

Ulas Karaoz

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

15,208
citations

186265

28
h-index

223800

46
g-index

53
all docs

53
docs citations

53
times ranked

24577
citing authors

#	ARTICLE	IF	CITATIONS
1	To rarefy or not to rarefy: robustness and efficiency trade-offs of rarefying microbiome data. <i>Bioinformatics</i> , 2022, 38, 2389-2396.	4.1	11
2	METABOLIC: high-throughput profiling of microbial genomes for functional traits, metabolism, biogeochemistry, and community-scale functional networks. <i>Microbiome</i> , 2022, 10, 33.	11.1	168
3	A novel d-xylose isomerase from the gut of the wood feeding beetle <i>Odontotaenius disjunctus</i> efficiently expressed in <i>Saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2021, 11, 4766.	3.3	11
4	Microbial Phosphorus Mobilization Strategies Across a Natural Nutrient Limitation Gradient and Evidence for Linkage With Iron Solubilization Traits. <i>Frontiers in Microbiology</i> , 2021, 12, 572212.	3.5	8
5	Presence and Persistence of Putative Lytic and Temperate Bacteriophages in Vaginal Metagenomes from South African Adolescents. <i>Viruses</i> , 2021, 13, 2341.	3.3	8
6	Hormonal contraception alters vaginal microbiota and cytokines in South African adolescents in a randomized trial. <i>Nature Communications</i> , 2020, 11, 5578.	12.8	30
7	The Snowmelt Niche Differentiates Three Microbial Life Strategies That Influence Soil Nitrogen Availability During and After Winter. <i>Frontiers in Microbiology</i> , 2020, 11, 871.	3.5	32
8	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	9.8	135
9	Paired RNA Radiocarbon and Sequencing Analyses Indicate the Importance of Autotrophy in a Shallow Alluvial Aquifer. <i>Scientific Reports</i> , 2019, 9, 10370.	3.3	1
10	Gut anatomical properties and microbial functional assembly promote lignocellulose deconstruction and colony subsistence of a wood-feeding beetle. <i>Nature Microbiology</i> , 2019, 4, 864-875.	13.3	68
11	P367â€¦Hormonal contraception and risk of STIs and bacterial vaginosis in south african adolescents: a randomized trial. , 2019, , .		0
12	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. <i>MBio</i> , 2019, 10, .	4.1	19
13	Large Blooms of <i>Bacillales</i> (<i>Firmicutes</i>) Underlie the Response to Wetting of Cyanobacterial Biofilms at Various Stages of Maturity. <i>MBio</i> , 2018, 9, .	4.1	28
14	Feeding-Related Gut Microbial Composition Associates With Peripheral T-Cell Activation and Mucosal Gene Expression in African Infants. <i>Clinical Infectious Diseases</i> , 2018, 67, 1237-1246.	5.8	31
15	Linking soil biology and chemistry in biological soil crust using isolate exometabolomics. <i>Nature Communications</i> , 2018, 9, 19.	12.8	129
16	Dynamic root exudate chemistry and microbial substrate preferences drive patterns in rhizosphere microbial community assembly. <i>Nature Microbiology</i> , 2018, 3, 470-480.	13.3	1,268
17	Next generation modeling of microbial souring â€“ Parameterization through genomic information. <i>International Biodeterioration and Biodegradation</i> , 2018, 126, 189-203.	3.9	21
18	Whole-genome sequencing and single nucleotide polymorphisms in multidrug-resistant clinical isolates of <i>Mycobacterium tuberculosis</i> from the Philippines. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 15, 239-245.	2.2	6

