

Scott Kelley

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

56,049
citations

81434

41
h-index

58552

86
g-index

103
all docs

103
docs citations

103
times ranked

66315
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative profiling of built environment bacterial and fungal communities reveals dynamic material dependent growth patterns and microbial interactions. <i>Indoor Air</i> , 2021, 31, 188-205.	2.0	10
2	Alterations in Gut Microbiota Do Not Play a Causal Role in Diet-independent Weight Gain Caused by Ovariectomy. <i>Journal of the Endocrine Society</i> , 2021, 5, bvaa173.	0.1	6
3	Building a Diverse Workforce and Thinkforce to Reduce Health Disparities. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 1569.	1.2	8
4	Compositional Data Analysis of Periodontal Disease Microbial Communities. <i>Frontiers in Microbiology</i> , 2021, 12, 617949.	1.5	12
5	Gut Metabolites Are More Predictive of Disease and Cohoused States than Gut Bacterial Features in a Polycystic Ovary Syndrome-Like Mouse Model. <i>MSystems</i> , 2021, 6, e0114920.	1.7	8
6	Automated high confidence compound identification of electron ionization mass spectra for nontargeted analysis. <i>Journal of Chromatography A</i> , 2021, 1660, 462656.	1.8	4
7	Viruses in the Built Environment (VIBE) meeting report. <i>Microbiome</i> , 2020, 8, 1.	4.9	345
8	An application of compositional data analysis to multiomic time-series data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa079.	1.5	15
9	Chemical composition of material extractives influences microbial growth and dynamics on wetted wood materials. <i>Scientific Reports</i> , 2020, 10, 14500.	1.6	4
10	Temporal variations in bacterial community diversity and composition throughout intensive care unit renovations. <i>Microbiome</i> , 2020, 8, 86.	4.9	14
11	Meta-SourceTracker: application of Bayesian source tracking to shotgun metagenomics. <i>PeerJ</i> , 2020, 8, e8783.	0.9	43
12	Discovery of a Novel Periodontal Disease-Associated Bacterium. <i>Microbial Ecology</i> , 2019, 77, 267-276.	1.4	26
13	Effects of moderate, voluntary ethanol consumption on the rat and human gut microbiome. <i>Addiction Biology</i> , 2019, 24, 617-630.	1.4	46
14	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	5.9	184
15	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
16	Letrozole treatment of pubertal female mice results in activational effects on reproduction, metabolism and the gut microbiome. <i>PLoS ONE</i> , 2019, 14, e0223274.	1.1	37
17	Geothermal steam vents of Hawaii™. , 2019, , 23-40.		2
18	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , 2019, 4, .	1.7	214

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19	Exposure to a Healthy Gut Microbiome Protects Against Reproductive and Metabolic Dysregulation in a PCOS Mouse Model. <i>Endocrinology</i> , 2019, 160, 1193-1204.	1.4	70
20	Microbial and metabolic succession on common building materials under high humidity conditions. <i>Nature Communications</i> , 2019, 10, 1767.	5.8	46
21	Letrozole treatment of adult female mice results in a similar reproductive phenotype but distinct changes in metabolism and the gut microbiome compared to pubertal mice. <i>BMC Microbiology</i> , 2019, 19, 57.	1.3	31
22	Seasonal dynamics of DNA and RNA viral bioaerosol communities in a daycare center. <i>Microbiome</i> , 2019, 7, 53.	4.9	30
23	Periodontal disease and its connection to systemic biomarkers of cardiovascular disease in young American Indian/Alaskan natives. <i>Journal of Periodontology</i> , 2018, 89, 219-227.	1.7	16
24	Gut Microbial Diversity in Women With Polycystic Ovary Syndrome Correlates With Hyperandrogenism. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 1502-1511.	1.8	224
25	Sampling, Extraction, and High-Throughput Sequencing Methods for Environmental Microbial and Viral Communities. <i>Methods in Molecular Biology</i> , 2018, 1712, 163-173.	0.4	2
26	Draft Genome Sequence of USA100 Methicillin-Resistant <i>Staphylococcus aureus</i> Strain 209. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
27	A new method for discovering EMAST sequences in animal models of cancer. <i>Scientific Reports</i> , 2018, 8, 13764.	1.6	2
28	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
29	Computational Biology: A Hypertextbook. , 2018, , .		2
30	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <i>MSystems</i> , 2017, 2, .	1.7	47
31	Endosymbiont interference and microbial diversity of the Pacific coast tick, <i>Dermacentor occidentalis</i> , in San Diego County, California. <i>PeerJ</i> , 2017, 5, e3202.	0.9	50
32	The Gut Microbiome Is Altered in a Letrozole-Induced Mouse Model of Polycystic Ovary Syndrome. <i>PLoS ONE</i> , 2016, 11, e0146509.	1.1	145
33	Rapid assemblage of diverse environmental fungal communities on public restroom floors. <i>Indoor Air</i> , 2016, 26, 869-879.	2.0	20
34	Geography and Location Are the Primary Drivers of Office Microbiome Composition. <i>MSystems</i> , 2016, 1, .	1.7	110
35	ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. <i>Microbiome</i> , 2016, 4, 11.	4.9	51
36	Biodiversity hot spot on a hot spot: novel extremophile diversity in Hawaiian fumaroles. <i>MicrobiologyOpen</i> , 2015, 4, 267-281.	1.2	16

