

Eric J Alm

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1578568/eric-j-alm-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
117	Inferring correlation networks from genomic survey data. <i>PLoS Computational Biology</i> , 2012 , 8, e1002683	37.7	1037
116	Ecology drives a global network of gene exchange connecting the human microbiome. <i>Nature</i> , 2011 , 480, 241-4	50.4	573
115	Salt-responsive gut commensal modulates T17 axis and disease. <i>Nature</i> , 2017 , 551, 585-589	50.4	553
114	Host lifestyle affects human microbiota on daily timescales. <i>Genome Biology</i> , 2014 , 15, R89	18.3	548
113	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. <i>Nature Communications</i> , 2017 , 8, 1784	17.4	425
112	SARS-CoV-2 Titers in Wastewater Are Higher than Expected from Clinically Confirmed Cases. <i>MSystems</i> , 2020 , 5,	7.6	385
111	Population genomics of early events in the ecological differentiation of bacteria. <i>Science</i> , 2012 , 336, 48-51	33.3	366
110	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016 , 10, 1669-81	11.9	365
109	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
108	A novel method for accurate operon predictions in all sequenced prokaryotes. <i>Nucleic Acids Research</i> , 2005 , 33, 880-92	20.1	279
107	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. <i>Trends in Genetics</i> , 2013 , 29, 170-5	8.5	273
106	Dissimilatory metabolism of nitrogen oxides in bacteria: comparative reconstruction of transcriptional networks. <i>PLoS Computational Biology</i> , 2005 , 1, e55	5	227
105	Non-invasive mapping of the gastrointestinal microbiota identifies children with inflammatory bowel disease. <i>PLoS ONE</i> , 2012 , 7, e39242	3.7	198
104	Unraveling the processes shaping mammalian gut microbiomes over evolutionary time. <i>Nature Communications</i> , 2017 , 8, 14319	17.4	195
103	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
102	The MicrobesOnline Web site for comparative genomics. <i>Genome Research</i> , 2005 , 15, 1015-22	9.7	160

101	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	159
100	Mobile genes in the human microbiome are structured from global to individual scales. <i>Nature</i> , 2016 , 535, 435-439	50.4	148
99	Adaptive Evolution within Gut Microbiomes of Healthy People. <i>Cell Host and Microbe</i> , 2019 , 25, 656-667.	28.4	133
98	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
97	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
96	The life-cycle of operons. <i>PLoS Genetics</i> , 2006 , 2, e96	6	120
95	Natural bacterial communities serve as quantitative geochemical biosensors. <i>MBio</i> , 2015 , 6, e00326-15	7.8	113
94	Operon formation is driven by co-regulation and not by horizontal gene transfer. <i>Genome Research</i> , 2005 , 15, 809-19	9.7	112
93	Detection of low-abundance bacterial strains in metagenomic datasets by eigengenome partitioning. <i>Nature Biotechnology</i> , 2015 , 33, 1053-60	44.5	111
92	Distribution-based clustering: using ecology to refine the operational taxonomic unit. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 6593-603	4.8	102
91	Transmission of human-associated microbiota along family and social networks. <i>Nature Microbiology</i> , 2019 , 4, 964-971	26.6	85
90	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
89	Making waves: Wastewater surveillance of SARS-CoV-2 for population-based health management. <i>Water Research</i> , 2020 , 184, 116181	12.5	80
88	Probiotic microbes sustain youthful serum testosterone levels and testicular size in aging mice. <i>PLoS ONE</i> , 2014 , 9, e84877	3.7	77
87	Looking for Darwin's footprints in the microbial world. <i>Trends in Microbiology</i> , 2009 , 17, 196-204	12.4	71
86	Dysbiosis is not an answer. <i>Nature Microbiology</i> , 2016 , 1, 16228	26.6	66
85	Metapopulation structure of Vibrionaceae among coastal marine invertebrates. <i>Environmental Microbiology</i> , 2011 , 13, 265-275	5.2	65
84	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. <i>Gut Microbes</i> , 2019 , 10, 358-366	8.8	65

