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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	Synthase-Selective Exploration of a Tunicate Microbiome by Activity-Guided Single-Cell Genomics. ACS Chemical Biology, 2021, 16, 813-819.	3.4	4
2	Detection of mixed-strain infections by FACS and ultra-low input genome sequencing. Gut Microbes, 2020, 11, 305-309.	9.8	4
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	Salivary microbiome composition changes after bariatric surgery. Scientific Reports, 2020, 10, 20086.	3.3	13
5	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
6	Defining the human gut host-phage network through single-cell viral tagging. Nature Microbiology, 2019, 4, 2192-2203.	13.3	95
7	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
8	Oxidative stress in the oral cavity is driven by individual-specific bacterial communities. Npj Biofilms and Microbiomes, 2018, 4, 29.	6.4	19
9	Flow Cytometry and Direct Sequencing of Viruses. Methods in Molecular Biology, 2018, 1838, 3-14.	0.9	0
10	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
11	Active and Secretory IgA-Coated Bacterial Fractions Elucidate Dysbiosis in Clostridium difficile Infection. MSphere, 2016, 1, .	2.9	20
12	Direct sequencing of human gut virome fractions obtained by flow cytometry. Frontiers in Microbiology, 2015, 6, 955.	3.5	18
13	Revealing microbial recognition by specific antibodies. BMC Microbiology, 2015, 15, 132.	3.3	28
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	Genome Sequence of Lactobacillus plantarum 19L3, a Strain Proposed as a Starter Culture for SlovenskÃ Bryndza Ovine Cheese. Genome Announcements, 2014, 2, .	0.8	1
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Characterisation of the Amaranth Genetic Resources in the Czech Gene Bank. , 2012, , .		2
20	Hybrid Sequencing Approach Applied to Human Fecal Metagenomic Clone Libraries Revealed Clones with Potential Biotechnological Applications. PLoS ONE, 2012, 7, e47654.	2.5	16
21	Glutelin protein fraction as a tool for clear identification of Amaranth accessions. Journal of Cereal Science, 2011, 53, 198-205.	3.7	19