

Eric J Alm

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.

118
papers

13,850
citations

49
h-index

117
g-index

131
ext. papers

21,676
ext. citations

13.6
avg, IF

6.53
L-index

#	Paper	IF	Citations
118	Gut Ruminococcaceae levels at baseline correlate with risk of antibiotic-associated diarrhea.. <i>IScience</i> , 2022 , 25, 103644	6.1	3
117	Effect of antibiotic pretreatment on bacterial engraftment after Fecal Microbiota Transplant (FMT) in IBS-D.. <i>Gut Microbes</i> , 2022 , 14, 2020067	8.8	5
116	Metrics to relate COVID-19 wastewater data to clinical testing dynamics.. <i>Water Research</i> , 2022 , 212, 118070	12.5	3
115	Anatomy promotes neutral coexistence of strains in the human skin microbiome.. <i>Cell Host and Microbe</i> , 2022 ,	23.4	6
114	SARS-CoV-2 RNA concentrations in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases. <i>Science of the Total Environment</i> , 2022 , 805, 150121	10.2	51
113	Development of an efficient wastewater testing protocol for high-throughput country-wide SARS-CoV-2 monitoring.. <i>Science of the Total Environment</i> , 2022 , 826, 154024	10.2	0
112	Making Waves: Wastewater Surveillance of SARS-CoV-2 in an Endemic Future. <i>Water Research</i> , 2022 , 118535	12.5	4
111	Wastewater network infrastructure in public health: Applications and learnings from the COVID-19 pandemic.. <i>PLOS Global Public Health</i> , 2021 , 1, e0000061		5
110	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021 , 184, 205357067-918	20.7	18
109	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. <i>MSystems</i> , 2021 , e0053721	7.6	3
108	Metrics to relate COVID-19 wastewater data to clinical testing dynamics 2021 ,		3
107	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	11	17
106	Functional heterogeneity in the fermentation capabilities of the healthy human gut microbiota. <i>PLoS ONE</i> , 2021 , 16, e0254004	3.7	1
105	Daily, oral FMT for long-term maintenance therapy in ulcerative colitis: results of a single-center, prospective, randomized pilot study. <i>BMC Gastroenterology</i> , 2021 , 21, 281	3	14
104	Wastewater Surveillance of SARS-CoV-2 across 40 U.S. states 2021 ,		12
103	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021 , 12, 4765	17.4	25
102	"Waste Not, Want Not" - Leveraging Sewer Systems and Wastewater-Based Epidemiology for Drug Use Trends and Pharmaceutical Monitoring. <i>Journal of Medical Toxicology</i> , 2021 , 17, 397-410	2.6	3

101	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	11	5
100	Dynamic Colonization of Microbes and Their Functions after Fecal Microbiota Transplantation for Inflammatory Bowel Disease. <i>MBio</i> , 2021 , 12, e0097521	7.8	5
99	Wastewater surveillance of SARS-CoV-2 across 40 U.S. states from February to June 2020. <i>Water Research</i> , 2021 , 202, 117400	12.5	35
98	Genome and sequence determinants governing the expression of horizontally acquired DNA in bacteria. <i>ISME Journal</i> , 2020 , 14, 2347-2357	11.9	4
97	Longitudinal wastewater sampling in buildings reveals temporal dynamics of metabolites. <i>PLoS Computational Biology</i> , 2020 , 16, e1008001	5	1
96	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	3	13
95	16S rRNA sequencing analysis: the devil is in the details. <i>Gut Microbes</i> , 2020 , 11, 1139-1142	8.8	1
94	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	5.7	5
93	SARS-CoV-2 titers in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases 2020 ,		56
92	Predicting human health from biofluid-based metabolomics using machine learning. <i>Scientific Reports</i> , 2020 , 10, 17635	4.9	8
91	Making waves: Wastewater surveillance of SARS-CoV-2 for population-based health management. <i>Water Research</i> , 2020 , 184, 116181	12.5	80
90	Co-evolution and Co-speciation of Host-Gut Bacteria Systems. <i>Cell Host and Microbe</i> , 2020 , 28, 12-22	23.4	42
89	SARS-CoV-2 Titers in Wastewater Are Higher than Expected from Clinically Confirmed Cases. <i>MSystems</i> , 2020 , 5,	7.6	385
88	Prebiotics and Community Composition Influence Gas Production of the Human Gut Microbiota. <i>MBio</i> , 2020 , 11,	7.8	8
87	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020 , 8, 51	16.6	64
86	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. <i>Nature Medicine</i> , 2019 , 25, 1442-1452	50.5	125
85	Longitudinal immunosequencing in healthy people reveals persistent T cell receptors rich in highly public receptors. <i>BMC Immunology</i> , 2019 , 20, 19	3.7	21
84	A practical guide to methods controlling false discoveries in computational biology. <i>Genome Biology</i> , 2019 , 20, 118	18.3	64

