

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	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	Community Genomics Among Stratified Microbial Assemblages in the Ocean's Interior. <i>Science</i> , 2006, 311, 496-503.	12.6	1,261
4	Reverse Methanogenesis: Testing the Hypothesis with Environmental Genomics. <i>Science</i> , 2004, 305, 1457-1462.	12.6	624
5	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
6	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
7	Microbial ecology of expanding oxygen minimum zones. <i>Nature Reviews Microbiology</i> , 2012, 10, 381-394.	28.6	454
8	Viral dark matter and virus-host interactions resolved from publicly available microbial genomes. <i>ELife</i> , 2015, 4, .	6.0	400
9	Identification of Methyl Coenzyme M Reductase A (mcrA) Genes Associated with Methane-Oxidizing Archaea. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5483-5491.	3.1	353
10	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
11	Metagenome of a Versatile Chemolithoautotroph from Expanding Oceanic Dead Zones. <i>Science</i> , 2009, 326, 578-582.	12.6	312
12	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	9.8	232
13	Major role of nitrite-oxidizing bacteria in dark ocean carbon fixation. <i>Science</i> , 2017, 358, 1046-1051.	12.6	229
14	Metabolic reprogramming by viruses in the sunlit and dark ocean. <i>Genome Biology</i> , 2013, 14, R123.	9.6	208
15	Single-cell genomics-based analysis of virus-host interactions in marine surface bacterioplankton. <i>ISME Journal</i> , 2015, 9, 2386-2399.	9.8	207
16	Microbial community dynamics in a seasonally anoxic fjord: Saanich Inlet, British Columbia. <i>Environmental Microbiology</i> , 2010, 12, 172-191.	3.8	198
17	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
18	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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19	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
20	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
21	Phylogeny and physiology of candidate phylum "Atribacteria"™ (OP9/JS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	9.8	166
22	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
23	Non-symbiotic <i>Bradyrhizobium</i> ecotypes dominate North American forest soils. <i>ISME Journal</i> , 2015, 9, 2435-2441.	9.8	142
24	Illuminating Microbial Dark Matter in Meromictic Sakinaw Lake. <i>Applied and Environmental Microbiology</i> , 2014, 80, 6807-6818.	3.1	109
25	Effect of oxygen minimum zone formation on communities of marine protists. <i>ISME Journal</i> , 2012, 6, 1586-1601.	9.8	108
26	MetaPathways: a modular pipeline for constructing pathway/genome databases from environmental sequence information. <i>BMC Bioinformatics</i> , 2013, 14, 202.	2.6	100
27	Diverse Marinimicrobia bacteria may mediate coupled biogeochemical cycles along eco-thermodynamic gradients. <i>Nature Communications</i> , 2017, 8, 1507.	12.8	99
28	Ecology of inorganic sulfur auxiliary metabolism in widespread bacteriophages. <i>Nature Communications</i> , 2021, 12, 3503.	12.8	97
29	Forest harvesting reduces the soil metagenomic potential for biomass decomposition. <i>ISME Journal</i> , 2015, 9, 2465-2476.	9.8	96
30	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
31	The art and design of functional metagenomic screens. <i>Current Opinion in Biotechnology</i> , 2011, 22, 465-472.	6.6	90
32	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
33	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
34	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
35	Mercury methylation by metabolically versatile and cosmopolitan marine bacteria. <i>ISME Journal</i> , 2021, 15, 1810-1825.	9.8	74
36	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

