

Xu Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

4,358
citations

182225

30
h-index

206121

51
g-index

72
all docs

72
docs citations

72
times ranked

6653
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. <i>Cancer Cell</i> , 2022, 40, 70-87.e15.	7.7	120
2	Evaluating live microbiota biobanking using an <i>ex vivo</i> microbiome assay and metaproteomics. <i>Gut Microbes</i> , 2022, 14, 2035658.	4.3	7
3	iMetaLab Suite: A one-stop toolset for metaproteomics. , 2022, 1, .		7
4	Comprehensive Assessment of Functional Effects of Commonly Used Sugar Substitute Sweeteners on <i>Ex Vivo</i> Human Gut Microbiome. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
5	Oxytetracycline stress reconstruct the core microbial community related to nitrogen transformation during composting. <i>Bioresource Technology</i> , 2021, 319, 124142.	4.8	59
6	Quantitative analysis of SARS-CoV-2 RNA from wastewater solids in communities with low COVID-19 incidence and prevalence. <i>Water Research</i> , 2021, 188, 116560.	5.3	297
7	<i>Sargassum fusiforme</i> fucoidan modifies gut microbiota and intestinal metabolites during alleviation of hyperglycemia in type 2 diabetic mice. <i>Food and Function</i> , 2021, 12, 3572-3585.	2.1	38
8	Exploring the Microbiome-Wide Lysine Acetylation, Succinylation, and Propionylation in Human Gut Microbiota. <i>Analytical Chemistry</i> , 2021, 93, 6594-6598.	3.2	6
9	Catching a resurgence: Increase in SARS-CoV-2 viral RNA identified in wastewater 48h before COVID-19 clinical tests and 96h before hospitalizations. <i>Science of the Total Environment</i> , 2021, 770, 145319.	3.9	159
10	Examining the Effects of an Anti-Salmonella Bacteriophage Preparation, BAFASAL [®] , on Ex-Vivo Human Gut Microbiome Composition and Function Using a Multi-Omics Approach. <i>Viruses</i> , 2021, 13, 1734.	1.5	5
11	Elevated colonic microbiota-associated paucimannosidic and truncated N-glycans in pediatric ulcerative colitis. <i>Journal of Proteomics</i> , 2021, 249, 104369.	1.2	4
12	Chemoenzymatic Method for Glycoproteomic N-Glycan Type Quantitation. <i>Analytical Chemistry</i> , 2020, 92, 1618-1627.	3.2	11
13	Studying the Temporal Dynamics of the Gut Microbiota Using Metabolic Stable Isotope Labeling and Metaproteomics. <i>Analytical Chemistry</i> , 2020, 92, 15711-15718.	3.2	5
14	Widespread protein lysine acetylation in gut microbiome and its alterations in patients with Crohn's disease. <i>Nature Communications</i> , 2020, 11, 4120.	5.8	32
15	A functional ecological network based on metaproteomics responses of individual gut microbiomes to resistant starches. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3833-3842.	1.9	15
16	pepFunk: a tool for peptide-centric functional analysis of metaproteomic human gut microbiome studies. <i>Bioinformatics</i> , 2020, 36, 4171-4179.	1.8	7
17	Berberine and its structural analogs have differing effects on functional profiles of individual gut microbiomes. <i>Gut Microbes</i> , 2020, 11, 1348-1361.	4.3	30
18	MetaLab 2.0 Enables Accurate Post-Translational Modifications Profiling in Metaproteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1473-1482.	1.2	21