83	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	3.7	13
82	Adaptive Evolution within Gut Microbiomes of Healthy People. <i>Cell Host and Microbe</i> , 2019 , 25, 656-667.e34	23.4	133
81	Transmission of human-associated microbiota along family and social networks. <i>Nature Microbiology</i> , 2019 , 4, 964-971	26.6	85
80	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
79	Framework for rational donor selection in fecal microbiota transplant clinical trials. <i>PLoS ONE</i> , 2019 , 14, e0222881	3.7	20
78	Interactions in self-assembled microbial communities saturate with diversity. <i>ISME Journal</i> , 2019 , 13, 1602-1617	11.9	26
77	Comprehensive analysis of chromosomal mobile genetic elements in the gut microbiome reveals phylum-level niche-adaptive gene pools. <i>PLoS ONE</i> , 2019 , 14, e0223680	3.7	26
76	Invertible promoters mediate bacterial phase variation, antibiotic resistance, and host adaptation in the gut. <i>Science</i> , 2019 , 363, 181-187	33.3	42
75	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019 , 10, 358-366	8.8	65
74	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018 , 9,	7.8	37
73	Random sequences rapidly evolve into de novo promoters. <i>Nature Communications</i> , 2018 , 9, 1530	17.4	51
72	Evolution of a Vegetarian Vibrio: Metabolic Specialization of <i>Vibrio breoganii</i> to Macroalgal Substrates. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	9
71	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	23.4	177
70	High resolution time series reveals cohesive but short-lived communities in coastal plankton. <i>Nature Communications</i> , 2018 , 9, 266	17.4	62
69	Searching for superstool: maximizing the therapeutic potential of FMT. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 387-388	24.2	16
68	Metagenomic mining of regulatory elements enables programmable species-selective gene expression. <i>Nature Methods</i> , 2018 , 15, 323-329	21.6	46
67	Designing fecal microbiota transplant trials that account for differences in donor stool efficacy. <i>Statistical Methods in Medical Research</i> , 2018 , 27, 2906-2917	2.3	12
66	Defining the gut microbiota in individuals with periodontal diseases: an exploratory study. <i>Journal of Oral Microbiology</i> , 2018 , 10, 1487741	6.3	55

65	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. <i>Scientific Reports</i> , 2018 , 8, 12699	4.9	27
64	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. <i>Cell Reports</i> , 2018 , 24, 1842-1851	10.6	52
63	Endospores and other lysis-resistant bacteria comprise a widely shared core community within the human microbiota. <i>ISME Journal</i> , 2018 , 12, 2403-2416	11.9	22
62	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	159
61	Correcting for batch effects in case-control microbiome studies. <i>PLoS Computational Biology</i> , 2018 , 14, e1006102	5	55
60	Unraveling the processes shaping mammalian gut microbiomes over evolutionary time. <i>Nature Communications</i> , 2017 , 8, 14319	17.4	195
59	A Mobile Element in mutS Drives Hypermutation in a Marine Vibrio. <i>MBio</i> , 2017 , 8,	7.8	14
58	Inoculum composition determines microbial community and function in an anaerobic sequential batch reactor. <i>PLoS ONE</i> , 2017 , 12, e0171369	3.7	17
57	dbOTU3: A new implementation of distribution-based OTU calling. <i>PLoS ONE</i> , 2017 , 12, e0176335	3.7	13
56	Two dynamic regimes in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017 , 13, e1005364	5	56
55	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. <i>Nature Communications</i> , 2017 , 8, 1784	17.4	425
54	Identifying predictive features of Clostridium difficile infection recurrence before, during, and after primary antibiotic treatment. <i>Microbiome</i> , 2017 , 5, 148	16.6	20
53	Salt-responsive gut commensal modulates T17 axis and disease. <i>Nature</i> , 2017 , 551, 585-589	50.4	553
52	Microbial lysate upregulates host oxytocin. <i>Brain, Behavior, and Immunity</i> , 2017 , 61, 36-49	16.6	62
51	Profiling Living Bacteria Informs Preparation of Fecal Microbiota Transplantations. <i>PLoS ONE</i> , 2017 , 12, e0170922	3.7	55
50	Massively parallel sequencing of single cells by epicPCR links functional genes with phylogenetic markers. <i>ISME Journal</i> , 2016 , 10, 427-36	11.9	125
49	Dysbiosis is not an answer. <i>Nature Microbiology</i> , 2016 , 1, 16228	26.6	66
48	Mobile genes in the human microbiome are structured from global to individual scales. <i>Nature</i> , 2016 , 535, 435-439	50.4	148