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37	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
38	Metagenomes Reveal Global Distribution of Bacterial Steroid Catabolism in Natural, Engineered, and Host Environments. <i>MBio</i> , 2018, 9, .	4.1	72
39	Potential virus-mediated nitrogen cycling in oxygen-depleted oceanic waters. <i>ISME Journal</i> , 2021, 15, 981-998.	9.8	71
40	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
41	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
42	Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. <i>PLoS Biology</i> , 2022, 20, e3001508.	5.6	62
43	MetaPathways v2.5: quantitative functional, taxonomic and usability improvements. <i>Bioinformatics</i> , 2015, 31, 3345-3347.	4.1	57
44	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
45	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
46	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
47	Metabolic pathways for the whole community. <i>BMC Genomics</i> , 2014, 15, 619.	2.8	50
48	Single cell genomics of uncultured marine alveolates shows paraphyly of basal dinoflagellates. <i>ISME Journal</i> , 2018, 12, 304-308.	9.8	40
49	DNA Extraction from 0.22 μm Sterivex Filters and Cesium Chloride Density Gradient Centrifugation. <i>Journal of Visualized Experiments</i> , 2009, , .	0.3	40
50	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
51	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
52	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
53	Biomining active cellulases from a mining bioremediation system. <i>Journal of Biotechnology</i> , 2013, 167, 462-471.	3.8	35
54	A compendium of multi-omic sequence information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170160.	5.3	35

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55	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021, 12, 3076.	12.8	35
56	Unexpected genomic features in widespread intracellular bacteria: evidence for motility of marine chlamydiae. <i>ISME Journal</i> , 2017, 11, 2334-2344.	9.8	34
57	Patterns of Endemism and Habitat Selection in Coalbed Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7924-7937.	3.1	31
58	A compendium of geochemical information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170159.	5.3	29
59	Biocatalysts for biomass deconstruction from environmental genomics. <i>Current Opinion in Chemical Biology</i> , 2015, 29, 18-25.	6.1	28
60	Nutrient Acquisition and the Metabolic Potential of Photoferrotrophic Chlorobi. <i>Frontiers in Microbiology</i> , 2017, 8, 1212.	3.5	28
61	Draft Genome Sequence of the Pelagic Photoferrotroph <i>Chlorobium phaeoferrooxidans</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	28
62	The information science of microbial ecology. <i>Current Opinion in Microbiology</i> , 2016, 31, 209-216.	5.1	26
63	LCA*: an entropy-based measure for taxonomic assignment within assembled metagenomes. <i>Bioinformatics</i> , 2016, 32, 3535-3542.	4.1	23
64	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
65	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
66	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
67	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
68	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
69	Pelagic Oxygen Minimum Zone Microbial Communities. , 2013, , 113-122.		18
70	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
71	Methanotrophic Community Dynamics in a Seasonally Anoxic Fjord: Saanich Inlet, British Columbia. <i>Frontiers in Marine Science</i> , 2016, 3, .	2.5	17
72	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

