

Steven J Hallam

List of Publications by Year in descending order

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Version: 2024-02-01

112
papers

14,272
citations

53794

45
h-index

30922

102
g-index

130
all docs

130
docs citations

130
times ranked

15093
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	5.6	62
2	Aggregating Statistically Correlated Metabolic Pathways Into Groups to Improve Prediction Performance. , 2022, , .		0
3	The nature of gas production patterns associated with methanol degradation in natural aquifer sediments: A microcosm study. <i>Journal of Contaminant Hydrology</i> , 2022, 247, 103988.	3.3	0
4	Pathway-Centric Analysis of Microbial Metabolic Potential and Expression Along Nutrient and Energy Gradients in the Western Atlantic Ocean. <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	1
5	Expanding the phylogenetic distribution of cytochrome <i>c</i> -containing methanogenic archaea sheds light on the evolution of methanogenesis. <i>ISME Journal</i> , 2022, 16, 2373-2387.	9.8	12
6	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
7	Hive Panel Explorer: an interactive network visualization tool. <i>Bioinformatics</i> , 2021, 37, 436-437.	4.1	1
8	Potential virus-mediated nitrogen cycling in oxygen-depleted oceanic waters. <i>ISME Journal</i> , 2021, 15, 981-998.	9.8	71
9	Mercury methylation by metabolically versatile and cosmopolitan marine bacteria. <i>ISME Journal</i> , 2021, 15, 1810-1825.	9.8	74
10	Metabolic Pathway Prediction using Non-negative Matrix Factorization with Improved Precision. <i>Lecture Notes in Computer Science</i> , 2021, , 33-44.	1.3	2
11	An integrated, modular approach to data science education in microbiology. <i>PLoS Computational Biology</i> , 2021, 17, e1008661.	3.2	8
12	The cyanobacterium <i>Prochlorococcus</i> has divergent light-harvesting antennae and may have evolved in a low-oxygen ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	20
13	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021, 12, 3076.	12.8	35
14	The Kwakshua Watersheds Observatory, central coast of British Columbia, Canada. <i>Hydrological Processes</i> , 2021, 35, e14198.	2.6	4
15	Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. <i>Nature Communications</i> , 2021, 12, 3503.	12.8	97
16	Discovery and Development of Promiscuous O-Glycan Hydrolases for Removal of Intact Sialyl T-Antigen. <i>ACS Chemical Biology</i> , 2021, 16, 2004-2015.	3.4	7
17	Metabolic Pathway Prediction Using Non-Negative Matrix Factorization with Improved Precision. <i>Journal of Computational Biology</i> , 2021, 28, 1075-1103.	1.6	4
18	Biochar amendment rapidly shifts microbial community structure with enhanced thermophilic digestion activity. <i>Bioresource Technology</i> , 2021, 341, 125864.	9.6	13

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19	Leveraging heterogeneous network embedding for metabolic pathway prediction. <i>Bioinformatics</i> , 2021, 37, 822-829.	4.1	9
20	Prokaryotic responses to a warm temperature anomaly in northeast subarctic Pacific waters. <i>Communications Biology</i> , 2021, 4, 1217.	4.4	14
21	The Bacteroidetes <i>Aequorivita</i> sp. and <i>Kaistella jeonii</i> Produce Promiscuous Esterases With PET-Hydrolyzing Activity. <i>Frontiers in Microbiology</i> , 2021, 12, 803896.	3.5	21
22	Metabolite composition of sinking particles differs from surface suspended particles across a latitudinal transect in the South Atlantic. <i>Limnology and Oceanography</i> , 2020, 65, 111-127.	3.1	39
23	CRAGE-mediated insertion of fluorescent chromosomal markers for accurate and scalable measurement of co-culture dynamics in <i>Escherichia coli</i> . <i>Synthetic Biology</i> , 2020, 5, ysaa015.	2.2	3
24	TreeSAPP: the Tree-based Sensitive and Accurate Phylogenetic Profiler. <i>Bioinformatics</i> , 2020, 36, 4706-4713.	4.1	8
25	Metabolic pathway inference using multi-label classification with rich pathway features. <i>PLoS Computational Biology</i> , 2020, 16, e1008174.	3.2	10
26	Metabolic pathway inference using multi-label classification with rich pathway features. , 2020, 16, e1008174.		0
27	Metabolic pathway inference using multi-label classification with rich pathway features. , 2020, 16, e1008174.		0
28	Metabolic pathway inference using multi-label classification with rich pathway features. , 2020, 16, e1008174.		0
29	Metabolic pathway inference using multi-label classification with rich pathway features. , 2020, 16, e1008174.		0
30	Time-series CH ₄ measurements from Saanich Inlet, BC, a seasonally anoxic fjord. <i>Marine Chemistry</i> , 2019, 215, 103664.	2.3	10
31	Prospecting for microbial β -N-acetylgalactosaminidases yields a new class of GH31 O-glycanase. <i>Journal of Biological Chemistry</i> , 2019, 294, 16400-16415.	3.4	22
32	An enzymatic pathway in the human gut microbiome that converts A to universal O type blood. <i>Nature Microbiology</i> , 2019, 4, 1475-1485.	13.3	56
33	Sampling and Processing Methods Impact Microbial Community Structure and Potential Activity in a Seasonally Anoxic Fjord: Saanich Inlet, British Columbia. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	16
34	High-Throughput Recovery and Characterization of Metagenome-Derived Glycoside Hydrolase-Containing Clones as a Resource for Biocatalyst Development. <i>MSystems</i> , 2019, 4, .	3.8	11
35	Development and Application of a High-Throughput Functional Metagenomic Screen for Glycoside Phosphorylases. <i>Cell Chemical Biology</i> , 2019, 26, 1001-1012.e5.	5.2	23
36	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. <i>Nature Microbiology</i> , 2019, 4, 603-613.	13.3	187

