

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

393982

19
h-index

610482

24
g-index

30
all docs

30
docs citations

30
times ranked

5612
citing authors

#	ARTICLE	IF	CITATIONS
1	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	9.4	628
2	CheckV assesses the quality and completeness of metagenome-assembled viral genomes. <i>Nature Biotechnology</i> , 2021, 39, 578-585.	9.4	569
3	New insights from uncultivated genomes of the global human gut microbiome. <i>Nature</i> , 2019, 568, 505-510.	13.7	505
4	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
5	An integrated metagenomics pipeline for strain profiling reveals novel patterns of bacterial transmission and biogeography. <i>Genome Research</i> , 2016, 26, 1612-1625.	2.4	405
6	Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. <i>Nature Microbiology</i> , 2021, 6, 960-970.	5.9	248
7	Toward Accurate and Quantitative Comparative Metagenomics. <i>Cell</i> , 2016, 166, 1103-1116.	13.5	247
8	IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. <i>Nucleic Acids Research</i> , 2021, 49, D764-D775.	6.5	240
9	Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. <i>Nature Microbiology</i> , 2019, 4, 1895-1906.	5.9	206
10	Modulation of a Circulating Uremic Solute via Rational Genetic Manipulation of the Gut Microbiota. <i>Cell Host and Microbe</i> , 2016, 20, 709-715.	5.1	201
11	Discovery of Reactive Microbiota-Derived Metabolites that Inhibit Host Proteases. <i>Cell</i> , 2017, 168, 517-526.e18.	13.5	173
12	A Metagenomic Meta-analysis Reveals Functional Signatures of Health and Disease in the Human Gut Microbiome. <i>MSystems</i> , 2019, 4, .	1.7	112
13	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.	5.9	63
14	Automated and Accurate Estimation of Gene Family Abundance from Shotgun Metagenomes. <i>PLoS Computational Biology</i> , 2015, 11, e1004573.	1.5	55
15	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	4.9	53
16	MetaQuery: a web server for rapid annotation and quantitative analysis of specific genes in the human gut microbiome. <i>Bioinformatics</i> , 2015, 31, 3368-3370.	1.8	50
17	Global ecotypes in the ubiquitous marine clade SAR86. <i>ISME Journal</i> , 2020, 14, 178-188.	4.4	49
18	Phylogeny-corrected identification of microbial gene families relevant to human gut colonization. <i>PLoS Computational Biology</i> , 2018, 14, e1006242.	1.5	39

#	ARTICLE	IF	CITATIONS
19	Ecology and molecular targets of hypermutation in the global microbiome. Nature Communications, 2021, 12, 3076.	5.8	35
20	Fast and accurate metagenotyping of the human gut microbiome with GT-Pro. Nature Biotechnology, 2022, 40, 507-516.	9.4	18
21	A most wanted list of conserved microbial protein families with no known domains. PLoS ONE, 2018, 13, e0205749.	1.1	17
22	Illuminating the Virosphere Through Global Metagenomics. Annual Review of Biomedical Data Science, 2021, 4, 369-391.	2.8	17
23	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. ISME Journal, 2022, 16, 1337-1347.	4.4	15