

# 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	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
2	Induction of Intestinal Th17 Cells by Segmented Filamentous Bacteria. <i>Cell</i> , 2009, 139, 485-498.	28.9	3,818
3	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
4	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	12.8	994
5	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
6	Airway Microbiota and Pathogen Abundance in Age-Stratified Cystic Fibrosis Patients. <i>PLoS ONE</i> , 2010, 5, e11044.	2.5	395
7	Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. <i>Nature Communications</i> , 2015, 6, 7618.	12.8	361
8	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
9	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
10	Use of 16S rRNA Gene for Identification of a Broad Range of Clinically Relevant Bacterial Pathogens. <i>PLoS ONE</i> , 2015, 10, e0117617.	2.5	293
11	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
12	Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. <i>ISME Journal</i> , 2012, 6, 531-541.	9.8	186
13	Exometabolite niche partitioning among sympatric soil bacteria. <i>Nature Communications</i> , 2015, 6, 8289.	12.8	178
14	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
15	Bacteria increase arid-land soil surface temperature through the production of sunscreens. <i>Nature Communications</i> , 2016, 7, 10373.	12.8	156
16	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	9.8	135
17	Linking soil biology and chemistry in biological soil crust using isolate exometabolomics. <i>Nature Communications</i> , 2018, 9, 19.	12.8	129
18	Metatranscriptomic evidence of pervasive and diverse chemolithoautotrophy relevant to C, S, N and Fe cycling in a shallow alluvial aquifer. <i>ISME Journal</i> , 2016, 10, 2106-2117.	9.8	119

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19	Human Papillomavirus Community in Healthy Persons, Defined by Metagenomics Analysis of Human Microbiome Project Shotgun Sequencing Data Sets. <i>Journal of Virology</i> , 2014, 88, 4786-4797.	3.4	108
20	Compartmentalized microbial composition, oxygen gradients and nitrogen fixation in the gut of <i>Odontotaenium disjunctum</i> . <i>ISME Journal</i> , 2014, 8, 6-18.	9.8	80
21	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
22	Genomic and Physiological Characterization of the Chromate-Reducing, Aquifer-Derived Firmicute <i>Pelosinus</i> sp. Strain HCF1. <i>Applied and Environmental Microbiology</i> , 2013, 79, 63-73.	3.1	65
23	Uncovering multiple molecular targets for caffeine using a drug target validation strategy combining A <sub>2A</sub> receptor knockout mice with microarray profiling. <i>Physiological Genomics</i> , 2009, 37, 199-210.	2.3	59
24	Isolation of a significant fraction of non-phototroph diversity from a desert Biological Soil Crust. <i>Frontiers in Microbiology</i> , 2015, 6, 277.	3.5	50
25	Microdiversity of an Abundant Terrestrial Bacterium Encompasses Extensive Variation in Ecologically Relevant Traits. <i>MBio</i> , 2017, 8, .	4.1	49
26	Coupled high-throughput functional screening and next generation sequencing for identification of plant polymer decomposing enzymes in metagenomic libraries. <i>Frontiers in Microbiology</i> , 2013, 4, 282.	3.5	44
27	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
28	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
29	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
30	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
31	Large Blooms of <i>Bacillales</i> ( <i>Firmicutes</i> ) Underlie the Response to Wetting of Cyanobacterial Biocrusts at Various Stages of Maturity. <i>MBio</i> , 2018, 9, .	4.1	28
32	Simrank: Rapid and sensitive general-purpose k-mer search tool. <i>BMC Ecology</i> , 2011, 11, 11.	3.0	24
33	Divergent Aquifer Biogeochemical Systems Converge on Similar and Unexpected Cr(VI) Reduction Products. <i>Environmental Science &amp; Technology</i> , 2014, 48, 10699-10706.	10.0	24
34	Next generation modeling of microbial souring – Parameterization through genomic information. <i>International Biodeterioration and Biodegradation</i> , 2018, 126, 189-203.	3.9	21
35	Diversity and structure of soil bacterial communities associated with vultures in an African savanna. <i>Ecosphere</i> , 2012, 3, 1-18.	2.2	19
36	Maintenance of Sympatric and Allopatric Populations in Free-Living Terrestrial Bacteria. <i>MBio</i> , 2019, 10, .	4.1	19

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37	Metatranscriptomic Analysis Reveals Unexpectedly Diverse Microbial Metabolism in a Biogeochemical Hot Spot in an Alluvial Aquifer. <i>Frontiers in Microbiology</i> , 2017, 8, 40.	3.5	14
38	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
39	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
40	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
41	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
42	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
43	Metagenomic analysis of intertidal hypersaline microbial mats from Elkhorn Slough, California, grown with and without molybdate. <i>Standards in Genomic Sciences</i> , 2017, 12, 67.	1.5	5
44	Metagenomics reveals niche partitioning within the phototrophic zone of a microbial mat. <i>PLoS ONE</i> , 2018, 13, e0202792.	2.5	5
45	Solid and Suspension Microarrays for Microbial Diagnostics. <i>Methods in Microbiology</i> , 2015, , 395-431.	0.8	4
46	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
47	P367â€¦Hormonal contraception and risk of STIs and bacterial vaginosis in south african adolescents: a randomized trial. , 2019, , .		0