

# Brian P Hedlund

## List of Publications by Year in descending order

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109  
papers

8,976  
citations

94433

37  
h-index

48315

88  
g-index

153  
all docs

153  
docs citations

153  
times ranked

8900  
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	27.8	2,239
2	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
3	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
4	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
5	A Comprehensive Census of Microbial Diversity in Hot Springs of Tengchong, Yunnan Province China Using 16S rRNA Gene Pyrosequencing. <i>PLoS ONE</i> , 2013, 8, e53350.	2.5	216
6	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. <i>Nature Communications</i> , 2013, 4, 1854.	12.8	199
7	Global Occurrence of Archaeal <i>amoA</i> Genes in Terrestrial Hot Springs. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6417-6426.	3.1	189
8	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016, 7, 10476.	12.8	189
9	Sediment microbial communities in Great Boiling Spring are controlled by temperature and distinct from water communities. <i>ISME Journal</i> , 2013, 7, 718-729.	9.8	182
10	Verrucomicrobia div. nov., a new division of the bacteria containing three new species of Prosthecobacter. <i>Antonie Van Leeuwenhoek</i> , 1997, 72, 29-38.	1.7	171
11	Phylogeny and physiology of candidate phylum "Atribacteria" (OP9/S1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	9.8	166
12	Microbiology and geochemistry of great boiling and mud hot springs in the United States Great Basin. <i>Extremophiles</i> , 2009, 13, 447-459.	2.3	157
13	Evaluation of the Antimicrobial Activity of Endophytic Bacterial Populations From Chinese Traditional Medicinal Plant Licorice and Characterization of the Bioactive Secondary Metabolites Produced by <i>Bacillus atrophaeus</i> Against <i>Verticillium dahliae</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 924.	3.5	150
14	Impact of single-cell genomics and metagenomics on the emerging view of extremophile "microbial dark matter". <i>Extremophiles</i> , 2014, 18, 865-875.	2.3	133
15	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> , 2011, 13, 2371-2386.	3.8	132
16	Moderately Thermophilic Magnetotactic Bacteria from Hot Springs in Nevada. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3740-3743.	3.1	127
17	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	13.3	115
18	Insights into ecological role of a new deltaproteobacterial order <i>Candidatus</i> Acidulodesulfobacterales by metagenomics and metatranscriptomics. <i>ISME Journal</i> , 2019, 13, 2044-2057.	9.8	112

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19	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <i>Nature Communications</i> , 2018, 9, 2832.	12.8	108
20	<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> , 2014, 64, 2119-2127.	1.7	90
21	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. <i>Nature Communications</i> , 2019, 10, 4574.	12.8	90
22	Microbial dark matter coming to light: challenges and opportunities. <i>National Science Review</i> , 2021, 8, nwaa280.	9.5	86
23	Uncultivated thermophiles: current status and spotlight on <i>Aigarchaeota</i> <sup>TM</sup> . <i>Current Opinion in Microbiology</i> , 2015, 25, 136-145.	5.1	70
24	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	9.8	69
25	Beneficial Endophytic Bacterial Populations Associated With Medicinal Plant <i>Thymus vulgaris</i> Alleviate Salt Stress and Confer Resistance to <i>Fusarium oxysporum</i> . <i>Frontiers in Plant Science</i> , 2020, 11, 47.	3.6	69
26	Cultivation and characterization of thermophilic <i>Nitrospira</i> species from geothermal springs in the US Great Basin, China, and Armenia. <i>FEMS Microbiology Ecology</i> , 2013, 85, 283-292.	2.7	64
27	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , 2020, 11, 1848.	3.5	62
28	A review of the microbiology of the Rehai geothermal field in Tengchong, Yunnan Province, China. <i>Geoscience Frontiers</i> , 2012, 3, 273-288.	8.4	59
29	Seasonal patterns in microbial communities inhabiting the hot springs of Tengchong, Yunnan Province, China. <i>Environmental Microbiology</i> , 2014, 16, 1579-1591.	3.8	57
30	Synergistic plant-microbe interactions between endophytic bacterial communities and the medicinal plant <i>Glycyrrhiza uralensis</i> F.. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 1735-1748.	1.7	55
31	Insight into the function and evolution of the Wood-Ljungdahl pathway in Actinobacteria. <i>ISME Journal</i> , 2021, 15, 3005-3018.	9.8	55
32	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. <i>Environmental Microbiology</i> , 2018, 20, 734-754.	3.8	53
33	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> , 2020, 70, 2937-2948.	1.7	51
34	<i>Kallotenue 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> , 2013, 63, 4675-4682.	1.7	50
35	Korarchaeota Diversity, Biogeography, and Abundance in Yellowstone and Great Basin Hot Springs and Ecological Niche Modeling Based on Machine Learning. <i>PLoS ONE</i> , 2012, 7, e35964.	2.5	43
36	Potential role of <i>Thermus thermophilus</i> and <i>T.Âoshimai</i> in high rates of nitrous oxide (N <sub>2</sub> O) production in 1480Â°C hot springs in the US Great Basin. <i>Geobiology</i> , 2011, 9, 471-480.	2.4	42

