

Brian P Hedlund

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	An aniline-substituted bile salt analog protects both mice and hamsters from multiple strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , AAC0143521	5.9	0
120	Microbial dark matter coming to light: challenges and opportunities. <i>National Science Review</i> , 2021 , 8, nwa280	10.8	17
119	Genomics, Exometabolomics, and Metabolic Probing Reveal Conserved Proteolytic Metabolism of and Three Candidate Species From China and Japan. <i>Frontiers in Microbiology</i> , 2021 , 12, 632731	5.7	2
118	Insight into the function and evolution of the Wood-Ljungdahl pathway in Actinobacteria. <i>ISME Journal</i> , 2021 , 15, 3005-3018	11.9	11
117	Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. <i>ISME Communications</i> , 2021 , 1,		4
116	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021 , 39, 499-509	44.5	120
115	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	5.7	2
114	Deciphering Symbiotic Interactions of "Aenigmarchaeota" with Inferred Horizontal Gene Transfers and Co-occurrence Networks. <i>MSystems</i> , 2021 , 6, e0060621	7.6	1
113	Comparative Genomics Reveals Thermal Adaptation and a High Metabolic Diversity in "Bathyarchaeia". <i>MSystems</i> , 2021 , 6, e0025221	7.6	4
112	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020 , 5, 987-994	26.6	64
111	Beneficial Endophytic Bacterial Populations Associated With Medicinal Plant Alleviate Salt Stress and Confer Resistance to. <i>Frontiers in Plant Science</i> , 2020 , 11, 47	6.2	30
110	A High-Fat/High-Protein, Atkins-Type Diet Exacerbates () Infection in Mice, whereas a High-Carbohydrate Diet Protects. <i>MSystems</i> , 2020 , 5,	7.6	20
109	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	3.3	2
108	Identification of the Gut Microbiome and its Role in Paradoxical Anaerobism in Desert Pupfish. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	1
107	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	2.2	24
106	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020 , 14, 659-675	11.9	29
105	The gut microbiome and its potential role in paradoxical anaerobism in pupfishes of the Mojave Desert. <i>Animal Microbiome</i> , 2020 , 2, 20	4.1	7

104	Diversity and Distribution of a Novel Genus of Hyperthermophilic Viruses Encoding a Proof-Reading Family-A DNA Polymerase. <i>Frontiers in Microbiology</i> , 2020 , 11, 583361	5.7	1
103	Impact of Terrestrial Input on Deep-Sea Benthic Archaeal Community Structure in South China Sea Sediments. <i>Frontiers in Microbiology</i> , 2020 , 11, 572017	5.7	3
102	Microbiome Shifts Associated With the Introduction of Wild Atlantic Horseshoe Crabs () Into a Touch-Tank Exhibit. <i>Frontiers in Microbiology</i> , 2020 , 11, 1398	5.7	5
101	Ancestral Absence of Electron Transport Chains in Patescibacteria and DPANN. <i>Frontiers in Microbiology</i> , 2020 , 11, 1848	5.7	29
100	Diverse respiratory capacity among Thermus strains from US Great Basin hot springs. <i>Extremophiles</i> , 2020 , 24, 71-80	3	2
99	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> , 2020 , 11, 608832	5.7	4
98	Position-Specific Metabolic Probing and Metagenomics of Microbial Communities Reveal Conserved Central Carbon Metabolic Network Activities at High Temperatures. <i>Frontiers in Microbiology</i> , 2019 , 10, 1427	5.7	3
97	Insights into ecological role of a new deltaproteobacterial order Candidatus Acidulodesulfobacterales by metagenomics and metatranscriptomics. <i>ISME Journal</i> , 2019 , 13, 2044-2057 ^{1.9}	7.1	36
96	Insights into the ecological roles and evolution of methyl-coenzyme M reductase-containing hot spring Archaea. <i>Nature Communications</i> , 2019 , 10, 4574	17.4	33
95	Synergistic plant-microbe interactions between endophytic bacterial communities and the medicinal plant Glycyrrhiza uralensis F. <i>Antonie Van Leeuwenhoek</i> , 2018 , 111, 1735-1748	2.1	24
94	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	10.2	26
93	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> , 2018 , 9, 924	5.7	68
92	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <i>Nature Communications</i> , 2018 , 9, 2832	17.4	50
91	Effect of the Synthetic Bile Salt Analog CamSA on the Hamster Model of Clostridium difficile Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2018 , 62,	5.9	12
90	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	5.2	27
89	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> , 2018 , 22, 983-991	3	8
88	Candidatus Nitrosocaldaceae 2017 , 1-2		1
87	Candidatus Nitrosocaldus 2017 , 1-5		1

