province, China. <i>Environmental Microbiology</i> , <b>2014</b> , 16, 1579-91	5.2	44
102	A review of the microbiology of the Rehai geothermal field in Tengchong, Yunnan Province, China. <i>Geoscience Frontiers</i> , <b>2012</b> , 3, 273-288	6	43
101	Insights into ecological role of a new deltaproteobacterial order Candidatus Acidulodesulfobacterales by metagenomics and metatranscriptomics. <i>ISME Journal</i> , <b>2019</b> , 13, 2044-2057	11.9	36
100	<i>Thermoflexus hugenholtzii</i> gen. nov., sp. nov., a thermophilic, microaerophilic, filamentous bacterium representing a novel class in the Chloroflexi, Thermoflexia classis nov., and description of Thermoflexaceae fam. nov. and Thermoflexales ord. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2014</b> , 64, 2119-2127	2.2	36
99	Exploring microbial dark matter to resolve the deep archaeal ancestry of eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2015</b> , 370, 20140328	5.8	35
98	Cultivation and characterization of thermophilic Nitrospira species from geothermal springs in the US Great Basin, China, and Armenia. <i>FEMS Microbiology Ecology</i> , <b>2013</b> , 85, 283-92	4.3	35
97	Potential role of <i>Thermus thermophilus</i> and <i>T. oshimai</i> in high rates of nitrous oxide (N <sub>2</sub> O) production in ~80 °C hot springs in the US Great Basin. <i>Geobiology</i> , <b>2011</b> , 9, 471-80	4.3	34
96	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. <i>Nature Communications</i> , <b>2019</b> , 10, 4574	17.4	33
95	Pyrosequencing reveals high-temperature cellulolytic microbial consortia in Great Boiling Spring after in situ lignocellulose enrichment. <i>PLoS ONE</i> , <b>2013</b> , 8, e59927	3.7	33
94	Uncultivated thermophiles: current status and spotlight on 'Aigarchaeota'. <i>Current Opinion in Microbiology</i> , <b>2015</b> , 25, 136-45	7.9	32
93	Bacterial succession within an ephemeral hypereutrophic Mojave Desert playa Lake. <i>Microbial Ecology</i> , <b>2009</b> , 57, 307-20	4.4	32
92	An integrated study reveals diverse methanogens, Thaumarchaeota, and yet-uncultivated archaeal lineages in Armenian hot springs. <i>Antonie Van Leeuwenhoek</i> , <b>2013</b> , 104, 71-82	2.1	31
91	Beneficial Endophytic Bacterial Populations Associated With Medicinal Plant Alleviate Salt Stress and Confer Resistance to. <i>Frontiers in Plant Science</i> , <b>2020</b> , 11, 47	6.2	30
90	Korarchaeota diversity, biogeography, and abundance in Yellowstone and Great Basin hot springs and ecological niche modeling based on machine learning. <i>PLoS ONE</i> , <b>2012</b> , 7, e35964	3.7	29
89	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , <b>2020</b> , 14, 659-675	11.9	29
88	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1848	5.7	29
87	Measuring nitrification, denitrification, and related biomarkers in terrestrial geothermal ecosystems. <i>Methods in Enzymology</i> , <b>2011</b> , 486, 171-203	1.7	27

86	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. <i>Environmental Microbiology</i> , <b>2018</b> , 20, 734-754	5.2	27
85	Association between degradation of pharmaceuticals and endocrine-disrupting compounds and microbial communities along a treated wastewater effluent gradient in Lake Mead. <i>Science of the Total Environment</i> , <b>2018</b> , 622-623, 1640-1648	10.2	26
84	Interdomain conjugal transfer of DNA from bacteria to archaea. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 5644-7	4.8	26
83	<i>Kallotenua papyrolyticum</i> gen. nov., sp. nov., a cellulolytic and filamentous thermophile that represents a novel lineage (Kallotenuales ord. nov., Kallotenuaceae fam. nov.) within the class Chloroflexia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2013</b> , 63, 4675-4682	2.2	25
82	Synergistic plant-microbe interactions between endophytic bacterial communities and the medicinal plant <i>Glycyrrhiza uralensis</i> F. <i>Antonie Van Leeuwenhoek</i> , <b>2018</b> , 111, 1735-1748	2.1	24
81	Lateral gene transfer of family A DNA polymerases between thermophilic viruses, aquificae, and apicomplexa. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1653-64	8.3	24
80	All ANIs are not created equal: implications for prokaryotic species boundaries and integration of ANIs into polyphasic taxonomy. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2020</b> , 70, 2937-2948	2.2	24
79	<i>Thermus oshimai</i> JL-2 and <i>T. thermophilus</i> JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. <i>Standards in Genomic Sciences</i> , <b>2013</b> , 7, 449-68		22
78	Distribution of ether lipids and composition of the archaeal community in terrestrial geothermal springs: impact of environmental variables. <i>Environmental Microbiology</i> , <b>2015</b> , 17, 1600-14	5.2	20
77	Isolation of diverse members of the Aquificales from geothermal springs in Tengchong, China. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 157	5.7	20
76	The changing landscape of microbial biodiversity exploration and its implications for systematics. <i>Systematic and Applied Microbiology</i> , <b>2015</b> , 38, 231-6	4.2	20
75	A High-Fat/High-Protein, Atkins-Type Diet Exacerbates () Infection in Mice, whereas a High-Carbohydrate Diet Protects. <i>MSystems</i> , <b>2020</b> , 5,	7.6	20
74	Molecular Phylogeny of Uncultivated Crenarchaeota in Great Basin Hot Springs of Moderately Elevated Temperature. <i>Geomicrobiology Journal</i> , <b>2007</b> , 24, 535-542	2.5	20
73	In situ production of branched glycerol dialkyl glycerol tetraethers in a great basin hot spring (USA). <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 181	5.7	17
72	Microbial dark matter coming to light: challenges and opportunities. <i>National Science Review</i> , <b>2021</b> , 8, nwaa280	10.8	17
71	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 992-1003	4.8	16
70	Calculation of total free energy yield as an alternative approach for predicting the importance of potential chemolithotrophic reactions in geothermal springs. <i>FEMS Microbiology Ecology</i> , <b>2012</b> , 81, 446-54	4.3	16
69	Whole Genome Sequencing of <i>Thermus oshimai</i> JL-2 and <i>Thermus thermophilus</i> JL-18, Incomplete Denitrifiers from the United States Great Basin. <i>Genome Announcements</i> , <b>2013</b> , 1,		15

