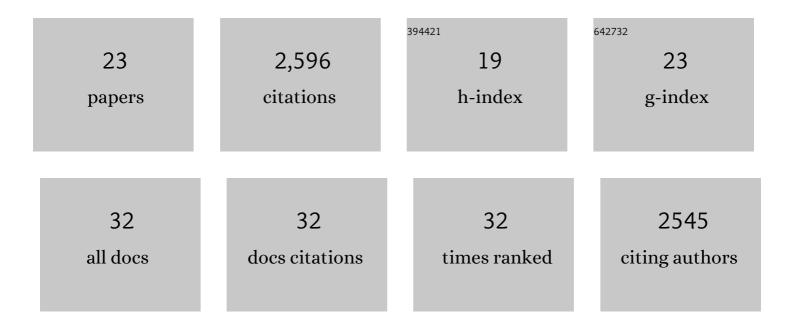
## Andrey N Shkoporov

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5051735/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Selective Isolation of Eggerthella lenta from Human Faeces and Characterisation of the Species Prophage Diversity. Microorganisms, 2022, 10, 195.	3.6	9
2	Phage-mediated horizontal gene transfer and its implications for the human gut microbiome. Gastroenterology Report, 2022, 10, goac012.	1.3	45
3	Roles of the gut virome and mycobiome in faecal microbiota transplantation. The Lancet Gastroenterology and Hepatology, 2022, 7, 472-484.	8.1	34
4	Mutualistic interplay between bacteriophages and bacteria in the human gut. Nature Reviews Microbiology, 2022, 20, 737-749.	28.6	47
5	Probing the Mobilome: Discoveries in the Dynamic Microbiome. Trends in Microbiology, 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. Frontiers in Cellular and Infection Microbiology, 2021, 11, 616918.	3.9	25
7	Biases in Viral Metagenomics-Based Detection, Cataloguing and Quantification of Bacteriophage Genomes in Human Faeces, a Review. Microorganisms, 2021, 9, 524.	3.6	18
8	Isolation and characterisation of ΦcrAss002, a crAss-like phage from the human gut that infects Bacteroides xylanisolvens. Microbiome, 2021, 9, 89.	11.1	48
9	Stability of the human gut virome and effect of gluten-free diet. Cell Reports, 2021, 35, 109132.	6.4	34
10	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. Archives of Virology, 2021, 166, 3239-3244.	2.1	24
11	Long-term persistence of crAss-like phage crAss001 is associated with phase variation in Bacteroides intestinalis. BMC Biology, 2021, 19, 163.	3.8	42
12	Leviviricetes: expanding and restructuring the taxonomy of bacteria-infecting single-stranded RNA viruses. Microbial Genomics, 2021, 7, .	2.0	18
13	Diverse Bacteriocins Produced by Strains From the Human Milk Microbiota. Frontiers in Microbiology, 2020, 11, 788.	3.5	23
14	Expansion of known ssRNA phage genomes: From tens to over a thousand. Science Advances, 2020, 6, eaay5981.	10.3	112
15	The Human Gut Virome Is Highly Diverse, Stable, and Individual Specific. Cell Host and Microbe, 2019, 26, 527-541.e5.	11.0	449
16	Bacteriophages of the Human Gut: The "Known Unknown―of the Microbiome. Cell Host and Microbe, 2019, 25, 195-209.	11.0	436
17	Whole-Virome Analysis Sheds Light on Viral Dark Matter in Inflammatory Bowel Disease. Cell Host and Microbe, 2019, 26, 764-778.e5.	11.0	287
18	Reproducible protocols for metagenomic analysis of human faecal phageomes. Microbiome, 2018, 6, 68.	11.1	162

#	Article	IF	CITATIONS
19	ΦCrAss001 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