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37	Rates and Pathways of N ₂ Production in a Persistently Anoxic Fjord: Saanich Inlet, British Columbia. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	9
38	Systematic Screening of Synthetic Gene-Encoded Enzymes for Synthesis of Modified Glycosides. <i>ACS Catalysis</i> , 2019, 9, 3219-3227.	11.2	17
39	Seasonal and ecohydrological regulation of active microbial populations involved in DOC, CO ₂ , and CH ₄ fluxes in temperate rainforest soil. <i>ISME Journal</i> , 2019, 13, 950-963.	9.8	37
40	Metagenomes Reveal Global Distribution of Bacterial Steroid Catabolism in Natural, Engineered, and Host Environments. <i>MBio</i> , 2018, 9, .	4.1	72
41	Single cell genomics of uncultured marine alveolates shows paraphyly of basal dinoflagellates. <i>ISME Journal</i> , 2018, 12, 304-308.	9.8	40
42	A multi-year time-series of N ₂ O dynamics in a seasonally anoxic fjord: Saanich Inlet, British Columbia. <i>Limnology and Oceanography</i> , 2018, 63, 524-539.	3.1	16
43	An Improved Whole-Cell Biosensor for the Discovery of Lignin-Transforming Enzymes in Functional Metagenomic Screens. <i>ACS Synthetic Biology</i> , 2018, 7, 392-398.	3.8	51
44	Recovering cellular biomass from fluids using chemical flocculation. <i>Environmental Microbiology Reports</i> , 2018, 10, 686-694.	2.4	2
45	Metagenomic discovery of a novel transaminase for valorization of monoaromatic compounds. <i>RSC Advances</i> , 2018, 8, 22490-22497.	3.6	10
46	Metagenomics reveals functional synergy and novel polysaccharide utilization loci in the <i>Castor canadensis</i> fecal microbiome. <i>ISME Journal</i> , 2018, 12, 2757-2769.	9.8	36
47	A geographically-diverse collection of 418 human gut microbiome pathway genome databases. <i>Scientific Data</i> , 2017, 4, 170035.	5.3	8
48	Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae. <i>ISME Journal</i> , 2017, 11, 2334-2344.	9.8	34
49	A metagenomic survey of forest soil microbial communities more than a decade after timber harvesting. <i>Scientific Data</i> , 2017, 4, 170092.	5.3	17
50	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
51	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. <i>Science</i> , 2017, 358, 1046-1051.	12.6	229
52	Monitoring microbial responses to ocean deoxygenation in a model oxygen minimum zone. <i>Scientific Data</i> , 2017, 4, 170158.	5.3	14
53	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	12.8	99
54	A compendium of geochemical information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170159.	5.3	29