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19	Metagenomics reveals niche partitioning within the phototrophic zone of a microbial mat. PLoS ONE, 2018, 13, e0202792.	2.5	5
20	Microdiversity of an Abundant Terrestrial Bacterium Encompasses Extensive Variation in Ecologically Relevant Traits. MBio, 2017, 8, .	4.1	49
21	Metatranscriptomic Analysis Reveals Unexpectedly Diverse Microbial Metabolism in a Biogeochemical Hot Spot in an Alluvial Aquifer. Frontiers in Microbiology, 2017, 8, 40.	3.5	14
22	Metagenomic analysis of intertidal hypersaline microbial mats from Elkhorn Slough, California, grown with and without molybdate. Standards in Genomic Sciences, 2017, 12, 67.	1.5	5
23	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. Nature Communications, 2016, 7, 13219.	12.8	994
24	Bacteria increase arid-land soil surface temperature through the production of sunscreens. Nature Communications, 2016, 7, 10373.	12.8	156
25	Metatranscriptomic evidence of pervasive and diverse chemolithoautotrophy relevant to C, S, N and Fe cycling in a shallow alluvial aquifer. ISME Journal, 2016, 10, 2106-2117.	9.8	119
26	Exometabolite niche partitioning among sympatric soil bacteria. Nature Communications, 2015, 6, 8289.	12.8	178
27	Use of 16S rRNA Gene for Identification of a Broad Range of Clinically Relevant Bacterial Pathogens. PLoS ONE, 2015, 10, e0117617.	2.5	293
28	Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. Nature Communications, 2015, 6, 7618.	12.8	361
29	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. Frontiers in Microbiology, 2015, 6, 277.	3.5	50
30	Solid and Suspension Microarrays for Microbial Diagnostics. Methods in Microbiology, 2015, , 395-431.	0.8	4
31	Human Papillomavirus Community in Healthy Persons, Defined by Metagenomics Analysis of Human Microbiome Project Shotgun Sequencing Data Sets. Journal of Virology, 2014, 88, 4786-4797.	3.4	108
32	Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of <i>Odontotaenius disjunctus</i> . ISME Journal, 2014, 8, 6-18.	9.8	80
33	Divergent Aquifer Biogeochemical Systems Converge on Similar and Unexpected Cr(VI) Reduction Products. Environmental Science & Technology, 2014, 48, 10699-10706.	10.0	24
34	Genomic and Physiological Characterization of the Chromate-Reducing, Aquifer-Derived Firmicute <i>Pelosinus</i> sp. Strain HCF1. Applied and Environmental Microbiology, 2013, 79, 63-73.	3.1	65
35	Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. Frontiers in Microbiology, 2013, 4, 282.	3.5	44
36	Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. ISME Journal, 2012, 6, 531-541.	9.8	186

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37	Diversity and structure of soil bacterial communities associated with vultures in an African savanna. <i>Ecosphere</i> , 2012, 3, 1-18.	2.2	19
38	Differential Growth Responses of Soil Bacterial Taxa to Carbon Substrates of Varying Chemical Recalcitrance. <i>Frontiers in Microbiology</i> , 2011, 2, 94.	3.5	504
39	Structure of the human gastric bacterial community in relation to <i>Helicobacter pylori</i> status. <i>ISME Journal</i> , 2011, 5, 574-579.	9.8	256
40	Simrank: Rapid and sensitive general-purpose k-mer search tool. <i>BMC Ecology</i> , 2011, 11, 11.	3.0	24
41	Airway Microbiota and Pathogen Abundance in Age-Stratified Cystic Fibrosis Patients. <i>PLoS ONE</i> , 2010, 5, e11044.	2.5	395
42	Uncovering multiple molecular targets for caffeine using a drug target validation strategy combining A _{2A} receptor knockout mice with microarray profiling. <i>Physiological Genomics</i> , 2009, 37, 199-210.	2.3	59
43	Induction of Intestinal Th17 Cells by Segmented Filamentous Bacteria. <i>Cell</i> , 2009, 139, 485-498.	28.9	3,818
44	The landscape of histone modifications across 1% of the human genome in five human cell lines. <i>Genome Research</i> , 2007, 17, 691-707.	5.5	353
45	Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. <i>Genome Research</i> , 2007, 17, 720-731.	5.5	31
46	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
47	Whole-genome annotation by using evidence integration in functional-linkage networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2888-2893.	7.1	293