

# Xiang Gao

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

626  
citations

759190

12  
h-index

752679

20  
g-index

21  
all docs

21  
docs citations

21  
times ranked

1117  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Bayesian framework for estimating the risk ratio of hospitalization for people with comorbidity infected by SARS-CoV-2 virus. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 472-476.	4.4	4
2	A primer on Bayesian estimation of prevalence of COVID-19 patient outcomes. <i>JAMIA Open</i> , 2021, 3, 628-631.	2.0	3
3	Evaluation of clinical, Gram stain, and microbiological cure outcomes in men receiving azithromycin for acute nongonococcal urethritis. <i>Sexually Transmitted Diseases</i> , 2021, Publish Ahead of Print, 67-75.	1.7	2
4	<i>Streptococcus pyogenes</i> Is Associated with Idiopathic Cutaneous Ulcers in Children on a Yaws-Endemic Island. <i>MBio</i> , 2021, 12, .	4.1	5
5	Bayesian estimation of the seroprevalence of antibodies to SARS-CoV-2. <i>JAMIA Open</i> , 2021, 3, 496-499.	2.0	3
6	The microbiome of calcium-based urinary stones. <i>Urolithiasis</i> , 2020, 48, 191-199.	2.0	49
7	Natural Polymorphisms Are Present in the Furin Cleavage Site of the SARS-CoV-2 Spike Glycoprotein. <i>Frontiers in Genetics</i> , 2020, 11, 783.	2.3	39
8	A logistic model for age-specific COVID-19 case-fatality rates. <i>JAMIA Open</i> , 2020, 3, 151-153.	2.0	7
9	Bladder bacterial diversity differs in continent and incontinent women: a cross-sectional study. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 223, 729.e1-729.e10.	1.3	29
10	MicroGMT: A Mutation Tracker for SARS-CoV-2 and Other Microbial Genome Sequences. <i>Frontiers in Microbiology</i> , 2020, 11, 1502.	3.5	23
11	Disease correlation network: a computational package for identifying temporal correlations between disease states from Large-Scale longitudinal medical records. <i>JAMIA Open</i> , 2019, 2, 353-359.	2.0	2
12	Bladder urinary oxygen tension is correlated with urinary microbiota composition. <i>International Urogynecology Journal</i> , 2019, 30, 1261-1267.	1.4	14
13	Characterization of Proximal Small Intestinal Microbiota in Patients With Suspected Small Intestinal Bacterial Overgrowth: A Cross-Sectional Study. <i>Clinical and Translational Gastroenterology</i> , 2019, 10, e00073.	2.5	13
14	Decreased microbial co-occurrence network stability and SCFA receptor level correlates with obesity in African-origin women. <i>Scientific Reports</i> , 2018, 8, 17135.	3.3	42
15	Urinary microbes and postoperative urinary tract infection risk in urogynecologic surgical patients. <i>International Urogynecology Journal</i> , 2018, 29, 1797-1805.	1.4	91
16	Urinary symptoms are associated with certain urinary microbes in urogynecologic surgical patients. <i>International Urogynecology Journal</i> , 2018, 29, 1765-1771.	1.4	68
17	A Dirichlet-Multinomial Bayes Classifier for Disease Diagnosis with Microbial Compositions. <i>MSphere</i> , 2017, 2, .	2.9	6
18	Household air pollution and the lung microbiome of healthy adults in Malawi: a cross-sectional study. <i>BMC Microbiology</i> , 2016, 16, 182.	3.3	49

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19	Effect of Advanced HIV Infection on the Respiratory Microbiome. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 226-235.	5.6	83
20	The Human Skin Microbiome Associates with the Outcome of and Is Influenced by Bacterial Infection. MBio, 2015, 6, e01315-15.	4.1	94