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73	Systematic Screening of Synthetic Gene-Encoded Enzymes for Synthesis of Modified Glycosides. ACS Catalysis, 2019, 9, 3219-3227.	11.2	17
74	A multi-year time-series of N ₂ O dynamics in a seasonally anoxic fjord: Saanich Inlet, British Columbia. Limnology and Oceanography, 2018, 63, 524-539.	3.1	16
75	Sampling and Processing Methods Impact Microbial Community Structure and Potential Activity in a Seasonally Anoxic Fjord: Saanich Inlet, British Columbia. Frontiers in Marine Science, 2019, 6, .	2.5	16
76	FragGeneScan-plus for scalable high-throughput short-read open reading frame prediction. , 2015, , .		15
77	Large Insert Environmental Genomic Library Production. Journal of Visualized Experiments, 2009, , .	0.3	14
78	Monitoring microbial responses to ocean deoxygenation in a model oxygen minimum zone. Scientific Data, 2017, 4, 170158.	5.3	14
79	Prokaryotic responses to a warm temperature anomaly in northeast subarctic Pacific waters. Communications Biology, 2021, 4, 1217.	4.4	14
80	Biochar amendment rapidly shifts microbial community structure with enhanced thermophilic digestion activity. Bioresource Technology, 2021, 341, 125864.	9.6	13
81	Extraction of High Molecular Weight Genomic DNA from Soils and Sediments. Journal of Visualized Experiments, 2009, , .	0.3	12
82	MetaPathways v2.0: A master-worker model for environmental Pathway/Genome Database construction on grids and clouds. , 2014, , .		12
83	Expanding the phylogenetic distribution of cytochrome <i>c</i> -containing methanogenic archaea sheds light on the evolution of methanogenesis. ISME Journal, 2022, 16, 2373-2387.	9.8	12
84	A High Throughput Screen for Biomining Cellulase Activity from Metagenomic Libraries. Journal of Visualized Experiments, 2011, , .	0.3	11
85	High-Throughput Recovery and Characterization of Metagenome-Derived Glycoside Hydrolase-Containing Clones as a Resource for Biocatalyst Development. MSystems, 2019, 4, .	3.8	11
86	Metagenomic discovery of a novel transaminase for valorization of monoaromatic compounds. RSC Advances, 2018, 8, 22490-22497.	3.6	10
87	Time-series CH ₄ measurements from Saanich Inlet, BC, a seasonally anoxic fjord. Marine Chemistry, 2019, 215, 103664.	2.3	10
88	Metabolic pathway inference using multi-label classification with rich pathway features. PLoS Computational Biology, 2020, 16, e1008174.	3.2	10
89	Rates and Pathways of N ₂ Production in a Persistently Anoxic Fjord: Saanich Inlet, British Columbia. Frontiers in Marine Science, 2019, 6, .	2.5	9
90	Leveraging heterogeneous network embedding for metabolic pathway prediction. Bioinformatics, 2021, 37, 822-829.	4.1	9

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91	A geographically-diverse collection of 418 human gut microbiome pathway genome databases. <i>Scientific Data</i> , 2017, 4, 170035.	5.3	8
92	TreeSAPP: the Tree-based Sensitive and Accurate Phylogenetic Profiler. <i>Bioinformatics</i> , 2020, 36, 4706-4713.	4.1	8
93	An integrated, modular approach to data science education in microbiology. <i>PLoS Computational Biology</i> , 2021, 17, e1008661.	3.2	8
94	Small Volume (1-3l) Filtration of Coastal Seawater Samples. <i>Journal of Visualized Experiments</i> , 2009, , .	0.3	7
95	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
96	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
97	The Kwakshua Watersheds Observatory, central coast of British Columbia, Canada. <i>Hydrological Processes</i> , 2021, 35, e14198.	2.6	4
98	Metabolic Pathway Prediction Using Non-Negative Matrix Factorization with Improved Precision. <i>Journal of Computational Biology</i> , 2021, 28, 1075-1103.	1.6	4
99	Molecular Tools for Investigating ANME Community Structure and Function. <i>Methods in Enzymology</i> , 2011, 494, 75-90.	1.0	3
100	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
101	FAST: Fast annotation with synchronized threads. , 2016, , .		2
102	Recovering cellular biomass from fluids using chemical flocculation. <i>Environmental Microbiology Reports</i> , 2018, 10, 686-694.	2.4	2
103	Metabolic Pathway Prediction using Non-negative Matrix Factorization with Improved Precision. <i>Lecture Notes in Computer Science</i> , 2021, , 33-44.	1.3	2
104	Hive Panel Explorer: an interactive network visualization tool. <i>Bioinformatics</i> , 2021, 37, 436-437.	4.1	1
105	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
106	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
107	Aggregating Statistically Correlated Metabolic Pathways Into Groups to Improve Prediction Performance. , 2022, , .		0
108	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

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109	Metabolic pathway inference using multi-label classification with rich pathway features. , 2020, 16, e1008174.		0
110	Metabolic pathway inference using multi-label classification with rich pathway features. , 2020, 16, e1008174.		0
111	Metabolic pathway inference using multi-label classification with rich pathway features. , 2020, 16, e1008174.		0
112	Metabolic pathway inference using multi-label classification with rich pathway features. , 2020, 16, e1008174.		0