

# Stephen Nayfach

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9395707/publications.pdf>

Version: 2024-02-01

23  
papers

4,475  
citations

394421  
19  
h-index

610901  
24  
g-index

30  
all docs

30  
docs citations

30  
times ranked

5612  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast and accurate metagenotyping of the human gut microbiome with GT-Pro. <i>Nature Biotechnology</i> , 2022, 40, 507-516.	17.5	18
2	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. <i>ISME Journal</i> , 2022, 16, 1337-1347.	9.8	15
3	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
4	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	17.5	628
5	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021, 49, D764-D775.	14.5	240
6	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. <i>Nature Biotechnology</i> , 2021, 39, 578-585.	17.5	569
7	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021, 12, 3076.	12.8	35
8	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	13.3	248
9	Illuminating the Virosphere Through Global Metagenomics. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 369-391.	6.5	17
10	Global ecotypes in the ubiquitous marine clade SAR86. <i>ISME Journal</i> , 2020, 14, 178-188.	9.8	49
11	Genetic basis for the cooperative bioactivation of plant lignans by <i>Eggerthella lenta</i> and other human gut bacteria. <i>Nature Microbiology</i> , 2020, 5, 56-66.	13.3	63
12	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	13.3	206
13	A Metagenomic Meta-analysis Reveals Functional Signatures of Health and Disease in the Human Gut Microbiome. <i>MSystems</i> , 2019, 4, .	3.8	112
14	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , 2019, 568, 505-510.	27.8	505
15	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	11.1	53
16	A most wanted list of conserved microbial protein families with no known domains. <i>PLoS ONE</i> , 2018, 13, e0205749.	2.5	17
17	Phylogeny-corrected identification of microbial gene families relevant to human gut colonization. <i>PLoS Computational Biology</i> , 2018, 14, e1006242.	3.2	39
18	Discovery of Reactive Microbiota-Derived Metabolites that Inhibit Host Proteases. <i>Cell</i> , 2017, 168, 517-526.e18.	28.9	173

#	ARTICLE	IF	CITATIONS
19	Modulation of a Circulating Uremic Solute via Rational Genetic Manipulation of the Gut Microbiota. Cell Host and Microbe, 2016, 20, 709-715.	11.0	201
20	Toward Accurate and Quantitative Comparative Metagenomics. Cell, 2016, 166, 1103-1116.	28.9	247
21	An integrated metagenomics pipeline for strain profiling reveals novel patterns of bacterial transmission and biogeography. Genome Research, 2016, 26, 1612-1625.	5.5	405
22	MetaQuery: a web server for rapid annotation and quantitative analysis of specific genes in the human gut microbiome. Bioinformatics, 2015, 31, 3368-3370.	4.1	50
23	Automated and Accurate Estimation of Gene Family Abundance from Shotgun Metagenomes. PLoS Computational Biology, 2015, 11, e1004573.	3.2	55