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37	Changes in microbial communities along redox gradients in polygonized <sc>A</sc>ctic wet tundra soils. Environmental Microbiology Reports, 2015, 7, 649-657.	1.0	42
38	Draft Genome Sequence of " Candidatus Bacteroides pericalifornicus," a New Member of the Bacteroidetes Phylum Found within the Oral Microbiome of Periodontitis Patients. Genome Announcements, 2015, 3, .	0.8	11
39	Ecological Succession and Viability of Human-Associated Microbiota on Restroom Surfaces. Applied and Environmental Microbiology, 2015, 81, 765-773.	1.4	89
40	Characterization of the salivary microbiome in patients with pancreatic cancer. PeerJ, 2015, 3, e1373.	0.9	150
41	The Personal Human Oral Microbiome Obscures the Effects of Treatment on Periodontal Disease. PLoS ONE, 2014, 9, e86708.	1.1	79
42	Advancing the Microbiome Research Community. Cell, 2014, 159, 227-230.	13.5	64
43	Studying the microbiology of the indoor environment. Genome Biology, 2013, 14, 202.	13.9	129
44	The Hospital Microbiome Project: Meeting Report for the 1st Hospital Microbiome Project Workshop on sampling design and building science measurements, Chicago, USA, June 7th-8th 2012. Standards in Genomic Sciences, 2013, 8, 112-117.	1.5	18
45	The Hospital Microbiome Project: Meeting report for the 2nd Hospital Microbiome Project, Chicago, USA, January 15th, 2013. Standards in Genomic Sciences, 2013, 8, 571-579.	1.5	11
46	Bacterial Diversity in Two Neonatal Intensive Care Units (NICUs). PLoS ONE, 2013, 8, e54703.	1.1	120
47	Microbial Diversity in Acidic High-Temperature Steam Vents. Cellular Origin and Life in Extreme Habitats, 2013, , 315-332.	0.3	2
48	Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. PLoS Computational Biology, 2012, 8, e1002358.	1.5	939
49	Ancestral State Reconstruction for Dendroctonus Bark Beetles: Evolution of a Tree Killer. Environmental Entomology, 2012, 41, 723-730.	0.7	22
50	Bacterial Flora of Dental Periradicular Lesions Analyzed by the 454-Pyrosequencing Technology. Journal of Endodontics, 2012, 38, 1484-1488.	1.4	37
51	Office Space Bacterial Abundance and Diversity in Three Metropolitan Areas. PLoS ONE, 2012, 7, e37849.	1.1	114
52	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MIXS) specifications. Nature Biotechnology, 2011, 29, 415-420.	9.4	608
53	Role of the terrestrial subsurface in shaping geothermal spring microbial communities. Environmental Microbiology Reports, 2011, 3, 491-499.	1.0	6
54	Microbial diversity in nonsulfur, sulfur and iron geothermal steam vents. FEMS Microbiology Ecology, 2011, 76, 74-88.	1.3	47

