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	An Aniline-Substituted Bile Salt Analog Protects both Mice and Hamsters from Multiple Clostridioides difficile Strains. Antimicrobial Agents and Chemotherapy, 2022, 66, AAC0143521.	3.2	4
2	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
3	A High-Carbohydrate Diet Prolongs Dysbiosis and Clostridioides difficile Carriage and Increases Delayed Mortality in a Hamster Model of Infection. Microbiology Spectrum, 2022, 10, .	3.0	4
4	Complete Genome Sequence of Klebsiella quasipneumoniae subsp. <i>similipneumoniae</i> Strain IF3SW-P1, Isolated from the International Space Station. Microbiology Resource Announcements, 2022, 11, .	0.6	4
5	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
6	Incomplete denitrification phenotypes in diverse Thermus species from diverse geothermal spring sediments and adjacent soils in southwest China. Extremophiles, 2022, 26, .	2.3	4
7	Compositional and Metabolic Responses of Autotrophic Microbial Community to Salinity in Lacustrine Environments. MSystems, 2022, 7, .	3.8	15
8	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
9	Diversity of Root Nodule-Associated Bacteria of Diverse Legumes Along an Elevation Gradient in the Kunlun Mountains, China. Frontiers in Microbiology, 2021, 12, 633141.	3.5	9
10	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of Thermoflexus hugenholtzii and Three Candidate Species From China and Japan. Frontiers in Microbiology, 2021, 12, 632731.	3.5	8
11	Insight into the function and evolution of the Woodâ€“Ljungdahl pathway in <i>Actinobacteria</i>. ISME Journal, 2021, 15, 3005-3018.	9.8	55
12	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. ISME Communications, 2021, 1, .	4.2	23
13	Deciphering Symbiotic Interactions of â€œ <i>Candidatus</i> Aenigmarchaeotaâ€•with Inferred Horizontal Gene Transfers and Co-occurrence Networks. MSystems, 2021, 6, e0060621.	3.8	11
14	Comparative Genomics Reveals Thermal Adaptation and a High Metabolic Diversity in â€œ <i>Candidatus</i> Bathyarchaeiaâ€• MSystems, 2021, 6, e0025221.	3.8	20
15	Microbial dark matter coming to light: challenges and opportunities. National Science Review, 2021, 8, nwaa280.	9.5	86
16	Editorial: Ecology, Metabolism and Evolution of Archaea-Perspectives From Proceedings of the International Workshop on Geo-Omics of Archaea. Frontiers in Microbiology, 2021, 12, 827229.	3.5	3
17	Diverse respiratory capacity among Thermus strains from US Great Basin hot springs. Extremophiles, 2020, 24, 71-80.	2.3	13
18	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. ISME Journal, 2020, 14, 659-675.	9.8	69

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19	The gut microbiome and its potential role in paradoxical anaerobism in pupfishes of the Mojave Desert. Animal Microbiome, 2020, 2, 20.	3.8	20
20	Diversity and Distribution of a Novel Genus of Hyperthermophilic Aquificae Viruses Encoding a Proof-Reading Family-A DNA Polymerase. Frontiers in Microbiology, 2020, 11, 583361.	3.5	7
21	Impact of Terrestrial Input on Deep-Sea Benthic Archaeal Community Structure in South China Sea Sediments. Frontiers in Microbiology, 2020, 11, 572017.	3.5	4
22	Microbiome Shifts Associated With the Introduction of Wild Atlantic Horseshoe Crabs (Limulus) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62	3.5	12
23	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. Frontiers in Microbiology, 2020, 11, 1848.	3.5	62
24	Roadmap for naming uncultivated Archaea and Bacteria. Nature Microbiology, 2020, 5, 987-994.	13.3	115
25	Beneficial Endophytic Bacterial Populations Associated With Medicinal Plant Thymus vulgaris Alleviate Salt Stress and Confer Resistance to Fusarium oxysporum. Frontiers in Plant Science, 2020, 11, 47.	3.6	69
26	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. MSystems, 2020, 5, .	3.8	36
27	Hydrogeology of desert springs in the Panamint Range, California, USA : Geologic controls on the geochemical kinetics, flowpaths, and mean residence times of springs. Hydrological Processes, 2020, 34, 2923-2948.	2.6	5
