

Matthew R Olm

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/258317/publications.pdf>

Version: 2024-02-01

36
papers

4,119
citations

304743

22
h-index

501196

28
g-index

57
all docs

57
docs citations

57
times ranked

4830
citing authors

#	ARTICLE	IF	CITATIONS
1	dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication. <i>ISME Journal</i> , 2017, 11, 2864-2868.	9.8	1,309
2	Measurement of bacterial replication rates in microbial communities. <i>Nature Biotechnology</i> , 2016, 34, 1256-1263.	17.5	342
3	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	27.8	331
4	Genome Sequencing of Sewage Detects Regionally Prevalent SARS-CoV-2 Variants. <i>MBio</i> , 2021, 12, .	4.1	284
5	inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. <i>Nature Biotechnology</i> , 2021, 39, 727-736.	17.5	238
6	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
7	Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. <i>Nature Communications</i> , 2017, 8, 1814.	12.8	162
8	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	13.3	141
9	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. <i>MSystems</i> , 2020, 5, .	3.8	135
10	Necrotizing enterocolitis is preceded by increased gut bacterial replication, <i>Klebsiella</i> , and fimbriae-encoding bacteria. <i>Science Advances</i> , 2019, 5, eaax5727.	10.3	120
11	Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. <i>Genome Research</i> , 2017, 27, 601-612.	5.5	99
12	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	12.8	87
13	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. <i>MSystems</i> , 2018, 3, .	3.8	68
14	The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms. <i>Microbiome</i> , 2018, 6, 112.	11.1	65
15	Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. <i>Science</i> , 2022, 376, 1220-1223.	12.6	63
16	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. <i>Microbiome</i> , 2019, 7, 26.	11.1	60
17	Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network. <i>ISME Journal</i> , 2019, 13, 1618-1634.	9.8	60
18	Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isozymes. <i>Journal of Virology</i> , 2014, 88, 2461-2480.	3.4	52

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19	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. ISME Journal, 2020, 14, 1834-1846.	9.8	43
20	Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. Cell Reports Medicine, 2021, 2, 100393.	6.5	39
21	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. MBio, 2018, 9, .	4.1	34
22	Function, expression, specificity, diversity and incompatibility of actinobacteriophage <i>parABS</i> systems. Molecular Microbiology, 2016, 101, 625-644.	2.5	29
23	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. Genome Research, 2021, 31, 239-250.	5.5	24
24	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. MBio, 2017, 8, .	4.1	17
25	Genetic and behavioral adaptation of <i>Candida parapsilosis</i> to the microbiome of hospitalized infants revealed by in situ genomics, transcriptomics, and proteomics. Microbiome, 2021, 9, 142.	11.1	14
26	Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale. Microbiome, 2021, 9, 121.	11.1	11
27	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut. PLoS ONE, 2020, 15, e0229537.	2.5	8
28	Microbiome assembly in The Gambia. Nature Microbiology, 2022, 7, 18-19.	13.3	1
29	Title is missing!. , 2020, 15, e0229537.		0
30	Title is missing!. , 2020, 15, e0229537.		0
31	Title is missing!. , 2020, 15, e0229537.		0
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