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55	Supervised classification of microbiota mitigates mislabeling errors. <i>ISME Journal</i> , 2011, 5, 570-573.	4.4	42
56	Comparative analysis of microbial diversity in Longitarsus flea beetles (Coleoptera: Chrysomelidae). <i>Genetica</i> , 2011, 139, 541-550.	0.5	39
57	Bayesian community-wide culture-independent microbial source tracking. <i>Nature Methods</i> , 2011, 8, 761-763.	9.0	1,284
58	Host-Associated and Free-Living Phage Communities Differ Profoundly in Phylogenetic Composition. <i>PLoS ONE</i> , 2011, 6, e16900.	1.1	43
59	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
60	Inbreeding variability and population structure in the invasive haplodiploid palm seed borer (<i>Coccotrypes dactyliperda</i>). <i>Journal of Evolutionary Biology</i> , 2009, 22, 1076-1087.	0.8	27
61	Mate availability contributes to maintain the mixed mating system in a scolytid beetle. <i>Journal of Evolutionary Biology</i> , 2009, 22, 1526-1534.	0.8	15
62	Rapid development of multiple nuclear loci for phylogenetic analysis using genomic resources: An example from squamate reptiles. <i>Molecular Phylogenetics and Evolution</i> , 2008, 47, 129-142.	1.2	229
63	Biodiversity and biogeography of phages in modern stromatolites and thrombolites. <i>Nature</i> , 2008, 452, 340-343.	13.7	251
64	Halophilic <i>Archaea</i> determined from geothermal steam vent aerosols. <i>Environmental Microbiology</i> , 2008, 10, 1582-1590.	1.8	35
65	Viral diversity and dynamics in an infant gut. <i>Research in Microbiology</i> , 2008, 159, 367-373.	1.0	288
66	Phylogenetic classification of short environmental DNA fragments. <i>Nucleic Acids Research</i> , 2008, 36, 2230-2239.	6.5	246
67	Effects of Abiotic Factors on the Phylogenetic Diversity of Bacterial Communities in Acidic Thermal Springs. <i>Applied and Environmental Microbiology</i> , 2007, 73, 2612-2623.	1.4	70
68	Murine Noroviruses Comprising a Single Genogroup Exhibit Biological Diversity despite Limited Sequence Divergence. <i>Journal of Virology</i> , 2007, 81, 10460-10473.	1.5	235
69	Quantitative and Qualitative $\hat{\alpha}^2$ Diversity Measures Lead to Different Insights into Factors That Structure Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1576-1585.	1.4	2,418
70	Phylogenetic diversity of Pasteurellaceae and horizontal gene transfer of leukotoxin in wild and domestic sheep. <i>Infection, Genetics and Evolution</i> , 2007, 7, 13-23.	1.0	14
71	Culture-independent analysis of bacterial diversity in a child-care facility. <i>BMC Microbiology</i> , 2007, 7, 27.	1.3	69
72	MICROBIAL DIVERSITY IN BIGHORN SHEEP REVEALED BY CULTURE-INDEPENDENT METHODS. <i>Journal of Wildlife Diseases</i> , 2006, 42, 545-555.	0.3	20

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73	The Marine Viromes of Four Oceanic Regions. <i>PLoS Biology</i> , 2006, 4, e368.	2.6	867
74	Molecular survey of aeroplane bacterial contamination. <i>Journal of Applied Microbiology</i> , 2005, 99, 502-508.	1.4	38
75	Structural implications of novel diversity in eucaryal RNase P RNA. <i>Rna</i> , 2005, 11, 739-751.	1.6	55
76	Microscopic examination of acidic hot springs of Waiotapu, North Island, New Zealand. <i>New Zealand Journal of Marine and Freshwater Research</i> , 2005, 39, 1001-1011.	0.8	12
77	Molecular identification of potential pathogens in water and air of a hospital therapy pool. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4860-4865.	3.3	210
78	Molecular Analysis of Shower Curtain Biofilm Microbes. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4187-4192.	1.4	128
79	New Perspective on Uncultured Bacterial Phylogenetic Division OP11. <i>Applied and Environmental Microbiology</i> , 2004, 70, 845-849.	1.4	190
80	The Genetic Core of the Universal Ancestor. <i>Genome Research</i> , 2003, 13, 407-412.	2.4	253
81	Evaluation and refinement of tmRNA structure using gene sequences from natural microbial communities. <i>Rna</i> , 2001, 7, 1310-1316.	1.6	11
82	Phylogeny and Host Specificity of Psoroptic Mange Mites (Acarina: Psoroptidae) as Indicated by ITS Sequence Data. <i>Journal of Medical Entomology</i> , 2000, 37, 791-796.	0.9	21
83	Reproductive Biology of Two <i>Coelioxys</i> Cleptoparasites in Relation to Their <i>Megachile</i> Hosts (Hymenoptera: Megachilidae). <i>Annals of the Entomological Society of America</i> , 2000, 93, 941-948.	1.3	18
84	Improved statistical methods reveal direct interactions between 16S and 23S rRNA. <i>Nucleic Acids Research</i> , 2000, 28, 4938-4943.	6.5	6
85	Strong Differentiation in Mitochondrial Dna of <i>Dendroctonus brevicomis</i> (Coleoptera: Scolytidae) on Different Subspecies of Ponderosa Pine. <i>Annals of the Entomological Society of America</i> , 1999, 92, 193-197.	1.3	39
86	Phylogenetic Analyses Reveal Ancient Duplication of Estrogen Receptor Isoforms. <i>Journal of Molecular Evolution</i> , 1999, 49, 609-614.	0.8	29
87	Evidence for high rates of self-fertilization in the alpine herb <i>Epilobium anagallidifolium</i> (Onagraceae). <i>Canadian Journal of Botany</i> , 1998, 76, 1978-1980.	1.2	2