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37	Measuring Nitrification, Denitrification, and Related Biomarkers in Terrestrial Geothermal Ecosystems. <i>Methods in Enzymology</i> , 2011, 486, 171-203.	1.0	42
38	Pyrosequencing Reveals High-Temperature Cellulolytic Microbial Consortia in Great Boiling Spring after In Situ Lignocellulose Enrichment. <i>PLoS ONE</i> , 2013, 8, e59927.	2.5	42
39	Exploring microbial dark matter to resolve the deep archaeal ancestry of eukaryotes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140328.	4.0	40
40	An integrated study reveals diverse methanogens, Thaumarchaeota, and yet-uncultivated archaeal lineages in Armenian hot springs. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 71-82.	1.7	38
41	Lateral Gene Transfer of Family A DNA Polymerases between Thermophilic Viruses, Aquificae, and Apicomplexa. <i>Molecular Biology and Evolution</i> , 2013, 30, 1653-1664.	8.9	36
42	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 992-1003.	3.1	36
43	A High-Fat/High-Protein, Atkins-Type Diet Exacerbates <i>Clostridioides</i> ( <i>Clostridium</i> ) <i>difficile</i> Infection in Mice, whereas a High-Carbohydrate Diet Protects. <i>MSystems</i> , 2020, 5, .	3.8	36
44	Bacterial Succession within an Ephemeral Hypereutrophic Mojave Desert Playa Lake. <i>Microbial Ecology</i> , 2009, 57, 307-320.	2.8	35
45	Interdomain Conjugal Transfer of DNA from Bacteria to Archaea. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5644-5647.	3.1	34
46	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> , 2012, 81, 446-454.	2.7	34
47	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> , 2018, 622-623, 1640-1648.	8.0	34
48	<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> , 2013, 7, 449-468.	1.5	31
49	Isolation of diverse members of the Aquificales from geothermal springs in Tengchong, China. <i>Frontiers in Microbiology</i> , 2015, 6, 157.	3.5	31
50	Distribution of ether lipids and composition of the archaeal community in terrestrial geothermal springs: impact of environmental variables. <i>Environmental Microbiology</i> , 2015, 17, 1600-1614.	3.8	29
51	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> , 2013, 79, 3306-3310.	3.1	28
52	The changing landscape of microbial biodiversity exploration and its implications for systematics. <i>Systematic and Applied Microbiology</i> , 2015, 38, 231-236.	2.8	26
53	Molecular Phylogeny of Uncultivated <i>Crenarchaeota</i> in Great Basin Hot Springs of Moderately Elevated Temperature. <i>Geomicrobiology Journal</i> , 2007, 24, 535-542.	2.0	23
54	Effect of the Synthetic Bile Salt Analog CamSA on the Hamster Model of <i>Clostridium difficile</i> Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	23

