

Eric J Alm

List of Publications by Year in descending order

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Version: 2024-02-01

104
papers

27,957
citations

28242

55
h-index

27389

106
g-index

131
all docs

131
docs citations

131
times ranked

32469
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	Inferring Correlation Networks from Genomic Survey Data. <i>PLoS Computational Biology</i> , 2012, 8, e1002687.	1.5	1,874
3	Salt-responsive gut commensal modulates TH17 axis and disease. <i>Nature</i> , 2017, 551, 585-589.	13.7	896
4	Ecology drives a global network of gene exchange connecting the human microbiome. <i>Nature</i> , 2011, 480, 241-244.	13.7	788
5	Host lifestyle affects human microbiota on daily timescales. <i>Genome Biology</i> , 2014, 15, R89.	13.9	735
6	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. <i>Nature Communications</i> , 2017, 8, 1784.	5.8	714
7	SARS-CoV-2 Titers in Wastewater Are Higher than Expected from Clinically Confirmed Cases. <i>MSystems</i> , 2020, 5, .	1.7	649
8	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	4.4	593
9	Population Genomics of Early Events in the Ecological Differentiation of Bacteria. <i>Science</i> , 2012, 336, 48-51.	6.0	484
10	Fecal Microbiota Transplant for Relapsing <i>Clostridium difficile</i> Infection Using a Frozen Inoculum From Unrelated Donors: A Randomized, Open-Label, Controlled Pilot Study. <i>Clinical Infectious Diseases</i> , 2014, 58, 1515-1522.	2.9	397
11	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. <i>Trends in Genetics</i> , 2013, 29, 170-175.	2.9	364
12	Unraveling the processes shaping mammalian gut microbiomes over evolutionary time. <i>Nature Communications</i> , 2017, 8, 14319.	5.8	357
13	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	351
14	A novel method for accurate operon predictions in all sequenced prokaryotes. <i>Nucleic Acids Research</i> , 2005, 33, 880-892.	6.5	316
15	Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Fecal Microbiota Transplantation. <i>Cell Host and Microbe</i> , 2018, 23, 229-240.e5.	5.1	292
16	Adaptive Evolution within Gut Microbiomes of Healthy People. <i>Cell Host and Microbe</i> , 2019, 25, 656-667.e8.	5.1	289
17	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. <i>PLoS Computational Biology</i> , 2005, 1, e55.	1.5	260
18	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. <i>Nature Medicine</i> , 2019, 25, 1442-1452.	15.2	255

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19	Non-Invasive Mapping of the Gastrointestinal Microbiota Identifies Children with Inflammatory Bowel Disease. PLoS ONE, 2012, 7, e39242.	1.1	252
20	An omics-based framework for assessing the health risk of antimicrobial resistance genes. Nature Communications, 2021, 12, 4765.	5.8	248
21	Mobile genes in the human microbiome are structured from global to individual scales. Nature, 2016, 535, 435-439.	13.7	233
22	A practical guide to methods controlling false discoveries in computational biology. Genome Biology, 2019, 20, 118.	3.8	222
23	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. Microbiome, 2020, 8, 51.	4.9	205
24	SARS-CoV-2 RNA concentrations in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases. Science of the Total Environment, 2022, 805, 150121.	3.9	192
25	Massively parallel sequencing of single cells by epicPCR links functional genes with phylogenetic markers. ISME Journal, 2016, 10, 427-436.	4.4	184
26	The MicrobesOnline Web site for comparative genomics. Genome Research, 2005, 15, 1015-1022.	2.4	176
27	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. MBio, 2015, 6, e00326-15.	1.8	173
28	Elevated rates of horizontal gene transfer in the industrialized human microbiome. Cell, 2021, 184, 2053-2067.e18.	13.5	167
29	Transmission of human-associated microbiota along family and social networks. Nature Microbiology, 2019, 4, 964-971.	5.9	149
30	The Life-Cycle of Operons. PLoS Genetics, 2006, 2, e96.	1.5	146
31	Detection of low-abundance bacterial strains in metagenomic datasets by eigengenome partitioning. Nature Biotechnology, 2015, 33, 1053-1060.	9.4	144
32	Distribution-Based Clustering: Using Ecology To Refine the Operational Taxonomic Unit. Applied and Environmental Microbiology, 2013, 79, 6593-6603.	1.4	140
33	Adaptive radiation by waves of gene transfer leads to fine-scale resource partitioning in marine microbes. Nature Communications, 2016, 7, 12860.	5.8	140
34	Making waves: Wastewater surveillance of SARS-CoV-2 for population-based health management. Water Research, 2020, 184, 116181.	5.3	138
35	Operon formation is driven by co-regulation and not by horizontal gene transfer. Genome Research, 2005, 15, 809-819.	2.4	131
36	Co-evolution and Co-speciation of Host-Gut Bacteria Systems. Cell Host and Microbe, 2020, 28, 12-22.	5.1	128