86	Reversible Reduction of Estrone to 17 β Estradiol by , , and Isolates from the Las Vegas Wash. <i>Journal of Environmental Quality</i> , 2017 , 46, 281-287	3.4	9
85	Candidatus Nitrosocaldales 2017 , 1-2		0
84	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	44.5	648
83	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> , 2017 , 8, 2082	5.7	4
82	Phylogeny and physiology of candidate phylum 'Atribacteria' (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016 , 10, 273-86	11.9	118
81	High-quality draft genome sequence of the <i>Thermus amyloliquefaciens</i> type strain YIM 77409(T) with an incomplete denitrification pathway. <i>Standards in Genomic Sciences</i> , 2016 , 11, 20		5
80	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	4.8	16
79	Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. <i>Nature Communications</i> , 2016 , 7, 10476	17.4	90
78	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,		3
77	Uncultivated thermophiles: current status and spotlight on 'Aigarchaeota'. <i>Current Opinion in Microbiology</i> , 2015 , 25, 136-45	7.9	32
76	Distribution of ether lipids and composition of the archaeal community in terrestrial geothermal springs: impact of environmental variables. <i>Environmental Microbiology</i> , 2015 , 17, 1600-14	5.2	20
75	Isolation of diverse members of the Aquificales from geothermal springs in Tengchong, China. <i>Frontiers in Microbiology</i> , 2015 , 6, 157	5.7	20
74	Distribution and Diversity of Aerobic Carbon Monoxide-Oxidizing Bacteria in Geothermal Springs of China, the Philippines, and the United States. <i>Geomicrobiology Journal</i> , 2015 , 32, 903-913	2.5	13
73	The changing landscape of microbial biodiversity exploration and its implications for systematics. <i>Systematic and Applied Microbiology</i> , 2015 , 38, 231-6	4.2	20
72	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	5.8	35
71	Chthoniobacterales ord. nov 2015 , 1-1		
70	Lentisphaeraceae fam. nov. 2015 , 1-1		
69	Victivallaceae fam. nov. 2015 , 1-1		

68 Opitutaceae **2015**, 1-1

67 Akkermansiaceae fam. nov. **2015**, 1-1

1

66 Rubritaleaceae fam. nov. **2015**, 1-1

65 Verrucomicrobiaceae **2015**, 1-2

64 Alterococcus **2015**, 1-3

63 Cerasicoccus **2015**, 1-4

62 Coraliomargarita **2015**, 1-4

1

61 Pelagicoccus **2015**, 1-7

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

59 Rubritalea **2015**, 1-7

1

58 Opitutales **2015**, 1-1

57 Puniceococcales **2015**, 1-1

56 Verrucomicrobiales **2015**, 1-1

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

54 Puniceococcaceae **2015**, 1-2

53 Lentisphaerae **2015**, 1-2

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

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

50	Opitutae 2015 , 1-4		1
49	Spartobacteria class. nov. 2015 , 1-4		
48	Verrucomicrobiae 2015 , 1-5		1
47	Chthoniobacteraceae fam. nov. 2015 , 1-1		
46	Life in High-Temperature Environments 2015 , 4.3.4-1-4.3.4-15		3
45	High-Quality Draft Genome Sequence of <i>Kallotenua papyrolyticum</i> JKG1T Reveals Broad Heterotrophic Capacity Focused on Carbohydrate and Amino Acid Metabolism. <i>Genome Announcements</i> , 2015 , 3,		3
44	<i>Thermocrinis jamiesonii</i> sp. nov., a thiosulfate-oxidizing, autotrophic thermophile isolated from a geothermal spring. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015 , 65, 4769-4775	2.2	8
43	<i>Thermoflexus hugenholtzii</i> gen. nov., sp. nov., a thermophilic, microaerophilic, filamentous bacterium representing a novel class in the Chloroflexi, <i>Thermoflexia</i> 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	2.2	36
42	Impact of single-cell genomics and metagenomics on the emerging view of extremophile "microbial dark matter". <i>Extremophiles</i> , 2014 , 18, 865-75	3	96
41	Seasonal patterns in microbial communities inhabiting the hot springs of Tengchong, Yunnan Province, China. <i>Environmental Microbiology</i> , 2014 , 16, 1579-91	5.2	44
40	Production of branched tetraether lipids in Tibetan hot springs: A possible linkage to nitrite reduction by thermotolerant or thermophilic bacteria?. <i>Chemical Geology</i> , 2014 , 386, 209-217	4.2	10
39	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013 , 499, 431-7	50.4	1484
38	<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> , 2013 , 63, 4675-4682	2.2	25
37	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	2.1	31
36	Sediment microbial communities in Great Boiling Spring are controlled by temperature and distinct from water communities. <i>ISME Journal</i> , 2013 , 7, 718-29	11.9	106
35	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. <i>Nature Communications</i> , 2013 , 4, 1854	17.4	143
34	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> , 2013 , 1,		15
33	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, 3306-10	4.8	9