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55	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. ISME Communications, 2021, 1, .	4.2	23
56	Thermocrinis jamiesonii sp. nov., a thiosulfate-oxidizing, autotrophic thermophile isolated from a geothermal spring. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4769-4775.	1.7	23
57	In situ production of branched glycerol dialkyl glycerol tetraethers in a great basin hot spring (USA). Frontiers in Microbiology, 2013, 4, 181.	3.5	22
58	Thermus sediminis sp. nov., a thiosulfate-oxidizing and arsenate-reducing organism isolated from Little Hot Creek in the Long Valley Caldera, California. Extremophiles, 2018, 22, 983-991.	2.3	20
59	The gut microbiome and its potential role in paradoxical anaerobism in pupfishes of the Mojave Desert. Animal Microbiome, 2020, 2, 20.	3.8	20
60	Comparative Genomics Reveals Thermal Adaptation and a High Metabolic Diversity in <i>Candidatus</i> Bathyarchaeia. MSystems, 2021, 6, e0025221.	3.8	20
61	Whole Genome Sequencing of Thermus oshimai JL-2 and Thermus thermophilus JL-18, Incomplete Denitrifiers from the United States Great Basin. Genome Announcements, 2013, 1, .	0.8	19
62	Distribution and Diversity of Aerobic Carbon Monoxide-Oxidizing Bacteria in Geothermal Springs of China, the Philippines, and the United States. Geomicrobiology Journal, 2015, 32, 903-913.	2.0	19
63	Genomic Comparison of Two Family-Level Groups of the Uncultivated NAG1 Archaeal Lineage from Chemically and Geographically Disparate Hot Springs. Frontiers in Microbiology, 2017, 8, 2082.	3.5	19
64	Stereo-Specific Glucose Consumption May Be Used to Distinguish Between Chemical and Biological Reactivity on Mars: A Preliminary Test on Earth. Astrobiology, 2009, 9, 443-446.	3.0	16
65	An essential role for tungsten in the ecology and evolution of a previously uncultivated lineage of anaerobic, thermophilic Archaea. Nature Communications, 2022, 13, .	12.8	16
66	Compositional and Metabolic Responses of Autotrophic Microbial Community to Salinity in Lacustrine Environments. MSystems, 2022, 7, .	3.8	15
67	Diverse respiratory capacity among Thermus strains from US Great Basin hot springs. Extremophiles, 2020, 24, 71-80.	2.3	13
68	Genomic Insights of <i>Candidatus</i> Nitrosocaldaceae-Based on Nine New Metagenome-Assembled Genomes, Including <i>Candidatus</i> Nitrosothermus Gen Nov. and Two New Species of <i>Candidatus</i> Nitrosocaldus. Frontiers in Microbiology, 2020, 11, 608832.	3.5	13
69	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.	3.3	12
70	Position-Specific Metabolic Probing and Metagenomics of Microbial Communities Reveal Conserved Central Carbon Metabolic Network Activities at High Temperatures. Frontiers in Microbiology, 2019, 10, 1427.	3.5	12
71	Microbiome Shifts Associated With the Introduction of Wild Atlantic Horseshoe Crabs ( <i>Limulus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock	3.5	12
72	It is time for a new type of type to facilitate naming the microbial world. New Microbes and New Infections, 2022, 47, 100991.	1.6	12

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73	Wide distribution of autochthonous branched glycerol dialkyl glycerol tetraethers (bGDGTs) in U.S. Great Basin hot springs. <i>Frontiers in Microbiology</i> , 2013, 4, 222.	3.5	11
74	Reversible Reduction of Estrone to 17 $\beta$ -Estradiol by <i>Rhizobium</i> , <i>Sphingopyxis</i> , and <i>Pseudomonas</i> Isolates from the Las Vegas Wash. <i>Journal of Environmental Quality</i> , 2017, 46, 281-287.	2.0	11
75	Deciphering Symbiotic Interactions of <i>Candidatus</i> <i>Aenigmarchaeota</i> with Inferred Horizontal Gene Transfers and Co-occurrence Networks. <i>MSystems</i> , 2021, 6, e0060621.	3.8	11
76	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> , 2010, 21, 315-318.	3.2	9
77	Diversity of Root Nodule-Associated Bacteria of Diverse Legumes Along an Elevation Gradient in the Kunlun Mountains, China. <i>Frontiers in Microbiology</i> , 2021, 12, 633141.	3.5	9
78	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of <i>Thermoflexus hugenholtzii</i> and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , 2021, 12, 632731.	3.5	8
79	The distribution and abundance of archaeal tetraether lipids in U.S. Great Basin hot springs. <i>Frontiers in Microbiology</i> , 2013, 4, 247.	3.5	7
80	Life in High-Temperature Environments. , 0, , 4.3.4-1-4.3.4-15.		7
81	High-quality draft genome sequence of the <i>Thermus amyloliquefaciens</i> type strain YIM 77409T with an incomplete denitrification pathway. <i>Standards in Genomic Sciences</i> , 2016, 11, 20.	1.5	7
82	Diversity and Distribution of a Novel Genus of Hyperthermophilic Aquificae Viruses Encoding a Proof-Reading Family-A DNA Polymerase. <i>Frontiers in Microbiology</i> , 2020, 11, 583361.	3.5	7
83	Geomicrobiological Changes in Two Ephemeral Desert Playa Lakes in the Western United States. <i>Geomicrobiology Journal</i> , 2008, 25, 250-259.	2.0	6
84	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> , 2016, 4, .	0.8	5
85	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> , 2020, 34, 2923-2948.	2.6	5
86	High-Quality Draft Genome Sequence of <i>Kallotenuis papyrolyticum</i> JKG1 T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
87	Impact of Terrestrial Input on Deep-Sea Benthic Archaeal Community Structure in South China Sea Sediments. <i>Frontiers in Microbiology</i> , 2020, 11, 572017.	3.5	4
88	An Aniline-Substituted Bile Salt Analog Protects both Mice and Hamsters from Multiple <i>Clostridioides difficile</i> Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0143521.	3.2	4
89	A High-Carbohydrate Diet Prolongs Dysbiosis and <i>Clostridioides difficile</i> Carriage and Increases Delayed Mortality in a Hamster Model of Infection. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	4
90	Complete Genome Sequence of <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> Strain IF3SW-P1, Isolated from the International Space Station. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.6	4