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37	High resolution time series reveals cohesive but short-lived communities in coastal plankton. <i>Nature Communications</i> , 2018, 9, 266.	5.8	122
38	Wastewater surveillance of SARS-CoV-2 across 40 U.S. states from February to June 2020. <i>Water Research</i> , 2021, 202, 117400.	5.3	119
39	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019, 10, 358-366.	4.3	118
40	Probiotic Microbes Sustain Youthful Serum Testosterone Levels and Testicular Size in Aging Mice. <i>PLoS ONE</i> , 2014, 9, e84877.	1.1	114
41	Correcting for batch effects in case-control microbiome studies. <i>PLoS Computational Biology</i> , 2018, 14, e1006102.	1.5	108
42	Random sequences rapidly evolve into de novo promoters. <i>Nature Communications</i> , 2018, 9, 1530.	5.8	105
43	Microbial lysate upregulates host oxytocin. <i>Brain, Behavior, and Immunity</i> , 2017, 61, 36-49.	2.0	101
44	Two dynamic regimes in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017, 13, e1005364.	1.5	101
45	High-throughput, single-microbe genomics with strain resolution, applied to a human gut microbiome. <i>Science</i> , 2022, 376, .	6.0	100
46	Dysbiosis is not an answer. <i>Nature Microbiology</i> , 2016, 1, 16228.	5.9	97
47	Defining the gut microbiota in individuals with periodontal diseases: an exploratory study. <i>Journal of Oral Microbiology</i> , 2018, 10, 1487741.	1.2	96
48	Looking for Darwin's footprints in the microbial world. <i>Trends in Microbiology</i> , 2009, 17, 196-204.	3.5	94
49	Invertible promoters mediate bacterial phase variation, antibiotic resistance, and host adaptation in the gut. <i>Science</i> , 2019, 363, 181-187.	6.0	85
50	Metagenomic mining of regulatory elements enables programmable species-selective gene expression. <i>Nature Methods</i> , 2018, 15, 323-329.	9.0	80
51	Virtual microfluidics for digital quantification and single-cell sequencing. <i>Nature Methods</i> , 2016, 13, 759-762.	9.0	79
52	Metapopulation structure of <i>Vibrionaceae</i> among coastal marine invertebrates. <i>Environmental Microbiology</i> , 2011, 13, 265-275.	1.8	76
53	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. <i>Cell Reports</i> , 2018, 24, 1842-1851.	2.9	72
54	Quantitative SARS-CoV-2 Alpha Variant B.1.1.7 Tracking in Wastewater by Allele-Specific RT-qPCR. <i>Environmental Science and Technology Letters</i> , 2021, 8, 675-682.	3.9	68