28	Genomic Insights of â€œCandidatus Nitrosocaldaceaeâ€• Based on Nine New Metagenome-Assembled Genomes, Including â€œCandidatus Nitrosothermusâ€• Gen Nov. and Two New Species of â€œCandidatus Nitrosocaldusâ€•. Frontiers in Microbiology, 2020, 11, 608832.	3.5	13
29	All ANIs are not created equal: implications for prokaryotic species boundaries and integration of ANIs into polyphasic taxonomy. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 2937-2948.	1.7	51
30	AN EVOLVING CONCEPTUAL FRAMEWORK DESCRIBING THE VULNERABILITY OF DESERT SPRINGS: AN EXAMPLE FROM THE PANAMINT RANGE, DEATH VALLEY, USA. , 2020, , .		0
31	Identification of the Gut Microbiome and its Role in Paradoxical Anaerobism in Desert Pupfish. FASEB Journal, 2020, 34, 1-1.	0.5	1
32	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. Nature Communications, 2019, 10, 4574.	12.8	90
33	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
34	Insights into ecological role of a new deltaproteobacterial order <i>Candidatus</i> Acidulodesulfobacterales by metagenomics and metatranscriptomics. ISME Journal, 2019, 13, 2044-2057.	9.8	112
35	HYDROLOGICAL FRAGMENTATION AND GENETIC ISOLATION OF SPRINGS FOLLOWING TECTONIC EXTENSION IN THE SOUTHERN GREAT BASIN OF NV AND CA. , 2019, , .		0
36	SIMILARITIES IN LARGE-SCALE ECOLOGICAL PATTERNS OF MICROBIAL AND BENTHIC MACROINVERTEBRATE COMMUNITIES IN DESERT SPRINGS OF THE PANAMINT MOUNTAIN RANGE. , 2019, , .		0

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37	HYDROGEOLOGY, MACRO- AND MICROFAUNA IN ISOLATED DESERT SPRINGS. ARE THERE SIMILAR PATTERNS IN THE BIOLOGICAL ORGANIZATION?. , 2019, , .		0
38	EXAMINING LANDSCAPE PLACEMENT AS A CONTROL ON SPRING HYDROCHEMISTRY AND ECOLOGICAL DIVERSITY. , 2019, , .		0
39	Synergistic plantâ€“microbe interactions between endophytic bacterial communities and the medicinal plant Glycyrrhiza uralensis F.. Antonie Van Leeuwenhoek, 2018, 111, 1735-1748.	1.7	55
40	Association between degradation of pharmaceuticals and endocrine-disrupting compounds and microbial communities along a treated wastewater effluent gradient in Lake Mead. Science of the Total Environment, 2018, 622-623, 1640-1648.	8.0	34
41	Localized high abundance of Marine Group II archaea in the subtropical Pearl River Estuary: implications for their niche adaptation. Environmental Microbiology, 2018, 20, 734-754.	3.8	53
42	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
43	Evaluation of the Antimicrobial Activity of Endophytic Bacterial Populations From Chinese Traditional Medicinal Plant Licorice and Characterization of the Bioactive Secondary Metabolites Produced by Bacillus atrophaeus Against Verticillium dahliae. Frontiers in Microbiology, 2018, 9, 924.	3.5	150
44	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. Nature Communications, 2018, 9, 2832.	12.8	108
45	Effect of the Synthetic Bile Salt Analog CamSA on the Hamster Model of Clostridium difficile Infection. Antimicrobial Agents and Chemotherapy, 2018, 62, .	3.2	23
46	GEOLOGIC CONTROLS ON GROUNDWATER FLOWPATHS IN THE SPRING MOUNTAINS, NV INFERRED FROM SPRING WATER GEOCHEMISTRY AND 87SR/86SR. , 2018, , .		0
47	DISSOLVED NOBLE GASES AS FORENSIC TRACERS TO INVESTIGATE MOUNTAIN FRONT SPRINGS IN OWENS VALLEY, CA. , 2018, , .		0
48	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
49	MICROBIAL DIVERSITY AND COMMUNITY STRUCTURE OF DESERT SPRINGS ACROSS HYDROGEOCHEMICAL GRADIENTS IN THE SOUTHERN HYDROGRAPHIC GREAT BASIN. , 2018, , .		0
50	Reversible Reduction of Estrone to 17Î²â€Estradiol by <i>Rhizobium</i>, <i>Sphingopyxis</i>, and <i>Pseudomonas</i> Isolates from the Las Vegas Wash. Journal of Environmental Quality, 2017, 46, 281-287.	2.0	11
51	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	17.5	1,512
52	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
53	MINERAL WEATHERING AND GROUNDWATER FLOW IN OWENS VALLEY SPRINGS. , 2017, , .		0
54	High-Quality Draft Genomes from <i>Thermus caliditerrae</i> YIM 77777 and <i>T.Âtengchongensis</i> YIM 77401, Isolates from Tengchong, China. Genome Announcements, 2016, 4, .	0.8	5

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55	High-Quality Draft Genome Sequence of Thermocrinis jamiesonii GBS1 ^T Isolated from Great Boiling Spring, Nevada. Genome Announcements, 2016, 4, .	0.8	0
