

Andrey N Shkoporov

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

2,596
citations

394421

19
h-index

642732

23
g-index

32
all docs

32
docs citations

32
times ranked

2545
citing authors

#	ARTICLE	IF	CITATIONS
1	Selective Isolation of Eggerthella lenta from Human Faeces and Characterisation of the Species Prophage Diversity. <i>Microorganisms</i> , 2022, 10, 195.	3.6	9
2	Phage-mediated horizontal gene transfer and its implications for the human gut microbiome. <i>Gastroenterology Report</i> , 2022, 10, goac012.	1.3	45
3	Roles of the gut virome and mycobiome in faecal microbiota transplantation. <i>The Lancet Gastroenterology and Hepatology</i> , 2022, 7, 472-484.	8.1	34
4	Mutualistic interplay between bacteriophages and bacteria in the human gut. <i>Nature Reviews Microbiology</i> , 2022, 20, 737-749.	28.6	47
5	Probing the Mobilome: Discoveries in the Dynamic Microbiome. <i>Trends in Microbiology</i> , 2021, 29, 158-170.	7.7	41
6	Probing the "Dark Matter" of the Human Gut Phageome: Culture Assisted Metagenomics Enables Rapid Discovery and Host-Linking for Novel Bacteriophages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 616918.	3.9	25
7	Biases in Viral Metagenomics-Based Detection, Cataloguing and Quantification of Bacteriophage Genomes in Human Faeces, a Review. <i>Microorganisms</i> , 2021, 9, 524.	3.6	18
8	Isolation and characterisation of Î crAss002, a crAss-like phage from the human gut that infects <i>Bacteroides xylanisolvens</i> . <i>Microbiome</i> , 2021, 9, 89.	11.1	48
9	Stability of the human gut virome and effect of gluten-free diet. <i>Cell Reports</i> , 2021, 35, 109132.	6.4	34
10	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. <i>Archives of Virology</i> , 2021, 166, 3239-3244.	2.1	24
11	Long-term persistence of crAss-like phage crAss001 is associated with phase variation in <i>Bacteroides intestinalis</i> . <i>BMC Biology</i> , 2021, 19, 163.	3.8	42
12	Leviviricetes: expanding and restructuring the taxonomy of bacteria-infecting single-stranded RNA viruses. <i>Microbial Genomics</i> , 2021, 7, .	2.0	18
13	Diverse Bacteriocins Produced by Strains From the Human Milk Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 788.	3.5	23
14	Expansion of known ssRNA phage genomes: From tens to over a thousand. <i>Science Advances</i> , 2020, 6, eaay5981.	10.3	112
15	The Human Gut Virome Is Highly Diverse, Stable, and Individual Specific. <i>Cell Host and Microbe</i> , 2019, 26, 527-541.e5.	11.0	449
16	Bacteriophages of the Human Gut: The "Known Unknown" of the Microbiome. <i>Cell Host and Microbe</i> , 2019, 25, 195-209.	11.0	436
17	Whole-Virome Analysis Sheds Light on Viral Dark Matter in Inflammatory Bowel Disease. <i>Cell Host and Microbe</i> , 2019, 26, 764-778.e5.	11.0	287
18	Reproducible protocols for metagenomic analysis of human faecal phageomes. <i>Microbiome</i> , 2018, 6, 68.	11.1	162

#	ARTICLE	IF	CITATIONS
19	∩ CrAss001 represents the most abundant bacteriophage family in the human gut and infects Bacteroides intestinalis. Nature Communications, 2018, 9, 4781.	12.8	244
20	Comparative analysis of Faecalibacterium prausnitzii genomes shows a high level of genome plasticity and warrants separation into new species-level taxa. BMC Genomics, 2018, 19, 931.	2.8	78
21	Biology and Taxonomy of crAss-like Bacteriophages, the Most Abundant Virus in the Human Gut. Cell Host and Microbe, 2018, 24, 653-664.e6.	11.0	233
22	RNA Phage Biology in a Metagenomic Era. Viruses, 2018, 10, 386.	3.3	45
23	Structural basis for the fast maturation of Arthropoda green fluorescent protein. EMBO Reports, 2006, 7, 1006-1012.	4.5	99