47	Surveys, simulation and single-cell assays relate function and phylogeny in a lake ecosystem. <i>Nature Microbiology</i> , 2016 , 1, 16130	26.6	24
46	Adaptive radiation by waves of gene transfer leads to fine-scale resource partitioning in marine microbes. <i>Nature Communications</i> , 2016 , 7, 12860	17.4	81
45	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016 , 10, 1669-81	11.9	365
44	A Novel Analysis Method for Paired-Sample Microbial Ecology Experiments. <i>PLoS ONE</i> , 2016 , 11, e0154804	9.4	5
43	Virtual microfluidics for digital quantification and single-cell sequencing. <i>Nature Methods</i> , 2016 , 13, 759-62	62.6	58
42	Detection of low-abundance bacterial strains in metagenomic datasets by eigengenome partitioning. <i>Nature Biotechnology</i> , 2015 , 33, 1053-60	44.5	111
41	Natural bacterial communities serve as quantitative geochemical biosensors. <i>MBio</i> , 2015 , 6, e00326-15	7.8	113
40	Dietary microbes modulate transgenerational cancer risk. <i>Cancer Research</i> , 2015 , 75, 1197-204	10.1	31
39	Improved gene tree error correction in the presence of horizontal gene transfer. <i>Bioinformatics</i> , 2015 , 31, 1211-8	7.2	37
38	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, 1515-22	11.6	313
37	Transfer of noncoding DNA drives regulatory rewiring in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 16112-7	11.5	47
36	Probiotic microbes sustain youthful serum testosterone levels and testicular size in aging mice. <i>PLoS ONE</i> , 2014 , 9, e84877	3.7	77
35	Host lifestyle affects human microbiota on daily timescales. <i>Genome Biology</i> , 2014 , 15, R89	18.3	548
34	Hygienic T lymphocytes convey increased cancer risk. <i>Journal of Analytical Oncology</i> , 2014 , 3, 113-121		4
33	Computational methods for high-throughput comparative analyses of natural microbial communities. <i>Methods in Enzymology</i> , 2013 , 531, 353-70	1.7	23
32	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. <i>Trends in Genetics</i> , 2013 , 29, 170-5	8.5	273
31	Distribution-based clustering: using ecology to refine the operational taxonomic unit. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6593-603	4.8	102
30	Population genomics of early events in the ecological differentiation of bacteria. <i>Science</i> , 2012 , 336, 48-51	33.3	366

29	Non-invasive mapping of the gastrointestinal microbiota identifies children with inflammatory bowel disease. <i>PLoS ONE</i> , 2012 , 7, e39242	3.7	198
28	Inferring correlation networks from genomic survey data. <i>PLoS Computational Biology</i> , 2012 , 8, e1002683	10.4	1037
27	Ecology drives a global network of gene exchange connecting the human microbiome. <i>Nature</i> , 2011 , 480, 241-4	50.4	573
26	Metapopulation structure of Vibrionaceae among coastal marine invertebrates. <i>Environmental Microbiology</i> , 2011 , 13, 265-275	5.2	65
25	Local gene regulation details a recognition code within the LacI transcriptional factor family. <i>PLoS Computational Biology</i> , 2010 , 6, e1000989	5	19
24	Engineering transcription factors with novel DNA-binding specificity using comparative genomics. <i>Nucleic Acids Research</i> , 2009 , 37, 2493-503	20.1	38
23	Looking for Darwin's footprints in the microbial world. <i>Trends in Microbiology</i> , 2009 , 17, 196-204	12.4	71
22	Comparing patterns of natural selection across species using selective signatures. <i>PLoS Genetics</i> , 2008 , 4, e23	6	32
21	The histidine operon is ancient. <i>Journal of Molecular Evolution</i> , 2006 , 62, 807-8	3.1	7
20	The life-cycle of operons. <i>PLoS Genetics</i> , 2006 , 2, e96	6	120
19	A novel method for accurate operon predictions in all sequenced prokaryotes. <i>Nucleic Acids Research</i> , 2005 , 33, 880-92	20.1	279
18	Dissimilatory metabolism of nitrogen oxides in bacteria: comparative reconstruction of transcriptional networks. <i>PLoS Computational Biology</i> , 2005 , 1, e55	5	227
17	Operon formation is driven by co-regulation and not by horizontal gene transfer. <i>Genome Research</i> , 2005 , 15, 809-19	9.7	112
16	The MicrobesOnline Web site for comparative genomics. <i>Genome Research</i> , 2005 , 15, 1015-22	9.7	160
15	Quantitative detection of SARS-CoV-2 Omicron BA.1 and BA.2 variants in wastewater through allele-specific RT-qPCR		3
14	Tracking strains predicts personal microbiomes and reveals recent adaptive evolution		2
13	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
12	Predicting human health from biofluid-based metabolomics using machine learning		1

11	Correcting for batch effects in case-control microbiome studies	3
10	Functional heterogeneity in the fermentation capabilities of the healthy human gut microbiota	2
9	Industrialization is associated with elevated rates of horizontal gene transfer in the human microbiome	1
8	Microbe-seq: high-throughput, single-microbe genomics with strain resolution, applied to a human gut microbiome	4
7	Adaptive evolution within the gut microbiome of individual people	17
6	A practical guide to methods controlling false discoveries in computational biology	4
5	Multi-site sampling and risk prioritization reveals the public health relevance of antibiotic resistance genes found in wastewater environments	1
4	24-hour multi-omics analysis of residential sewage reflects human activity and informs public health	5
3	Quantitative detection of SARS-CoV-2 B.1.1.7 variant in wastewater by allele-specific RT-qPCR	5
2	Anatomy promotes neutral coexistence of strains in the human skin microbiome	2
1	Quantitative SARS-CoV-2 tracking of variants Delta, Delta plus, Kappa and Beta in wastewater by allele-specific RT-qPCR	3