83	A practical guide to methods controlling false discoveries in computational biology. <i>Genome Biology</i> , 2019 , 20, 118	18.3	64
82	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020 , 8, 51	16.6	64
81	High resolution time series reveals cohesive but short-lived communities in coastal plankton. <i>Nature Communications</i> , 2018 , 9, 266	17.4	62
80	Microbial lysate upregulates host oxytocin. <i>Brain, Behavior, and Immunity</i> , 2017 , 61, 36-49	16.6	62
79	Virtual microfluidics for digital quantification and single-cell sequencing. <i>Nature Methods</i> , 2016 , 13, 759-626	62.6	58
78	Two dynamic regimes in the human gut microbiome. <i>PLoS Computational Biology</i> , 2017 , 13, e1005364	5	56
77	SARS-CoV-2 titers in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases 2020 ,		56
76	Defining the gut microbiota in individuals with periodontal diseases: an exploratory study. <i>Journal of Oral Microbiology</i> , 2018 , 10, 1487741	6.3	55
75	Profiling Living Bacteria Informs Preparation of Fecal Microbiota Transplantations. <i>PLoS ONE</i> , 2017 , 12, e0170922	3.7	55
74	Correcting for batch effects in case-control microbiome studies. <i>PLoS Computational Biology</i> , 2018 , 14, e1006102	5	55
73	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. <i>Cell Reports</i> , 2018 , 24, 1842-1851	10.6	52
72	Random sequences rapidly evolve into de novo promoters. <i>Nature Communications</i> , 2018 , 9, 1530	17.4	51
71	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
70	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
69	Metagenomic mining of regulatory elements enables programmable species-selective gene expression. <i>Nature Methods</i> , 2018 , 15, 323-329	21.6	46
68	Co-evolution and Co-speciation of Host-Gut Bacteria Systems. <i>Cell Host and Microbe</i> , 2020 , 28, 12-22	23.4	42
67	Invertible promoters mediate bacterial phase variation, antibiotic resistance, and host adaptation in the gut. <i>Science</i> , 2019 , 363, 181-187	33.3	42
66	Engineering transcription factors with novel DNA-binding specificity using comparative genomics. <i>Nucleic Acids Research</i> , 2009 , 37, 2493-503	20.1	38

65	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018 , 9,	7.8	37
64	Improved gene tree error correction in the presence of horizontal gene transfer. <i>Bioinformatics</i> , 2015 , 31, 1211-8	7.2	37
63	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
62	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
61	Comparing patterns of natural selection across species using selective signatures. <i>PLoS Genetics</i> , 2008 , 4, e23	6	32
60	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021 , 184, 2053-2067.e18	20.7	31
59	Dietary microbes modulate transgenerational cancer risk. <i>Cancer Research</i> , 2015 , 75, 1197-204	10.1	31
58	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. <i>Scientific Reports</i> , 2018 , 8, 12699	4.9	27
57	Interactions in self-assembled microbial communities saturate with diversity. <i>ISME Journal</i> , 2019 , 13, 1602-1617	11.9	26
56	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
55	An omics-based framework for assessing the health risk of antimicrobial resistance genes. <i>Nature Communications</i> , 2021 , 12, 4765	17.4	25
54	Surveys, simulation and single-cell assays relate function and phylogeny in a lake ecosystem. <i>Nature Microbiology</i> , 2016 , 1, 16130	26.6	24
53	Computational methods for high-throughput comparative analyses of natural microbial communities. <i>Methods in Enzymology</i> , 2013 , 531, 353-70	1.7	23
52	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
51	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
50	Identifying predictive features of <i>Clostridium difficile</i> infection recurrence before, during, and after primary antibiotic treatment. <i>Microbiome</i> , 2017 , 5, 148	16.6	20
49	Framework for rational donor selection in fecal microbiota transplant clinical trials. <i>PLoS ONE</i> , 2019 , 14, e0222881	3.7	20
48	Local gene regulation details a recognition code within the LacI transcriptional factor family. <i>PLoS Computational Biology</i> , 2010 , 6, e1000989	5	19

