

# Xin Fang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10740690/publications.pdf>

Version: 2024-02-01

24  
papers

716  
citations

840119

11  
h-index

1058022

14  
g-index

25  
all docs

25  
docs citations

25  
times ranked

1008  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reconstructing organisms in silico: genome-scale models and their emerging applications. <i>Nature Reviews Microbiology</i> , 2020, 18, 731-743.	13.6	158
2	Genome-scale metabolic reconstructions of multiple <i>Salmonella</i> strains reveal serovar-specific metabolic traits. <i>Nature Communications</i> , 2018, 9, 3771.	5.8	109
3	Global transcriptional regulatory network for <i>Escherichia coli</i> robustly connects gene expression to transcription factor activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10286-10291.	3.3	89
4	Systematic discovery of uncharacterized transcription factors in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2018, 46, 10682-10696.	6.5	65
5	A workflow for generating multi-strain genome-scale metabolic models of prokaryotes. <i>Nature Protocols</i> , 2020, 15, 1-14.	5.5	62
6	A unified resource for transcriptional regulation in <i>Escherichia coli</i> K-12 incorporating high-throughput-generated binding data into RegulonDB version 10.0. <i>BMC Biology</i> , 2018, 16, 91.	1.7	42
7	<i>Escherichia coli</i> B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. <i>BMC Systems Biology</i> , 2018, 12, 66.	3.0	39
8	Metagenomics-Based, Strain-Level Analysis of <i>Escherichia coli</i> From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <i>Frontiers in Microbiology</i> , 2018, 9, 2559.	1.5	37
9	Genome-scale model of metabolism and gene expression provides a multi-scale description of acid stress responses in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2019, 15, e1007525.	1.5	37
10	Adaptive laboratory evolution of <i>Escherichia coli</i> under acid stress. <i>Microbiology (United Kingdom)</i> , 2020, 166, 141-148.	0.7	28
11	Gastrointestinal Surgery for Inflammatory Bowel Disease Persistently Lowers Microbiome and Metabolome Diversity. <i>Inflammatory Bowel Diseases</i> , 2021, 27, 603-616.	0.9	25
12	Reconstruction and Validation of a Genome-Scale Metabolic Model of <i>Streptococcus oralis</i> (iCJ415), a Human Commensal and Opportunistic Pathogen. <i>Frontiers in Genetics</i> , 2020, 11, 116.	1.1	11
13	Genome-scale metabolic models highlight stage-specific differences in essential metabolic pathways in <i>Trypanosoma cruzi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008728.	1.3	8
14	Adaptations of <i>Escherichia coli</i> strains to oxidative stress are reflected in properties of their structural proteomes. <i>BMC Bioinformatics</i> , 2020, 21, 162.	1.2	5
15	Title is missing!. , 2019, 15, e1007525.		0
16	Title is missing!. , 2019, 15, e1007525.		0
17	Title is missing!. , 2019, 15, e1007525.		0
18	Title is missing!. , 2019, 15, e1007525.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 14, e0008728.		0
20	Title is missing!. , 2020, 14, e0008728.		0
21	Title is missing!. , 2020, 14, e0008728.		0
22	Title is missing!. , 2020, 14, e0008728.		0
23	Title is missing!. , 2020, 14, e0008728.		0
24	Title is missing!. , 2020, 14, e0008728.		0