Eric J Alm

List of Publications by Year
in descending order

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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	Sustained Ability of a Natural Microbial Community to Remove Nitrate from Groundwater. Ground Water, 2022, 60, 99-111.	0.7	6
2	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
3	Anatomy promotes neutral coexistence of strains in the human skin microbiome. Cell Host and Microbe, 2022, 30, 171-182.e7.	5.1	62
4	Gut Ruminococcaceae levels at baseline correlate with risk of antibiotic-associated diarrhea. IScience, 2022, 25, 103644.	1.9	28
5	Effect of antibiotic pretreatment on bacterial engraftment after Fecal Microbiota Transplant (FMT) in IBS-D. Gut Microbes, 2022, 14, 2020067.	4.3	30
6	Metrics to relate COVID-19 wastewater data to clinical testing dynamics. Water Research, 2022, 212, 118070.	5.3	68
7	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
8	Making waves: Wastewater surveillance of SARS-CoV-2 in an endemic future. Water Research, 2022, 219, 118535.	5.3	37
9	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
10	High-throughput, single-microbe genomics with strain resolution, applied to a human gut microbiome. Science, 2022, 376, .	6.0	100
11	Rapid displacement of SARS-CoV-2 variant Delta by Omicron revealed by allele-specific PCR in wastewater. Water Research, 2022, 221, 118809.	5.3	30
12	Elevated rates of horizontal gene transfer in the industrialized human microbiome. Cell, 2021, 184, 2053-2067.e18.	13.5	167
13	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. MSystems, 2021, 6, e0053721.	1.7	8
14	Quantitative SARS-CoV-2 Alpha Variant B.1.1.7 Tracking in Wastewater by Allele-Specific RT-qPCR. Environmental Science and Technology Letters, 2021, 8, 675-682.	3.9	68
15	Functional heterogeneity in the fermentation capabilities of the healthy human gut microbiota. PLoS ONE, 2021, 16, e0254004.	1.1	11
16	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
17	An omics-based framework for assessing the health risk of antimicrobial resistance genes. Nature Communications, 2021, 12, 4765.	5.8	248
18	â€œWaste Not, Want Notâ€•â€” 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

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19	Persistence of Dengue (Serotypes 2 and 3), Zika, Yellow Fever, and Murine Hepatitis Virus RNA in Untreated Wastewater. Environmental Science and Technology Letters, 2021, 8, 785-791.	3.9	23
20	Dynamic Colonization of Microbes and Their Functions after Fecal Microbiota Transplantation for Inflammatory Bowel Disease. MBio, 2021, 12, e0097521.	1.8	26
21	Wastewater surveillance of SARS-CoV-2 across 40 U.S. states from February to June 2020. Water Research, 2021, 202, 117400.	5.3	119
22	Wastewater network infrastructure in public health: Applications and learnings from the COVID-19 pandemic. PLOS Global Public Health, 2021, 1, e0000061.	0.5	23
23	Predicting human health from biofluid-based metabolomics using machine learning. Scientific Reports, 2020, 10, 17635.	1.6	16
24	Making waves: Wastewater surveillance of SARS-CoV-2 for population-based health management. Water Research, 2020, 184, 116181.	5.3	138
25	Co-evolution and Co-speciation of Host-Gut Bacteria Systems. Cell Host and Microbe, 2020, 28, 12-22.	5.1	128
26	SARS-CoV-2 Titers in Wastewater Are Higher than Expected from Clinically Confirmed Cases. MSystems, 2020, 5, .	1.7	649
27	Prebiotics and Community Composition Influence Gas Production of the Human Gut Microbiota. MBio, 2020, 11, .	1.8	23
28	Genome and sequence determinants governing the expression of horizontally acquired DNA in bacteria. ISME Journal, 2020, 14, 2347-2357.	4.4	16
29	Longitudinal wastewater sampling in buildings reveals temporal dynamics of metabolites. PLoS Computational Biology, 2020, 16, e1008001.	1.5	2
30	The Vaginal Microbiome as a Tool to Predict rASRM Stage of Disease in Endometriosis: a Pilot Study. Reproductive Sciences, 2020, 27, 1064-1073.	1.1	35
31	16S rRNA sequencing analysis: the devil is in the details. Gut Microbes, 2020, 11, 1139-1142.	4.3	6
32	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. Microbiome, 2020, 8, 51.	4.9	205
33	Culturing of â€œUnculturableâ€•Subsurface Microbes: Natural Organic Carbon Source Fuels the Growth of Diverse and Distinct Bacteria From Groundwater. Frontiers in Microbiology, 2020, 11, 610001.	1.5	26
34	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
35	Framework for rational donor selection in fecal microbiota transplant clinical trials. PLoS ONE, 2019, 14, e0222881.	1.1	36
36	A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. Nature Medicine, 2019, 25, 1442-1452.	15.2	255