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55	Profiling Living Bacteria Informs Preparation of Fecal Microbiota Transplantations. PLoS ONE, 2017, 12, e0170922.	1.1	68
56	Metrics to relate COVID-19 wastewater data to clinical testing dynamics. Water Research, 2022, 212, 118070.	5.3	68
57	Improved gene tree error correction in the presence of horizontal gene transfer. Bioinformatics, 2015, 31, 1211-1218.	1.8	64
58	Anatomy promotes neutral coexistence of strains in the human skin microbiome. Cell Host and Microbe, 2022, 30, 171-182.e7.	5.1	62
59	Daily, oral FMT for long-term maintenance therapy in ulcerative colitis: results of a single-center, prospective, randomized pilot study. BMC Gastroenterology, 2021, 21, 281.	0.8	61
60	Transfer of noncoding DNA drives regulatory rewiring in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16112-16117.	3.3	59
61	Comprehensive analysis of chromosomal mobile genetic elements in the gut microbiome reveals phylum-level niche-adaptive gene pools. PLoS ONE, 2019, 14, e0223680.	1.1	59
62	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. MBio, 2018, 9, .	1.8	57
63	Interactions in self-assembled microbial communities saturate with diversity. ISME Journal, 2019, 13, 1602-1617.	4.4	54
64	Nationwide Trends in COVID-19 Cases and SARS-CoV-2 RNA Wastewater Concentrations in the United States. ACS ES&T Water, 2022, 2, 1899-1909.	2.3	46
65	Dietary Microbes Modulate Transgenerational Cancer Risk. Cancer Research, 2015, 75, 1197-1204.	0.4	43
66	Longitudinal immunosequencing in healthy people reveals persistent T cell receptors rich in highly public receptors. BMC Immunology, 2019, 20, 19.	0.9	42
67	Comparing Patterns of Natural Selection across Species Using Selective Signatures. PLoS Genetics, 2008, 4, e23.	1.5	40
68	Endospores and other lysis-resistant bacteria comprise a widely shared core community within the human microbiota. ISME Journal, 2018, 12, 2403-2416.	4.4	40
69	Engineering transcription factors with novel DNA-binding specificity using comparative genomics. Nucleic Acids Research, 2009, 37, 2493-2503.	6.5	39
70	Computational Methods for High-Throughput Comparative Analyses of Natural Microbial Communities. Methods in Enzymology, 2013, 531, 353-370.	0.4	38
71	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. Scientific Reports, 2018, 8, 12699.	1.6	37
72	Making waves: Wastewater surveillance of SARS-CoV-2 in an endemic future. Water Research, 2022, 219, 118535.	5.3	37