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55	A compendium of multi-omic sequence information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170160.	5.3	35
56	Nutrient Acquisition and the Metabolic Potential of Photoferrotrophic Chlorobi. <i>Frontiers in Microbiology</i> , 2017, 8, 1212.	3.5	28
57	Draft Genome Sequence of the Pelagic Photoferrotroph <i>Chlorobium phaeoferrooxidans</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	28
58	Methanotrophic Community Dynamics in a Seasonally Anoxic Fjord: Saanich Inlet, British Columbia. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	17
59	FAST: Fast annotation with synchronized threads. , 2016, , .		2
60	The information science of microbial ecology. <i>Current Opinion in Microbiology</i> , 2016, 31, 209-216.	5.1	26
61	Editorial overview: Remapping the body of the world: Exploring interactions at the interface of microbial ecology, biological engineering and information science. <i>Current Opinion in Microbiology</i> , 2016, 31, v-vii.	5.1	0
62	Ammonium and nitrite oxidation at nanomolar oxygen concentrations in oxygen minimum zone waters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10601-10606.	7.1	195
63	Integrating biogeochemistry with multiomic sequence information in a model oxygen minimum zone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5925-E5933.	7.1	94
64	LCA*: an entropy-based measure for taxonomic assignment within assembled metagenomes. <i>Bioinformatics</i> , 2016, 32, 3535-3542.	4.1	23
65	Synthesis and evaluation of a series of 6-chloro-4-methylumbelliferyl glycosides as fluorogenic reagents for screening metagenomic libraries for glycosidase activity. <i>Carbohydrate Research</i> , 2016, 421, 33-39.	2.3	20
66	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	9.8	232
67	Phylogeny and physiology of candidate phylum <i>Atribacteria</i> [™] (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	9.8	166
68	FragGeneScan-plus for scalable high-throughput short-read open reading frame prediction. , 2015, , .		15
69	Rare taxa have potential to make metabolic contributions in enhanced biological phosphorus removal ecosystems. <i>Environmental Microbiology</i> , 2015, 17, 4979-4993.	3.8	68
70	The Microbial Community of a Passive Biochemical Reactor Treating Arsenic, Zinc, and Sulfate-Rich Seepage. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 27.	4.1	88
71	Combining genomic sequencing methods to explore viral diversity and reveal potential virus-host interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 265.	3.5	72
72	Previously unknown evolutionary groups dominate the ssDNA gokushoviruses in oxic and anoxic waters of a coastal marine environment. <i>Frontiers in Microbiology</i> , 2015, 6, 315.	3.5	18

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73	Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. <i>ELife</i> , 2015, 4, .	6.0	400
74	Non-symbiotic <i>Bradyrhizobium</i> ecotypes dominate North American forest soils. <i>ISME Journal</i> , 2015, 9, 2435-2441.	9.8	142
75	Biocatalysts for biomass deconstruction from environmental genomics. <i>Current Opinion in Chemical Biology</i> , 2015, 29, 18-25.	6.1	28
76	Single-cell genomics-based analysis of virus-host interactions in marine surface bacterioplankton. <i>ISME Journal</i> , 2015, 9, 2386-2399.	9.8	207
77	Forest harvesting reduces the soil metagenomic potential for biomass decomposition. <i>ISME Journal</i> , 2015, 9, 2465-2476.	9.8	96
78	Microbes don't play solitaire: how cooperation trumps isolation in the microbial world. <i>Environmental Microbiology Reports</i> , 2015, 7, 26-28.	2.4	78
79	MetaPathways v2.5: quantitative functional, taxonomic and usability improvements. <i>Bioinformatics</i> , 2015, 31, 3345-3347.	4.1	57
80	Patterns of Endemism and Habitat Selection in Coalbed Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7924-7937.	3.1	31
81	Genomic properties of Marine Group A bacteria indicate a role in the marine sulfur cycle. <i>ISME Journal</i> , 2014, 8, 455-468.	9.8	84
82	Illuminating Microbial Dark Matter in Meromictic Sakinaw Lake. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6807-6818.	3.1	109
83	Metaproteomics reveals differential modes of metabolic coupling among ubiquitous oxygen minimum zone microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11395-11400.	7.1	157
84	MetaPathways v2.0: A master-worker model for environmental Pathway/Genome Database construction on grids and clouds. , 2014, , .		12
85	Metagenomic scaffolds enable combinatorial lignin transformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10143-10148.	7.1	72
86	Metabolic pathways for the whole community. <i>BMC Genomics</i> , 2014, 15, 619.	2.8	50
87	Ecology and evolution of viruses infecting uncultivated SUP05 bacteria as revealed by single-cell- and meta-genomics. <i>ELife</i> , 2014, 3, e03125.	6.0	186
88	Biomining active cellulases from a mining bioremediation system. <i>Journal of Biotechnology</i> , 2013, 167, 462-471.	3.8	35
89	Insights into the phylogeny and coding potential of microbial dark matter. <i>Nature</i> , 2013, 499, 431-437.	27.8	2,239
90	MetaPathways: a modular pipeline for constructing pathway/genome databases from environmental sequence information. <i>BMC Bioinformatics</i> , 2013, 14, 202.	2.6	100

