

Kaisa Koskinen Mora

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/348323/publications.pdf>

Version: 2024-02-01

24
papers

3,722
citations

430874

18
h-index

610901

24
g-index

25
all docs

25
docs citations

25
times ranked

6753
citing authors

#	ARTICLE	IF	CITATIONS
1	Gut microbiota are related to Parkinson's disease and clinical phenotype. <i>Movement Disorders</i> , 2015, 30, 350-358.	3.9	1,457
2	Environmental biodiversity, human microbiota, and allergy are interrelated. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8334-8339.	7.1	856
3	The microbiome of the upper respiratory tract in health and disease. <i>BMC Biology</i> , 2019, 17, 87.	3.8	243
4	First Insights into the Diverse Human Archaeome: Specific Detection of Archaea in the Gastrointestinal Tract, Lung, and Nose and on Skin. <i>MBio</i> , 2017, 8, .	4.1	169
5	Probiotics drive gut microbiome triggering emotional brain signatures. <i>Gut Microbes</i> , 2018, 9, 1-11.	9.8	146
6	Microorganisms in Confined Habitats: Microbial Monitoring and Control of Intensive Care Units, Operating Rooms, Cleanrooms and the International Space Station. <i>Frontiers in Microbiology</i> , 2016, 7, 1573.	3.5	106
7	Comparison of microbial communities in marinated and unmarinated broiler meat by metagenomics. <i>International Journal of Food Microbiology</i> , 2012, 157, 142-149.	4.7	101
8	Bacterial diversity and community structure along different peat soils in boreal forest. <i>Applied Soil Ecology</i> , 2014, 74, 37-45.	4.3	89
9	Human age and skin physiology shape diversity and abundance of Archaea on skin. <i>Scientific Reports</i> , 2017, 7, 4039.	3.3	78
10	The nasal microbiome mirrors and potentially shapes olfactory function. <i>Scientific Reports</i> , 2018, 8, 1296.	3.3	76
11	The salivary microbiome as an indicator of carcinogenesis in patients with oropharyngeal squamous cell carcinoma: A pilot study. <i>Scientific Reports</i> , 2017, 7, 5867.	3.3	70
12	Preparing for the crewed Mars journey: microbiota dynamics in the confined Mars500 habitat during simulated Mars flight and landing. <i>Microbiome</i> , 2017, 5, 129.	11.1	47
13	Spatially differing bacterial communities in water columns of the northern Baltic Sea. <i>FEMS Microbiology Ecology</i> , 2011, 75, 99-110.	2.7	41
14	The microbiome of the human lower airways: a next generation sequencing perspective. <i>World Allergy Organization Journal</i> , 2015, 8, 23.	3.5	36
15	Molecular analysis of meso- and thermophilic microbiota associated with anaerobic biowaste degradation. <i>BMC Microbiology</i> , 2012, 12, 121.	3.3	30
16	Microbial biodiversity assessment of the European Space Agency's ExoMars 2016 mission. <i>Microbiome</i> , 2017, 5, 143.	11.1	27
17	Skin microbiome in melanomas and melanocytic nevi. <i>European Journal of Dermatology</i> , 2016, 26, 49-55.	0.6	26
18	Microbiome dynamics during the HI-SEAS IV mission, and implications for future crewed missions beyond Earth. <i>Microbiome</i> , 2021, 9, 27.	11.1	21

#	ARTICLE	IF	CITATIONS
19	A Combined LC-MS Metabolomics- and 16S rRNA Sequencing Platform to Assess Interactions between Herbal Medicinal Products and Human Gut Bacteria in Vitro: a Pilot Study on Willow Bark Extract. <i>Frontiers in Pharmacology</i> , 2017, 8, 893.	3.5	20
20	The influence of human exploration on the microbial community structure and ammonia oxidizing potential of the Su Bentu limestone cave in Sardinia, Italy. <i>PLoS ONE</i> , 2017, 12, e0180700.	2.5	20
21	Removal by Sorption and In Situ Biodegradation of Oil Spills Limits Damage to Marine Biota: A Laboratory Simulation. <i>Ambio</i> , 2007, 36, 173-179.	5.5	16
22	The effect of marination on lactic acid bacteria communities in raw broiler fillet strips. <i>Frontiers in Microbiology</i> , 2012, 3, 376.	3.5	16
23	The impacts of treatment with biocontrol fungus (<i>Phlebiopsis gigantea</i>) on bacterial diversity in Norway spruce stumps. <i>Biological Control</i> , 2013, 64, 238-246.	3.0	15
24	Inconsistent Denoising and Clustering Algorithms for Amplicon Sequence Data. <i>Journal of Computational Biology</i> , 2015, 22, 743-751.	1.6	15