

# Mã;ria DÅ¾unkovã;

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

469  
citations

759233

12  
h-index

794594

19  
g-index

21  
all docs

21  
docs citations

21  
times ranked

907  
citing authors

#	ARTICLE	IF	CITATIONS
1	Defining the human gut host-phage network through single-cell viral tagging. <i>Nature Microbiology</i> , 2019, 4, 2192-2203.	13.3	95
2	Evaluation of a concatenated protein phylogeny for classification of tailed double-stranded DNA viruses belonging to the order Caudovirales. <i>Nature Microbiology</i> , 2019, 4, 1306-1315.	13.3	69
3	Insights into the dynamics between viruses and their hosts in a hot spring microbial mat. <i>ISME Journal</i> , 2020, 14, 2527-2541.	9.8	42
4	Active and secreted IgA-coated bacterial fractions from the human gut reveal an under-represented microbiota core. <i>Scientific Reports</i> , 2013, 3, 3515.	3.3	41
5	Revealing microbial recognition by specific antibodies. <i>BMC Microbiology</i> , 2015, 15, 132.	3.3	28
6	The Monoclonal Antitoxin Antibodies (Actoxumab-Bezlotoxumab) Treatment Facilitates Normalization of the Gut Microbiota of Mice with <i>Clostridium difficile</i> Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 119.	3.9	26
7	Active and Secretory IgA-Coated Bacterial Fractions Elucidate Dysbiosis in <i>Clostridium difficile</i> Infection. <i>MSphere</i> , 2016, 1, .	2.9	20
8	Glutelin protein fraction as a tool for clear identification of <i>Amaranth</i> accessions. <i>Journal of Cereal Science</i> , 2011, 53, 198-205.	3.7	19
9	Oxidative stress in the oral cavity is driven by individual-specific bacterial communities. <i>Npj Biofilms and Microbiomes</i> , 2018, 4, 29.	6.4	19
10	Intraspecific sequence comparisons reveal similar rates of non-collinear gene insertion in the B and D genomes of bread wheat. <i>BMC Plant Biology</i> , 2012, 12, 155.	3.6	18
11	Direct sequencing of human gut virome fractions obtained by flow cytometry. <i>Frontiers in Microbiology</i> , 2015, 6, 955.	3.5	18
12	Hybrid Sequencing Approach Applied to Human Fecal Metagenomic Clone Libraries Revealed Clones with Potential Biotechnological Applications. <i>PLoS ONE</i> , 2012, 7, e47654.	2.5	16
13	Salivary microbiome composition changes after bariatric surgery. <i>Scientific Reports</i> , 2020, 10, 20086.	3.3	13
14	Direct Sequencing from the Minimal Number of DNA Molecules Needed to Fill a 454 Picotiterplate. <i>PLoS ONE</i> , 2014, 9, e97379.	2.5	12
15	Selective growth-inhibitory effect of 8-hydroxyquinoline towards <i>Clostridium difficile</i> and <i>Bifidobacterium longum</i> subsp. <i>longum</i> in co-culture analysed by flow cytometry. <i>Journal of Medical Microbiology</i> , 2014, 63, 1663-1669.	1.8	11
16	<i>Clostridioides difficile</i> Toxin A Remodels Membranes and Mediates DNA Entry Into Cells to Activate Toll-Like Receptor 9 Signaling. <i>Gastroenterology</i> , 2020, 159, 2181-2192.e1.	1.3	11
17	Detection of mixed-strain infections by FACS and ultra-low input genome sequencing. <i>Gut Microbes</i> , 2020, 11, 305-309.	9.8	4
18	Synthase-Selective Exploration of a Tunicate Microbiome by Activity-Guided Single-Cell Genomics. <i>ACS Chemical Biology</i> , 2021, 16, 813-819.	3.4	4

#	ARTICLE	IF	CITATIONS
19	Characterisation of the Amaranth Genetic Resources in the Czech Gene Bank. , 2012, , .		2
20	Genome Sequence of Lactobacillus plantarum 19L3, a Strain Proposed as a Starter Culture for SlovenskĀ; Bryndza Ovine Cheese. Genome Announcements, 2014, 2, .	0.8	1
21	Flow Cytometry and Direct Sequencing of Viruses. Methods in Molecular Biology, 2018, 1838, 3-14.	0.9	0