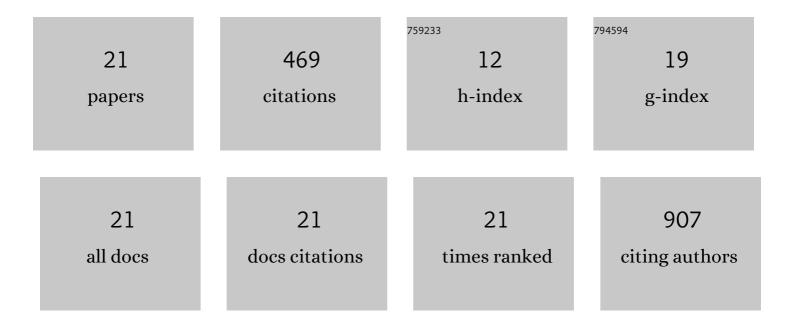
MÃ;ria DžunkovÃ;

List of Publications by Year in descending order

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