68	Stereo-specific glucose consumption may be used to distinguish between chemical and biological reactivity on Mars: a preliminary test on Earth. <i>Astrobiology</i> , <b>2009</b> , 9, 443-6	3.7	14
67	Distribution and Diversity of Aerobic Carbon Monoxide-Oxidizing Bacteria in Geothermal Springs of China, the Philippines, and the United States. <i>Geomicrobiology Journal</i> , <b>2015</b> , 32, 903-913	2.5	13
66	Effect of the Synthetic Bile Salt Analog CamSA on the Hamster Model of Clostridium difficile Infection. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2018</b> , 62,	5.9	12
65	Wide distribution of autochthonous branched glycerol dialkyl glycerol tetraethers (bGDGTs) in U.S. Great Basin hot springs. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 222	5.7	11
64	Insight into the function and evolution of the Wood-Ljungdahl pathway in Actinobacteria. <i>ISME Journal</i> , <b>2021</b> , 15, 3005-3018	11.9	11
63	Production of branched tetraether lipids in Tibetan hot springs: A possible linkage to nitrite reduction by thermotolerant or thermophilic bacteria?. <i>Chemical Geology</i> , <b>2014</b> , 386, 209-217	4.2	10
62	Reversible Reduction of Estrone to 17 $\beta$ Estradiol by , , and Isolates from the Las Vegas Wash. <i>Journal of Environmental Quality</i> , <b>2017</b> , 46, 281-287	3.4	9
61	Community microrespirometry and molecular analyses reveal a diverse energy economy in Great Boiling Spring and Sandy's Spring West in the U.S. Great Basin. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 3306-10	4.8	9
60	Microbiology and geochemistry of smith creek and grass valley hot springs: Emerging evidence for wide distribution of novel thermophilic lineages in the US Great Basin. <i>Journal of Earth Science (Wuhan, China)</i> , <b>2010</b> , 21, 315-318	2.2	9
59	Thermocrinis jamiesonii sp. nov., a thiosulfate-oxidizing, autotrophic thermophile isolated from a geothermal spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , <b>2015</b> , 65, 4769-4775	2.2	8
58	Thermus sediminis sp. nov., a thiosulfate-oxidizing and arsenate-reducing organism isolated from Little Hot Creek in the Long Valley Caldera, California. <i>Extremophiles</i> , <b>2018</b> , 22, 983-991	3	8
57	The gut microbiome and its potential role in paradoxical anaerobism in pupfishes of the Mojave Desert. <i>Animal Microbiome</i> , <b>2020</b> , 2, 20	4.1	7
56	Geomicrobiological Changes in Two Ephemeral Desert Playa Lakes in the Western United States. <i>Geomicrobiology Journal</i> , <b>2008</b> , 25, 250-259	2.5	6
55	High-quality draft genome sequence of the Thermus amyloliquefaciens type strain YIM 77409(T) with an incomplete denitrification pathway. <i>Standards in Genomic Sciences</i> , <b>2016</b> , 11, 20		5
54	The distribution and abundance of archaeal tetraether lipids in U.S. Great Basin hot springs. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 247	5.7	5
53	Diversity of Archaea in Terrestrial Hot Springs and Role in Ammonia Oxidation <b>2011</b> , 381-394		5
52	Microbiome Shifts Associated With the Introduction of Wild Atlantic Horseshoe Crabs ( ) Into a Touch-Tank Exhibit. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1398	5.7	5
51	Genomic Comparison of Two Family-Level Groups of the Uncultivated NAG1 Archaeal Lineage from Chemically and Geographically Disparate Hot Springs. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 2082	5.7	4