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37	Longitudinal immunosequencing in healthy people reveals persistent T cell receptors rich in highly public receptors. BMC Immunology, 2019, 20, 19.	0.9	42
38	A practical guide to methods controlling false discoveries in computational biology. Genome Biology, 2019, 20, 118.	3.8	222
39	Using fecal microbiota as biomarkers for predictions of performance in the selective breeding process of pedigree broiler breeders. PLoS ONE, 2019, 14, e0216080.	1.1	27
40	Adaptive Evolution within Gut Microbiomes of Healthy People. Cell Host and Microbe, 2019, 25, 656-667.e8.	5.1	289
41	Transmission of human-associated microbiota along family and social networks. Nature Microbiology, 2019, 4, 964-971.	5.9	149
42	Interactions in self-assembled microbial communities saturate with diversity. ISME Journal, 2019, 13, 1602-1617.	4.4	54
43	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
44	Invertible promoters mediate bacterial phase variation, antibiotic resistance, and host adaptation in the gut. Science, 2019, 363, 181-187.	6.0	85
45	Analysis of 1135 gut metagenomes identifies sex-specific resistome profiles. Gut Microbes, 2019, 10, 358-366.	4.3	118
46	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. MBio, 2018, 9, .	1.8	57
47	Random sequences rapidly evolve into de novo promoters. Nature Communications, 2018, 9, 1530.	5.8	105
48	Evolution of a Vegetarian Vibrio: Metabolic Specialization of Vibrio breoganii to Macroalgal Substrates. Journal of Bacteriology, 2018, 200, .	1.0	24
49	Strain Tracking Reveals the Determinants of Bacterial Engraftment in the Human Gut Following Fecal Microbiota Transplantation. Cell Host and Microbe, 2018, 23, 229-240.e5.	5.1	292
50	High resolution time series reveals cohesive but short-lived communities in coastal plankton. Nature Communications, 2018, 9, 266.	5.8	122
51	Searching for superstool: maximizing the therapeutic potential of FMT. Nature Reviews Gastroenterology and Hepatology, 2018, 15, 387-388.	8.2	22
52	Metagenomic mining of regulatory elements enables programmable species-selective gene expression. Nature Methods, 2018, 15, 323-329.	9.0	80
53	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
54	Gut microbiota composition and functional changes in inflammatory bowel disease and irritable bowel syndrome. Science Translational Medicine, 2018, 10, .	5.8	351

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55	Correcting for batch effects in case-control microbiome studies. PLoS Computational Biology, 2018, 14, e1006102.	1.5	108
56	Defining the gut microbiota in individuals with periodontal diseases: an exploratory study. Journal of Oral Microbiology, 2018, 10, 1487741.	1.2	96
57	Predictability and persistence of prebiotic dietary supplementation in a healthy human cohort. Scientific Reports, 2018, 8, 12699.	1.6	37
58	Orthogonal Dietary Niche Enables Reversible Engraftment of a Gut Bacterial Commensal. Cell Reports, 2018, 24, 1842-1851.	2.9	72
59	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
60	Unraveling the processes shaping mammalian gut microbiomes over evolutionary time. Nature Communications, 2017, 8, 14319.	5.8	357
61	A Mobile Element in <i>mutS</i> Drives Hypermutation in a Marine <i>Vibrio</i>. MBio, 2017, 8, .	1.8	26
62	Salt-responsive gut commensal modulates TH17 axis and disease. Nature, 2017, 551, 585-589.	13.7	896
63	Microbial lysate upregulates host oxytocin. Brain, Behavior, and Immunity, 2017, 61, 36-49.	2.0	101
64	Inoculum composition determines microbial community and function in an anaerobic sequential batch reactor. PLoS ONE, 2017, 12, e0171369.	1.1	23
65	dbOTU3: A new implementation of distribution-based OTU calling. PLoS ONE, 2017, 12, e0176335.	1.1	24
66	Two dynamic regimes in the human gut microbiome. PLoS Computational Biology, 2017, 13, e1005364.	1.5	101
67	Meta-analysis of gut microbiome studies identifies disease-specific and shared responses. Nature Communications, 2017, 8, 1784.	5.8	714
68	Identifying predictive features of Clostridium difficile infection recurrence before, during, and after primary antibiotic treatment. Microbiome, 2017, 5, 148.	4.9	36
69	Profiling Living Bacteria Informs Preparation of Fecal Microbiota Transplantations. PLoS ONE, 2017, 12, e0170922.	1.1	68
70	A Novel Analysis Method for Paired-Sample Microbial Ecology Experiments. PLoS ONE, 2016, 11, e0154804.	1.1	9
71	Virtual microfluidics for digital quantification and single-cell sequencing. Nature Methods, 2016, 13, 759-762.	9.0	79
72	Dysbiosis is not an answer. Nature Microbiology, 2016, 1, 16228.	5.9	97