56	High-quality draft genome sequence of the Thermus amyloliquefaciens type strain YIM 77409T with an incomplete denitrification pathway. Standards in Genomic Sciences, 2016, 11, 20.	1.5	7
57	Single-Cell-Genomics-Facilitated Read Binning of Candidate Phylum EM19 Genomes from Geothermal Spring Metagenomes. Applied and Environmental Microbiology, 2016, 82, 992-1003.	3.1	36
58	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. Nature Communications, 2016, 7, 10476.	12.8	189
59	Phylogeny and physiology of candidate phylum â€˜Atribacteriaâ€™ (OP9/JS1) inferred from cultivation-independent genomics. ISME Journal, 2016, 10, 273-286.	9.8	166
60	DESERT SPRING CHARACTERIZATION FROM HYDROCHEMICAL DATA ANALYSIS. , 2016, , .		0
61	High-Quality Draft Genome Sequence of Kallotenue papyrolyticum JKG1 T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. Genome Announcements, 2015, 3, .	0.8	4
62	Uncultivated thermophiles: current status and spotlight on â€˜Aigarchaeotaâ€™. Current Opinion in Microbiology, 2015, 25, 136-145.	5.1	70
63	Distribution of ether lipids and composition of the archaeal community in terrestrial geothermal springs: impact of environmental variables. Environmental Microbiology, 2015, 17, 1600-1614.	3.8	29
64	Isolation of diverse members of the Aquificales from geothermal springs in Tengchong, China. Frontiers in Microbiology, 2015, 6, 157.	3.5	31
65	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
66	The changing landscape of microbial biodiversity exploration and its implications for systematics. Systematic and Applied Microbiology, 2015, 38, 231-236.	2.8	26
67	Exploring microbial dark matter to resolve the deep archaeal ancestry of eukaryotes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140328.	4.0	40
68	Thermocrinis jamiesonii sp. nov., a thiosulfate-oxidizing, autotropic thermophile isolated from a geothermal spring. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 4769-4775.	1.7	23
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	Thermoflexus hugenholtzii 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.. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 2119-2127.	1.7	90
71	Impact of single-cell genomics and metagenomics on the emerging view of extremophile â€œmicrobial dark matterâ€• Extremophiles, 2014, 18, 865-875.	2.3	133
72	Seasonal patterns in microbial communities inhabiting the hot springs of <scp>T</scp>engchong, <scp>Y</scp>unnan Province, <scp>C</scp>hina. Environmental Microbiology, 2014, 16, 1579-1591.	3.8	57

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73	Insights into the phylogeny and coding potential of microbial dark matter. Nature, 2013, 499, 431-437.	27.8	2,239
74	Kallotenue papyrolyticum gen. nov., sp. nov., a cellulolytic and filamentous thermophile that represents a novel lineage (Kallotenuales ord. nov., Kallotenuaceae fam. nov.) within the class Chloroflexia. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 4675-4682.	1.7	50
75	An integrated study reveals diverse methanogens, Thaumarchaeota, and yet-uncultivated archaeal lineages in Armenian hot springs. Antonie Van Leeuwenhoek, 2013, 104, 71-82.	1.7	38
76	Sediment microbial communities in Great Boiling Spring are controlled by temperature and distinct from water communities. ISME Journal, 2013, 7, 718-729.	9.8	182
77	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. Nature Communications, 2013, 4, 1854.	12.8	199
78	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
79	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. Applied and Environmental Microbiology, 2013, 79, 3306-3310.	3.1	28
80	Cultivation and characterization of thermophilic<i>Nitrospira</i>species from geothermal springs in the US Great Basin, China, and Armenia. FEMS Microbiology Ecology, 2013, 85, 283-292.	2.7	64
81	Addressing Questions on Life in Terrestrial Geothermal Systems. Eos, 2013, 94, 325-325.	0.1	1
82	Thermus oshimai JL-2 and T. thermophilus JL-18 genome analysis illuminates pathways for carbon, nitrogen, and sulfur cycling. Standards in Genomic Sciences, 2013, 7, 449-468.	1.5	31