50	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <i>ISME Communications</i> , <b>2021</b> , 1,		4
49	Genomic Insights of " Nitrosocaldaceae" Based on Nine New Metagenome-Assembled Genomes, Including " Nitrosothermus" Gen Nov. and Two New Species of " Nitrosocaldus". <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 608832	5-7	4
48	Comparative Genomics Reveals Thermal Adaptation and a High Metabolic Diversity in " Bathyarchaeia". <i>MSystems</i> , <b>2021</b> , 6, e0025221	7-6	4
47	Position-Specific Metabolic Probing and Metagenomics of Microbial Communities Reveal Conserved Central Carbon Metabolic Network Activities at High Temperatures. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 1427	5-7	3
46	Life in High-Temperature Environments <b>2015</b> , 4.3.4-1-4.3.4-15		3
45	High-Quality Draft Genome Sequence of <i>Kallotenue papyrolyticum</i> JKG1T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. <i>Genome Announcements</i> , <b>2015</b> , 3,		3
44	Ancestral absence of electron transport chains in Patescibacteria and DPANN		3
43	Impact of Terrestrial Input on Deep-Sea Benthic Archaeal Community Structure in South China Sea Sediments. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 572017	5-7	3
42	High-Quality Draft Genomes from <i>Thermus caliditerrae</i> YIM 77777 and <i>T. tengchongensis</i> YIM 77401, Isolates from Tengchong, China. <i>Genome Announcements</i> , <b>2016</b> , 4,		3
41	Hydrogeology of desert springs in the Panamint Range, California, USA: Geologic controls on the geochemical kinetics, flowpaths, and mean residence times of springs. <i>Hydrological Processes</i> , <b>2020</b> , 34, 2923-2948	3-3	2
40	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 632731	5-7	2
39	Diverse respiratory capacity among <i>Thermus</i> strains from US Great Basin hot springs. <i>Extremophiles</i> , <b>2020</b> , 24, 71-80	3	2
38	Diversity of Root Nodule-Associated Bacteria of Diverse Legumes Along an Elevation Gradient in the Kunlun Mountains, China. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 633141	5-7	2
37	Candidatus Nitrosocaldaceae <b>2017</b> , 1-2		1
36	Candidatus Nitrosocaldus <b>2017</b> , 1-5		1
35	Akkermansiaceae fam. nov. <b>2015</b> , 1-1		1
34	<i>Coraliomargarita</i> <b>2015</b> , 1-4		1
33	<i>Rubritalea</i> <b>2015</b> , 1-7		1

32	Opitutae <b>2015</b> , 1-4			1
31	Verrucomicrobiae <b>2015</b> , 1-5			1
30	Addressing Questions on Life in Terrestrial Geothermal Systems. <i>Eos</i> , <b>2013</b> , 94, 325-325	1.5		1
29	Identification of the Gut Microbiome and its Role in Paradoxical Anaerobism in Desert Pupfish. <i>FASEB Journal</i> , <b>2020</b> , 34, 1-1	0.9		1
28	Diversity and Distribution of a Novel Genus of Hyperthermophilic Aquificae Viruses Encoding a Proof-reading Family-A DNA Polymerase			1
27	Diversity and Distribution of a Novel Genus of Hyperthermophilic Viruses Encoding a Proof-Reading Family-A DNA Polymerase. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 583361	5.7		1
26	Deciphering Symbiotic Interactions of "Aenigmarchaeota" with Inferred Horizontal Gene Transfers and Co-occurrence Networks. <i>MSystems</i> , <b>2021</b> , 6, e0060621	7.6		1
25	Candidatus Nitrosocaldales <b>2017</b> , 1-2			0
24	An aniline-substituted bile salt analog protects both mice and hamsters from multiple strains. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , AAC0143521	5.9		0
23	Chthoniobacterales ord. nov <b>2015</b> , 1-1			
22	Lentisphaeraceae fam. nov. <b>2015</b> , 1-1			
21	Victivallaceae fam. nov. <b>2015</b> , 1-1			
20	Opitutaceae <b>2015</b> , 1-1			
19	Rubritaleaceae fam. nov. <b>2015</b> , 1-1			
18	Verrucomicrobiaceae <b>2015</b> , 1-2			
17	Alterococcus <b>2015</b> , 1-3			
16	Cerasicoccus <b>2015</b> , 1-4			
15	Pelagicoccus <b>2015</b> , 1-7			

14 Candidatus Xiphinematobacter **2015**, 1-5

13 Opitutales **2015**, 1-1

12 Puniceococcales **2015**, 1-1

11 Verrucomicrobiales **2015**, 1-1

10 Verrucomicrobia phyl. nov. **2015**, 1-2

9 Puniceococcaceae **2015**, 1-2

8 Lentisphaerae **2015**, 1-2

7 Prostheco bacter **2015**, 1-5

6 Lentisphaeria class. nov. **2015**, 1-1

5 Spartobacteria class. nov. **2015**, 1-4

4 Chthoniobacteraceae fam. nov. **2015**, 1-1

3 Response to Dr. Levin's Comment. *Astrobiology*, **2009**, 9, 505-505

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2 Lentisphaerales 1-1

1 Victivallales 1-1