

# Andrey N Shkoporov

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5051735/publications.pdf>

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	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
2	Bacteriophages of the Human Gut: The “Known Unknown” of the Microbiome. <i>Cell Host and Microbe</i> , 2019, 25, 195-209.	11.0	436
3	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
4	∫ CrAss001 represents the most abundant bacteriophage family in the human gut and infects <i>Bacteroides intestinalis</i> . <i>Nature Communications</i> , 2018, 9, 4781.	12.8	244
5	Biology and Taxonomy of crAss-like Bacteriophages, the Most Abundant Virus in the Human Gut. <i>Cell Host and Microbe</i> , 2018, 24, 653-664.e6.	11.0	233
6	Reproducible protocols for metagenomic analysis of human faecal phageomes. <i>Microbiome</i> , 2018, 6, 68.	11.1	162
7	Expansion of known ssRNA phage genomes: From tens to over a thousand. <i>Science Advances</i> , 2020, 6, eaay5981.	10.3	112
8	Structural basis for the fast maturation of Arthropoda green fluorescent protein. <i>EMBO Reports</i> , 2006, 7, 1006-1012.	4.5	99
9	Comparative analysis of <i>Faecalibacterium prausnitzii</i> genomes shows a high level of genome plasticity and warrants separation into new species-level taxa. <i>BMC Genomics</i> , 2018, 19, 931.	2.8	78
10	Isolation and characterisation of ∫ crAss002, a crAss-like phage from the human gut that infects <i>Bacteroides xylanisolvens</i> . <i>Microbiome</i> , 2021, 9, 89.	11.1	48
11	Mutualistic interplay between bacteriophages and bacteria in the human gut. <i>Nature Reviews Microbiology</i> , 2022, 20, 737-749.	28.6	47
12	RNA Phage Biology in a Metagenomic Era. <i>Viruses</i> , 2018, 10, 386.	3.3	45
13	Phage-mediated horizontal gene transfer and its implications for the human gut microbiome. <i>Gastroenterology Report</i> , 2022, 10, goac012.	1.3	45
14	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
15	Probing the Mobilome: Discoveries in the Dynamic Microbiome. <i>Trends in Microbiology</i> , 2021, 29, 158-170.	7.7	41
16	Stability of the human gut virome and effect of gluten-free diet. <i>Cell Reports</i> , 2021, 35, 109132.	6.4	34
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	Diverse Bacteriocins Produced by Strains From the Human Milk Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 788.	3.5	23
21	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
22	Leviviricetes: expanding and restructuring the taxonomy of bacteria-infecting single-stranded RNA viruses. <i>Microbial Genomics</i> , 2021, 7, .	2.0	18
23	Selective Isolation of <i>Eggerthella lenta</i> from Human Faeces and Characterisation of the Species Prophage Diversity. <i>Microorganisms</i> , 2022, 10, 195.	3.6	9