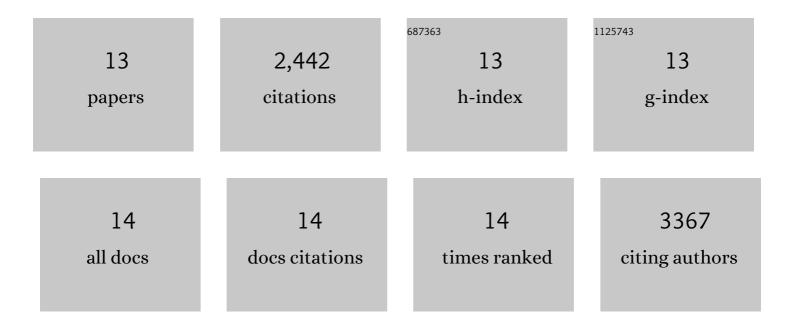
## Katherine H Huang

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10943942/publications.pdf Version: 2024-02-01



KATHEDINE H HUANC

#	Article	IF	CITATIONS
1	SARS-CoV-2 RNA concentrations in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases. Science of the Total Environment, 2022, 805, 150121.	8.0	192
2	Wastewater surveillance of SARS-CoV-2 across 40 U.S. states from February to June 2020. Water Research, 2021, 202, 117400.	11.3	119
3	Genetic diversity in cultured and wild marine cyanomyoviruses reveals phosphorus stress as a strong selective agent. ISME Journal, 2013, 7, 1827-1841.	9.8	67
4	Ecology of uncultured <i>Prochlorococcus</i> clades revealed through single-cell genomics and biogeographic analysis. ISME Journal, 2013, 7, 184-198.	9.8	105
5	ProPortal: a resource for integrated systems biology of Prochlorococcus and its phage. Nucleic Acids Research, 2012, 40, D632-D640.	14.5	33
6	Phage auxiliary metabolic genes and the redirection of cyanobacterial host carbon metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E757-64.	7.1	394
7	Genomic analysis of oceanic cyanobacterial myoviruses compared with T4â€like myoviruses from diverse hosts and environments. Environmental Microbiology, 2010, 12, 3035-3056.	3.8	318
8	MicrobesOnline: an integrated portal for comparative and functional genomics. Nucleic Acids Research, 2010, 38, D396-D400.	14.5	408
9	Analysis of a Ferric Uptake Regulator (Fur) Mutant of <i>Desulfovibrio vulgaris</i> Hildenborough. Applied and Environmental Microbiology, 2007, 73, 5389-5400.	3.1	70
10	Energetic Consequences of Nitrite Stress in Desulfovibrio vulgaris Hildenborough, Inferred from Global Transcriptional Analysis. Applied and Environmental Microbiology, 2006, 72, 4370-4381.	3.1	92
11	Operon formation is driven by co-regulation and not by horizontal gene transfer. Genome Research, 2005, 15, 809-819.	5.5	131
12	The MicrobesOnline Web site for comparative genomics. Genome Research, 2005, 15, 1015-1022.	5.5	176
13	A novel method for accurate operon predictions in all sequenced prokaryotes. Nucleic Acids Research, 2005, 33, 880-892.	14.5	316