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73	Identifying predictive features of <i>Clostridium difficile</i> infection recurrence before, during, and after primary antibiotic treatment. <i>Microbiome</i> , 2017, 5, 148.	4.9	36
74	Framework for rational donor selection in fecal microbiota transplant clinical trials. <i>PLoS ONE</i> , 2019, 14, e0222881.	1.1	36
75	The Vaginal Microbiome as a Tool to Predict rASRM Stage of Disease in Endometriosis: a Pilot Study. <i>Reproductive Sciences</i> , 2020, 27, 1064-1073.	1.1	35
76	Surveys, simulation and single-cell assays relate function and phylogeny in a lake ecosystem. <i>Nature Microbiology</i> , 2016, 1, 16130.	5.9	33
77	Effect of antibiotic pretreatment on bacterial engraftment after Fecal Microbiota Transplant (FMT) in IBS-D. <i>Gut Microbes</i> , 2022, 14, 2020067.	4.3	30
78	Rapid displacement of SARS-CoV-2 variant Delta by Omicron revealed by allele-specific PCR in wastewater. <i>Water Research</i> , 2022, 221, 118809.	5.3	30
79	Gut Ruminococcaceae levels at baseline correlate with risk of antibiotic-associated diarrhea. <i>IScience</i> , 2022, 25, 103644.	1.9	28
80	Using fecal microbiota as biomarkers for predictions of performance in the selective breeding process of pedigree broiler breeders. <i>PLoS ONE</i> , 2019, 14, e0216080.	1.1	27
81	A Mobile Element in <i>mutS</i> Drives Hypermutation in a Marine <i>Vibrio</i> . <i>MBio</i> , 2017, 8, .	1.8	26
82	Dynamic Colonization of Microbes and Their Functions after Fecal Microbiota Transplantation for Inflammatory Bowel Disease. <i>MBio</i> , 2021, 12, e0097521.	1.8	26
83	Culturing of "Unculturable" Subsurface Microbes: Natural Organic Carbon Source Fuels the Growth of Diverse and Distinct Bacteria From Groundwater. <i>Frontiers in Microbiology</i> , 2020, 11, 610001.	1.5	26
84	dbOTU3: A new implementation of distribution-based OTU calling. <i>PLoS ONE</i> , 2017, 12, e0176335.	1.1	24
85	Evolution of a Vegetarian <i>Vibrio</i> : Metabolic Specialization of <i>Vibrio breoganii</i> to Macroalgal Substrates. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	24
86	Inoculum composition determines microbial community and function in an anaerobic sequential batch reactor. <i>PLoS ONE</i> , 2017, 12, e0171369.	1.1	23
87	Prebiotics and Community Composition Influence Gas Production of the Human Gut Microbiota. <i>MBio</i> , 2020, 11, .	1.8	23
88	Persistence of Dengue (Serotypes 2 and 3), Zika, Yellow Fever, and Murine Hepatitis Virus RNA in Untreated Wastewater. <i>Environmental Science and Technology Letters</i> , 2021, 8, 785-791.	3.9	23
89	Wastewater network infrastructure in public health: Applications and learnings from the COVID-19 pandemic. <i>PLOS Global Public Health</i> , 2021, 1, e0000061.	0.5	23
90	Searching for superstool: maximizing the therapeutic potential of FMT. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018, 15, 387-388.	8.2	22

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91	Local Gene Regulation Details a Recognition Code within the LacI Transcriptional Factor Family. PLoS Computational Biology, 2010, 6, e1000989.	1.5	20
92	Development of an efficient wastewater testing protocol for high-throughput country-wide SARS-CoV-2 monitoring. Science of the Total Environment, 2022, 826, 154024.	3.9	17
93	Predicting human health from biofluid-based metabolomics using machine learning. Scientific Reports, 2020, 10, 17635.	1.6	16
94	Genome and sequence determinants governing the expression of horizontally acquired DNA in bacteria. ISME Journal, 2020, 14, 2347-2357.	4.4	16
95	“Waste Not, Want Not” Leveraging Sewer Systems and Wastewater-Based Epidemiology for Drug Use Trends and Pharmaceutical Monitoring. Journal of Medical Toxicology, 2021, 17, 397-410.	0.8	15
96	Designing fecal microbiota transplant trials that account for differences in donor stool efficacy. Statistical Methods in Medical Research, 2018, 27, 2906-2917.	0.7	13
97	Functional heterogeneity in the fermentation capabilities of the healthy human gut microbiota. PLoS ONE, 2021, 16, e0254004.	1.1	11
98	The Histidine Operon Is Ancient. Journal of Molecular Evolution, 2006, 62, 807-808.	0.8	9
99	A Novel Analysis Method for Paired-Sample Microbial Ecology Experiments. PLoS ONE, 2016, 11, e0154804.	1.1	9
100	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. MSystems, 2021, 6, e0053721.	1.7	8
101	16S rRNA sequencing analysis: the devil is in the details. Gut Microbes, 2020, 11, 1139-1142.	4.3	6
102	Sustained Ability of a Natural Microbial Community to Remove Nitrate from Groundwater. Ground Water, 2022, 60, 99-111.	0.7	6
103	“Hygienic” Lymphocytes Convey Increased Cancer Risk. Journal of Analytical Oncology, 2014, 3, 113-121-113-121.	0.1	4
104	Longitudinal wastewater sampling in buildings reveals temporal dynamics of metabolites. PLoS Computational Biology, 2020, 16, e1008001.	1.5	2