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19	Exosome-mediated effects and applications in inflammatory bowel disease. <i>Biological Reviews</i> , 2020, 95, 1287-1307.	4.7	89
20	RapidAIM: a culture- and metaproteomics-based Rapid Assay of Individual Microbiome responses to drugs. <i>Microbiome</i> , 2020, 8, 33.	4.9	209
21	Differential Lysis Approach Enables Selective Extraction of Taxon-Specific Proteins for Gut Metaproteomics. <i>Analytical Chemistry</i> , 2020, 92, 5379-5386.	3.2	4
22	Comparative proteomic analysis reveals metabolic variability of probiotic <i>Enterococcus durans</i> during aerobic and anaerobic cultivation. <i>Journal of Proteomics</i> , 2020, 220, 103764.	1.2	8
23	Metaproteomics Reveals Growth Phase-Dependent Responses of an <i>In Vitro</i> Gut Microbiota to Metformin. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1448-1458.	1.2	7
24	Metaproteomic and Metabolomic Approaches for Characterizing the Gut Microbiome. <i>Proteomics</i> , 2019, 19, e1800363.	1.3	28
25	Exploring the effects of operational mode and microbial interactions on bacterial community assembly in a one-stage partial-nitritation anammox reactor using integrated multi-omics. <i>Microbiome</i> , 2019, 7, 122.	4.9	65
26	An in vitro model maintaining taxon-specific functional activities of the gut microbiome. <i>Nature Communications</i> , 2019, 10, 4146.	5.8	70
27	Perspective and Guidelines for Metaproteomics in Microbiome Studies. <i>Journal of Proteome Research</i> , 2019, 18, 2370-2380.	1.8	63
28	Advancing functional and translational microbiome research using meta-omics approaches. <i>Microbiome</i> , 2019, 7, 154.	4.9	177
29	Ageing Disrupts the Circadian Patterns of Protein Expression in the Murine Hippocampus. <i>Frontiers in Aging Neuroscience</i> , 2019, 11, 368.	1.7	25
30	Open: Mucosal-luminal interface proteomics reveals biomarkers of pediatric inflammatory bowel disease-associated colitis. <i>American Journal of Gastroenterology</i> , 2018, 113, 713-724.	0.2	23
31	Assessing the impact of protein extraction methods for human gut metaproteomics. <i>Journal of Proteomics</i> , 2018, 180, 120-127.	1.2	115
32	Proteomic and Metaproteomic Approaches to Understand Host-Microbe Interactions. <i>Analytical Chemistry</i> , 2018, 90, 86-109.	3.2	44
33	Evaluating in Vitro Culture Medium of Gut Microbiome with Orthogonal Experimental Design and a Metaproteomics Approach. <i>Journal of Proteome Research</i> , 2018, 17, 154-163.	1.8	41
34	Separation and characterization of human microbiomes by metaproteomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 108, 221-230.	5.8	4
35	Metaproteomics reveals associations between microbiome and intestinal extracellular vesicle proteins in pediatric inflammatory bowel disease. <i>Nature Communications</i> , 2018, 9, 2873.	5.8	209
36	iMetaLab 1.0: a web platform for metaproteomics data analysis. <i>Bioinformatics</i> , 2018, 34, 3954-3956.	1.8	64

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37	Deep Metaproteomics Approach for the Study of Human Microbiomes. <i>Analytical Chemistry</i> , 2017, 89, 9407-9415.	3.2	83
38	Proteomic analysis of ascending colon biopsies from a paediatric inflammatory bowel disease inception cohort identifies protein biomarkers that differentiate Crohn's disease from UC. <i>Gut</i> , 2017, 66, 1573-1583.	6.1	69
39	Gut Microbial Dysbiosis Is Associated with Altered Hepatic Functions and Serum Metabolites in Chronic Hepatitis B Patients. <i>Frontiers in Microbiology</i> , 2017, 8, 2222.	1.5	172
40	MetaLab: an automated pipeline for metaproteomic data analysis. <i>Microbiome</i> , 2017, 5, 157.	4.9	128
41	The structural alteration of gut microbiota in low-birth-weight mice undergoing accelerated postnatal growth. <i>Scientific Reports</i> , 2016, 6, 27780.	1.6	34
42	<i>In Vitro</i> Metabolic Labeling of Intestinal Microbiota for Quantitative Metaproteomics. <i>Analytical Chemistry</i> , 2016, 88, 6120-6125.	3.2	40
43	MetaPro-IQ: a universal metaproteomic approach to studying human and mouse gut microbiota. <i>Microbiome</i> , 2016, 4, 31.	4.9	154
44	Peptide-Centric Approaches Provide an Alternative Perspective To Re-Examine Quantitative Proteomic Data. <i>Analytical Chemistry</i> , 2016, 88, 1973-1978.	3.2	14
45	Bottom-Up Proteomics (2013–2015): Keeping up in the Era of Systems Biology. <i>Analytical Chemistry</i> , 2016, 88, 95-121.	3.2	52
46	Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. <i>Scientific Reports</i> , 2015, 5, 14405.	1.6	499
47	Structural modulation of gut microbiota during alleviation of type 2 diabetes with a Chinese herbal formula. <i>ISME Journal</i> , 2015, 9, 552-562.	4.4	362
48	Structural changes of gut microbiota in a rat non-alcoholic fatty liver disease model treated with a Chinese herbal formula. <i>Systematic and Applied Microbiology</i> , 2013, 36, 188-196.	1.2	83
49	Structural Changes of Gut Microbiota during Berberine-Mediated Prevention of Obesity and Insulin Resistance in High-Fat Diet-Fed Rats. <i>PLoS ONE</i> , 2012, 7, e42529.	1.1	435
50	Targeting the Human Genome–Microbiome Axis for Drug Discovery: Inspirations from Global Systems Biology and Traditional Chinese Medicine. <i>Journal of Proteome Research</i> , 2012, 11, 3509-3519.	1.8	57
51	Biological extraction of realgar by <i>Acidithiobacillus ferrooxidans</i> and its <i>in vitro</i> and <i>in vivo</i> antitumor activities. <i>Pharmaceutical Biology</i> , 2010, 48, 40-47.	1.3	16
52	Bioleaching of arsenic from medicinal realgar by pure and mixed cultures. <i>Process Biochemistry</i> , 2007, 42, 1265-1271.	1.8	65