

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	Microbiome assembly in The Gambia. <i>Nature Microbiology</i> , 2022, 7, 18-19.	13.3	1
2	Robust variation in infant gut microbiome assembly across a spectrum of lifestyles. <i>Science</i> , 2022, 376, 1220-1223.	12.6	63
3	Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale. <i>Microbiome</i> , 2021, 9, 121.	11.1	11
4	Genetic and behavioral adaptation of <i>Candida parapsilosis</i> to the microbiome of hospitalized infants revealed by in situ genomics, transcriptomics, and proteomics. <i>Microbiome</i> , 2021, 9, 142.	11.1	14
5	Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. <i>Cell Reports Medicine</i> , 2021, 2, 100393.	6.5	39
6	inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. <i>Nature Biotechnology</i> , 2021, 39, 727-736.	17.5	238
7	Genome Sequencing of Sewage Detects Regionally Prevalent SARS-CoV-2 Variants. <i>MBio</i> , 2021, 12, .	4.1	284
8	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. <i>Genome Research</i> , 2021, 31, 239-250.	5.5	24
9	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	30.7	170
10	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. <i>MSystems</i> , 2020, 5, .	3.8	135
11	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut. <i>PLoS ONE</i> , 2020, 15, e0229537.	2.5	8
12	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	27.8	331
13	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. <i>ISME Journal</i> , 2020, 14, 1834-1846.	9.8	43
14	Title is missing!. , 2020, 15, e0229537.		0
15	Title is missing!. , 2020, 15, e0229537.		0
16	Title is missing!. , 2020, 15, e0229537.		0
17	Title is missing!. , 2020, 15, e0229537.		0
18	Title is missing!. , 2020, 15, e0229537.		0

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19	Title is missing!. , 2020, 15, e0229537.		0
20	Title is missing!. , 2020, 15, e0229537.		0
21	Title is missing!. , 2020, 15, e0229537.		0
22	Megaphages infect Prevotella and variants are widespread in gut microbiomes. Nature Microbiology, 2019, 4, 693-700.	13.3	141
23	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. Nature Communications, 2019, 10, 463.	12.8	87
24	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. Microbiome, 2019, 7, 26.	11.1	60
25	Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network. ISME Journal, 2019, 13, 1618-1634.	9.8	60
26	Necrotizing enterocolitis is preceded by increased gut bacterial replication, <i>Klebsiella</i> , and fimbriae-encoding bacteria. Science Advances, 2019, 5, eaax5727.	10.3	120
27	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. MBio, 2018, 9, .	4.1	34
28	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. MSystems, 2018, 3, .	3.8	68
29	The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms. Microbiome, 2018, 6, 112.	11.1	65
30	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. MBio, 2017, 8, .	4.1	17
31	Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. Genome Research, 2017, 27, 601-612.	5.5	99
32	dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication. ISME Journal, 2017, 11, 2864-2868.	9.8	1,309
33	Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. Nature Communications, 2017, 8, 1814.	12.8	162
34	Function, expression, specificity, diversity and incompatibility of actinobacteriophage <i>parABS</i> systems. Molecular Microbiology, 2016, 101, 625-644.	2.5	29
35	Measurement of bacterial replication rates in microbial communities. Nature Biotechnology, 2016, 34, 1256-1263.	17.5	342
36	Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isozymes. Journal of Virology, 2014, 88, 2461-2480.	3.4	52