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91	Incomplete denitrification phenotypes in diverse <i>Thermus</i> species from diverse geothermal spring sediments and adjacent soils in southwest China. <i>Extremophiles</i> , 2022, 26, .	2.3	4
92	<i>Marinobacter</i> strain NCE312 has a <i>Pseudomonas</i> -like naphthalene dioxygenase. <i>FEMS Microbiology Letters</i> , 2001, 201, 47-51.	1.8	3
93	Editorial: Ecology, Metabolism and Evolution of Archaea-Perspectives From Proceedings of the International Workshop on Geo-Omics of Archaea. <i>Frontiers in Microbiology</i> , 2021, 12, 827229.	3.5	3
94	Comparative genomic analysis of <i>Thermus</i> provides insights into the evolutionary history of an incomplete denitrification pathway. , 0, , .		3
95	Addressing Questions on Life in Terrestrial Geothermal Systems. <i>Eos</i> , 2013, 94, 325-325.	0.1	1
96	Identification of the Gut Microbiome and its Role in Paradoxical Anaerobism in Desert Pupfish. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	1
97	Response to Dr. Levin's Comment. <i>Astrobiology</i> , 2009, 9, 505-505.	3.0	0
98	High-Quality Draft Genome Sequence of <i>Thermocrinis jamiesonii</i> GBS1 <sup>T</sup> Isolated from Great Boiling Spring, Nevada. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
99	DESERT SPRING CHARACTERIZATION FROM HYDROCHEMICAL DATA ANALYSIS. , 2016, , .		0
100	MINERAL WEATHERING AND GROUNDWATER FLOW IN OWENS VALLEY SPRINGS. , 2017, , .		0
101	GEOLOGIC CONTROLS ON GROUNDWATER FLOWPATHS IN THE SPRING MOUNTAINS, NV INFERRED FROM SPRING WATER GEOCHEMISTRY AND 87SR/86SR. , 2018, , .		0
102	DISSOLVED NOBLE GASES AS FORENSIC TRACERS TO INVESTIGATE MOUNTAIN FRONT SPRINGS IN OWENS VALLEY, CA. , 2018, , .		0
103	LIFE IN THE RAIN SHADOW: UNDERSTANDING SOURCES OF RECHARGE AND GROUNDWATER FLOWPATHS TO GROUNDWATER DEPENDENT ECOSYSTEMS IN THE PANAMINT RANGE, DEATH VALLEY, CALIFORNIA, USA. , 2018, , .		0
104	MICROBIAL DIVERSITY AND COMMUNITY STRUCTURE OF DESERT SPRINGS ACROSS HYDROGEOCHEMICAL GRADIENTS IN THE SOUTHERN HYDROGRAPHIC GREAT BASIN. , 2018, , .		0
105	HYDROLOGICAL FRAGMENTATION AND GENETIC ISOLATION OF SPRINGS FOLLOWING TECTONIC EXTENSION IN THE SOUTHERN GREAT BASIN OF NV AND CA. , 2019, , .		0
106	SIMILARITIES IN LARGE-SCALE ECOLOGICAL PATTERNS OF MICROBIAL AND BENTHIC MACROINVERTEBRATE COMMUNITIES IN DESERT SPRINGS OF THE PANAMINT MOUNTAIN RANGE. , 2019, , .		0
107	HYDROGEOLOGY, MACRO- AND MICROFAUNA IN ISOLATED DESERT SPRINGS. ARE THERE SIMILAR PATTERNS IN THE BIOLOGICAL ORGANIZATION?. , 2019, , .		0
108	EXAMINING LANDSCAPE PLACEMENT AS A CONTROL ON SPRING HYDROCHEMISTRY AND ECOLOGICAL DIVERSITY. , 2019, , .		0

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109	AN EVOLVING CONCEPTUAL FRAMEWORK DESCRIBING THE VULNERABILITY OF DESERT SPRINGS: AN EXAMPLE FROM THE PANAMINT RANGE, DEATH VALLEY, USA. , 2020, , .		0