47	Inoculum composition determines microbial community and function in an anaerobic sequential batch reactor. <i>PLoS ONE</i> , 2017 , 12, e0171369	3.7	17
46	Adaptive evolution within the gut microbiome of individual people		17
45	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
44	Searching for superstool: maximizing the therapeutic potential of FMT. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 387-388	24.2	16
43	A Mobile Element in mutS Drives Hypermutation in a Marine Vibrio. <i>MBio</i> , 2017 , 8,	7.8	14
42	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
41	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
40	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
39	dbOTU3: A new implementation of distribution-based OTU calling. <i>PLoS ONE</i> , 2017 , 12, e0176335	3.7	13
38	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
37	Wastewater Surveillance of SARS-CoV-2 across 40 U.S. states 2021 ,		12
36	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
35	Predicting human health from biofluid-based metabolomics using machine learning. <i>Scientific Reports</i> , 2020 , 10, 17635	4.9	8
34	Prebiotics and Community Composition Influence Gas Production of the Human Gut Microbiota. <i>MBio</i> , 2020 , 11,	7.8	8
33	The histidine operon is ancient. <i>Journal of Molecular Evolution</i> , 2006 , 62, 807-8	3.1	7
32	Anatomy promotes neutral coexistence of strains in the human skin microbiome.. <i>Cell Host and Microbe</i> , 2022 ,	23.4	6
31	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
30	Wastewater network infrastructure in public health: Applications and learnings from the COVID-19 pandemic.. <i>PLOS Global Public Health</i> , 2021 , 1, e0000061		5

29	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
28	24-hour multi-omics analysis of residential sewage reflects human activity and informs public health		5
27	Quantitative detection of SARS-CoV-2 B.1.1.7 variant in wastewater by allele-specific RT-qPCR		5
26	A Novel Analysis Method for Paired-Sample Microbial Ecology Experiments. <i>PLoS ONE</i> , 2016 , 11, e0154804	9.4	5
25	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
24	Dynamic Colonization of Microbes and Their Functions after Fecal Microbiota Transplantation for Inflammatory Bowel Disease. <i>MBio</i> , 2021 , 12, e0097521	7.8	5
23	Genome and sequence determinants governing the expression of horizontally acquired DNA in bacteria. <i>ISME Journal</i> , 2020 , 14, 2347-2357	11.9	4
22	Microbe-seq: high-throughput, single-microbe genomics with strain resolution, applied to a human gut microbiome		4
21	A practical guide to methods controlling false discoveries in computational biology		4
20	Hygienic T lymphocytes convey increased cancer risk. <i>Journal of Analytical Oncology</i> , 2014 , 3, 113-121		4
19	Making Waves: Wastewater Surveillance of SARS-CoV-2 in an Endemic Future. <i>Water Research</i> , 2022 , 118535	12.5	4
18	Gut Ruminococcaceae levels at baseline correlate with risk of antibiotic-associated diarrhea. <i>iScience</i> , 2022 , 25, 103644	6.1	3
17	Metrics to relate COVID-19 wastewater data to clinical testing dynamics. <i>Water Research</i> , 2022 , 212, 118070	12.5	3
16	Quantitative detection of SARS-CoV-2 Omicron BA.1 and BA.2 variants in wastewater through allele-specific RT-qPCR		3
15	Correcting for batch effects in case-control microbiome studies		3
14	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. <i>MSystems</i> , 2021 , e0053721	7.6	3
13	Metrics to relate COVID-19 wastewater data to clinical testing dynamics 2021 ,		3
12	"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

11	Quantitative SARS-CoV-2 tracking of variants Delta, Delta plus, Kappa and Beta in wastewater by allele-specific RT-qPCR		3
10	Tracking strains predicts personal microbiomes and reveals recent adaptive evolution		2
9	Functional heterogeneity in the fermentation capabilities of the healthy human gut microbiota		2
8	Anatomy promotes neutral coexistence of strains in the human skin microbiome		2
7	Longitudinal wastewater sampling in buildings reveals temporal dynamics of metabolites. <i>PLoS Computational Biology</i> , 2020 , 16, e1008001	5	1
6	16S rRNA sequencing analysis: the devil is in the details. <i>Gut Microbes</i> , 2020 , 11, 1139-1142	8.8	1
5	Predicting human health from biofluid-based metabolomics using machine learning		1
4	Industrialization is associated with elevated rates of horizontal gene transfer in the human microbiome		1
3	Multi-site sampling and risk prioritization reveals the public health relevance of antibiotic resistance genes found in wastewater environments		1
2	Functional heterogeneity in the fermentation capabilities of the healthy human gut microbiota. <i>PLoS ONE</i> , 2021 , 16, e0254004	3.7	1
1	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