32	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, 283-92	4.3	35
31	Addressing Questions on Life in Terrestrial Geothermal Systems. <i>Eos</i> , 2013 , 94, 325-325	1.5	1
30	<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, 449-68		22
29	Lateral gene transfer of family A DNA polymerases between thermophilic viruses, aquificae, and apicomplexa. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1653-64	8.3	24
28	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	3.7	14 ⁰
27	Pyrosequencing reveals high-temperature cellulolytic microbial consortia in Great Boiling Spring after in situ lignocellulose enrichment. <i>PLoS ONE</i> , 2013 , 8, e59927	3.7	33
26	In situ production of branched glycerol dialkyl glycerol tetraethers in a great basin hot spring (USA). <i>Frontiers in Microbiology</i> , 2013 , 4, 181	5.7	17
25	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	5.7	11
24	The distribution and abundance of archaeal tetraether lipids in U.S. Great Basin hot springs. <i>Frontiers in Microbiology</i> , 2013 , 4, 247	5.7	5
23	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, 446-54	4.3	16
22	A review of the microbiology of the Rehai geothermal field in Tengchong, Yunnan Province, China. <i>Geoscience Frontiers</i> , 2012 , 3, 273-288	6	43
21	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	3.7	29
20	Diversity of Archaea in Terrestrial Hot Springs and Role in Ammonia Oxidation 2011 , 381-394		5
19	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, 2371-86	5.2	83
18	Potential role of <i>Thermus thermophilus</i> and <i>T. oshimai</i> in high rates of nitrous oxide (N ₂ O) production in ~80 °C hot springs in the US Great Basin. <i>Geobiology</i> , 2011 , 9, 471-80	4.3	34
17	Measuring nitrification, denitrification, and related biomarkers in terrestrial geothermal ecosystems. <i>Methods in Enzymology</i> , 2011 , 486, 171-203	1.7	27
16	Interdomain conjugal transfer of DNA from bacteria to archaea. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5644-7	4.8	26
15	Moderately thermophilic magnetotactic bacteria from hot springs in Nevada. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 3740-3	4.8	103

14	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	2.2	9
13	Stereo-specific glucose consumption may be used to distinguish between chemical and biological reactivity on Mars: a preliminary test on Earth. <i>Astrobiology</i> , 2009 , 9, 443-6	3.7	14
12	Response to Dr. Levin's Comment. <i>Astrobiology</i> , 2009 , 9, 505-505	3.7	
11	Microbiology and geochemistry of great boiling and mud hot springs in the United States Great Basin. <i>Extremophiles</i> , 2009 , 13, 447-59	3	131
10	Bacterial succession within an ephemeral hypereutrophic Mojave Desert playa Lake. <i>Microbial Ecology</i> , 2009 , 57, 307-20	4.4	32
9	Geomicrobiological Changes in Two Ephemeral Desert Playa Lakes in the Western United States. <i>Geomicrobiology Journal</i> , 2008 , 25, 250-259	2.5	6
8	Global occurrence of archaeal amoA genes in terrestrial hot springs. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 6417-26	4.8	156
7	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, 8102-7	11.5	214
6	Molecular Phylogeny of Uncultivated Crenarchaeota in Great Basin Hot Springs of Moderately Elevated Temperature. <i>Geomicrobiology Journal</i> , 2007 , 24, 535-542	2.5	20
5	Verrucomicrobia div. nov., a new division of the bacteria containing three new species of Prosthecobacter. <i>Antonie Van Leeuwenhoek</i> , 1997 , 72, 29-38	2.1	127
4	Diversity and Distribution of a Novel Genus of Hyperthermophilic Aquificae Viruses Encoding a Proof-reading Family-A DNA Polymerase		1
3	Ancestral absence of electron transport chains in Patescibacteria and DPANN		3
2	Lentisphaerales1-1		
1	Victivallales1-1		