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73	Mobile genes in the human microbiome are structured from global to individual scales. Nature, 2016, 535, 435-439.	13.7	233
74	Surveys, simulation and single-cell assays relate function and phylogeny in a lake ecosystem. Nature Microbiology, 2016, 1, 16130.	5.9	33
75	Adaptive radiation by waves of gene transfer leads to fine-scale resource partitioning in marine microbes. Nature Communications, 2016, 7, 12860.	5.8	140
76	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681.	4.4	593
77	Massively parallel sequencing of single cells by epicPCR links functional genes with phylogenetic markers. ISME Journal, 2016, 10, 427-436.	4.4	184
78	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. MBio, 2015, 6, e00326-15.	1.8	173
79	Dietary Microbes Modulate Transgenerational Cancer Risk. Cancer Research, 2015, 75, 1197-1204.	0.4	43
80	Improved gene tree error correction in the presence of horizontal gene transfer. Bioinformatics, 2015, 31, 1211-1218.	1.8	64
81	Detection of low-abundance bacterial strains in metagenomic datasets by eigengenome partitioning. Nature Biotechnology, 2015, 33, 1053-1060.	9.4	144
82	Probiotic Microbes Sustain Youthful Serum Testosterone Levels and Testicular Size in Aging Mice. PLoS ONE, 2014, 9, e84877.	1.1	114
83	Host lifestyle affects human microbiota on daily timescales. Genome Biology, 2014, 15, R89.	13.9	735
84	Fecal Microbiota Transplant for Relapsing Clostridium difficile Infection Using a Frozen Inoculum From Unrelated Donors: A Randomized, Open-Label, Controlled Pilot Study. Clinical Infectious Diseases, 2014, 58, 1515-1522.	2.9	397
85	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
86	â€˜Hygienicâ€™ Lymphocytes Convey Increased Cancer Risk. Journal of Analytical Oncology, 2014, 3, 113-121-113-121.	0.1	4
87	Computational Methods for High-Throughput Comparative Analyses of Natural Microbial Communities. Methods in Enzymology, 2013, 531, 353-370.	0.4	38
88	Horizontal gene transfer and the evolution of bacterial and archaeal population structure. Trends in Genetics, 2013, 29, 170-175.	2.9	364
89	Distribution-Based Clustering: Using Ecology To Refine the Operational Taxonomic Unit. Applied and Environmental Microbiology, 2013, 79, 6593-6603.	1.4	140
90	Inferring Correlation Networks from Genomic Survey Data. PLoS Computational Biology, 2012, 8, e1002687.	1.5	1,874

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91	Population Genomics of Early Events in the Ecological Differentiation of Bacteria. Science, 2012, 336, 48-51.	6.0	484
92	Non-Invasive Mapping of the Gastrointestinal Microbiota Identifies Children with Inflammatory Bowel Disease. PLoS ONE, 2012, 7, e39242.	1.1	252
93	Ecology drives a global network of gene exchange connecting the human microbiome. Nature, 2011, 480, 241-244.	13.7	788
94	Metapopulation structure of <i>Vibrionaceae</i> among coastal marine invertebrates. Environmental Microbiology, 2011, 13, 265-275.	1.8	76
95	Local Gene Regulation Details a Recognition Code within the LacI Transcriptional Factor Family. PLoS Computational Biology, 2010, 6, e1000989.	1.5	20
96	Engineering transcription factors with novel DNA-binding specificity using comparative genomics. Nucleic Acids Research, 2009, 37, 2493-2503.	6.5	39
97	Looking for Darwin's footprints in the microbial world. Trends in Microbiology, 2009, 17, 196-204.	3.5	94
98	Comparing Patterns of Natural Selection across Species Using Selective Signatures. PLoS Genetics, 2008, 4, e23.	1.5	40
99	The Histidine Operon Is Ancient. Journal of Molecular Evolution, 2006, 62, 807-808.	0.8	9
100	The Life-Cycle of Operons. PLoS Genetics, 2006, 2, e96.	1.5	146
101	Dissimilatory Metabolism of Nitrogen Oxides in Bacteria: Comparative Reconstruction of Transcriptional Networks. PLoS Computational Biology, 2005, 1, e55.	1.5	260
102	Operon formation is driven by co-regulation and not by horizontal gene transfer. Genome Research, 2005, 15, 809-819.	2.4	131
103	The MicrobesOnline Web site for comparative genomics. Genome Research, 2005, 15, 1015-1022.	2.4	176
104	A novel method for accurate operon predictions in all sequenced prokaryotes. Nucleic Acids Research, 2005, 33, 880-892.	6.5	316