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91	Molecular Tools for Investigating Microbial Community Structure and Function in Oxygen-Deficient Marine Waters. <i>Methods in Enzymology</i> , 2013, 531, 305-329.	1.0	6
92	Diversity and population structure of Marine Group A bacteria in the Northeast subarctic Pacific Ocean. <i>ISME Journal</i> , 2013, 7, 256-268.	9.8	63
93	Microbial community structure across fluid gradients in the Juan de Fuca Ridge hydrothermal system. <i>FEMS Microbiology Ecology</i> , 2013, 83, 324-339.	2.7	53
94	Pelagic Oxygen Minimum Zone Microbial Communities. , 2013, , 113-122.		18
95	Metagenomics of Hydrocarbon Resource Environments Indicates Aerobic Taxa and Genes to be Unexpectedly Common. <i>Environmental Science & Technology</i> , 2013, 47, 10708-10717.	10.0	179
96	Prevalent genome streamlining and latitudinal divergence of planktonic bacteria in the surface ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11463-11468.	7.1	328
97	Metabolic reprogramming by viruses in the sunlit and dark ocean. <i>Genome Biology</i> , 2013, 14, R123.	9.6	208
98	Effect of oxygen minimum zone formation on communities of marine protists. <i>ISME Journal</i> , 2012, 6, 1586-1601.	9.8	108
99	Microbial ecology of expanding oxygen minimum zones. <i>Nature Reviews Microbiology</i> , 2012, 10, 381-394.	28.6	454
100	Molecular Tools for Investigating ANME Community Structure and Function. <i>Methods in Enzymology</i> , 2011, 494, 75-90.	1.0	3
101	A High Throughput Screen for Biomining Cellulase Activity from Metagenomic Libraries. <i>Journal of Visualized Experiments</i> , 2011, , .	0.3	11
102	The art and design of functional metagenomic screens. <i>Current Opinion in Biotechnology</i> , 2011, 22, 465-472.	6.6	90
103	Microbial community dynamics in a seasonally anoxic fjord: Saanich Inlet, British Columbia. <i>Environmental Microbiology</i> , 2010, 12, 172-191.	3.8	198
104	Small Volume (1-3l) Filtration of Coastal Seawater Samples. <i>Journal of Visualized Experiments</i> , 2009, , .	0.3	7
105	Metagenome of a Versatile Chemolithoautotroph from Expanding Oceanic Dead Zones. <i>Science</i> , 2009, 326, 578-582.	12.6	312
106	Large Insert Environmental Genomic Library Production. <i>Journal of Visualized Experiments</i> , 2009, , .	0.3	14
107	Extraction of High Molecular Weight Genomic DNA from Soils and Sediments. <i>Journal of Visualized Experiments</i> , 2009, , .	0.3	12
108	DNA Extraction from 0.22 μm Sterivex Filters and Cesium Chloride Density Gradient Centrifugation. <i>Journal of Visualized Experiments</i> , 2009, , .	0.3	40

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109	Community Genomics Among Stratified Microbial Assemblages in the Ocean's Interior. <i>Science</i> , 2006, 311, 496-503.	12.6	1,261
110	Pathways of Carbon Assimilation and Ammonia Oxidation Suggested by Environmental Genomic Analyses of Marine Crenarchaeota. <i>PLoS Biology</i> , 2006, 4, e95.	5.6	554
111	Reverse Methanogenesis: Testing the Hypothesis with Environmental Genomics. <i>Science</i> , 2004, 305, 1457-1462.	12.6	624
112	Identification of Methyl Coenzyme M Reductase A (<i>mcrA</i>) Genes Associated with Methane-Oxidizing Archaea. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5483-5491.	3.1	353