83	Lateral Gene Transfer of Family A DNA Polymerases between Thermophilic Viruses, Aquificae, and Apicomplexa. Molecular Biology and Evolution, 2013, 30, 1653-1664.	8.9	36
84	A Comprehensive Census of Microbial Diversity in Hot Springs of Tengchong, Yunnan Province China Using 16S rRNA Gene Pyrosequencing. PLoS ONE, 2013, 8, e53350.	2.5	216
85	Pyrosequencing Reveals High-Temperature Cellulolytic Microbial Consortia in Great Boiling Spring after In Situ Lignocellulose Enrichment. PLoS ONE, 2013, 8, e59927.	2.5	42
86	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
87	Wide distribution of autochthonous branched glycerol dialkyl glycerol tetraethers (bGDGTs) in U.S. Great Basin hot springs. Frontiers in Microbiology, 2013, 4, 222.	3.5	11
88	The distribution and abundance of archaeal tetraether lipids in U.S. Great Basin hot springs. Frontiers in Microbiology, 2013, 4, 247.	3.5	7
89	A review of the microbiology of the Rehai geothermal field in Tengchong, Yunnan Province, China. Geoscience Frontiers, 2012, 3, 273-288.	8.4	59
90	Korarchaeota Diversity, Biogeography, and Abundance in Yellowstone and Great Basin Hot Springs and Ecological Niche Modeling Based on Machine Learning. PLoS ONE, 2012, 7, e35964.	2.5	43

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91	Calculation of total free energy yield as an alternative approach for predicting the importance of potential chemolithotrophic reactions in geothermal springs. FEMS Microbiology Ecology, 2012, 81, 446-454.	2.7	34
92	Ammonia oxidation, denitrification and dissimilatory nitrate reduction to ammonium in two US Great Basin hot springs with abundant ammoniaâ€oxidizing archaea. Environmental Microbiology, 2011, 13, 2371-2386.	3.8	132
93	Potential role of Thermus thermophilus and T.Âoshimai in high rates of nitrous oxide (N2O) production in âˆ¼80â€ƒÂ°C hot springs in the US Great Basin. Geobiology, 2011, 9, 471-480.	2.4	42
94	Measuring Nitrification, Denitrification, and Related Biomarkers in Terrestrial Geothermal Ecosystems. Methods in Enzymology, 2011, 486, 171-203.	1.0	42
95	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. Journal of Earth Science (Wuhan, China), 2010, 21, 315-318.	3.2	9
96	Interdomain Conjugal Transfer of DNA from Bacteria to Archaea. Applied and Environmental Microbiology, 2010, 76, 5644-5647.	3.1	34
97	Moderately Thermophilic Magnetotactic Bacteria from Hot Springs in Nevada. Applied and Environmental Microbiology, 2010, 76, 3740-3743.	3.1	127
98	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
99	Response to Dr. Levin's Comment. Astrobiology, 2009, 9, 505-505.	3.0	0
100	Microbiology and geochemistry of great boiling and mud hot springs in the United States Great Basin. Extremophiles, 2009, 13, 447-459.	2.3	157
101	Bacterial Succession within an Ephemeral Hypereutrophic Mojave Desert Playa Lake. Microbial Ecology, 2009, 57, 307-320.	2.8	35
102	Geomicrobiological Changes in Two Ephemeral Desert Playa Lakes in the Western United States. Geomicrobiology Journal, 2008, 25, 250-259.	2.0	6
103	Global Occurrence of Archaeal <i>amoA</i> Genes in Terrestrial Hot Springs. Applied and Environmental Microbiology, 2008, 74, 6417-6426.	3.1	189
104	A korarchaeal genome reveals insights into the evolution of the Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8102-8107.	7.1	253
105	Molecular Phylogeny of Uncultivated<i>Crenarchaeota</i>in Great Basin Hot Springs of Moderately Elevated Temperature. Geomicrobiology Journal, 2007, 24, 535-542.	2.0	23
106	Marinobacter strain NCE312 has a Pseudomonas-like naphthalene dioxygenase. FEMS Microbiology Letters, 2001, 201, 47-51.	1.8	3
107	Verrucomicrobia div. nov., a new division of the bacteria containing three new species of Prosthecobacter. Antonie Van Leeuwenhoek, 1997, 72, 29-38.	1.7	171
108	Life in High-Temperature Environments. , 0, , 4.3.4-1-4.3.4-15.		7

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109	Comparative genomic analysis of <i>Thermus</i> provides insights into the evolutionary history of an incomplete denitrification pathway. , 0, , .		3