Xu Zhang

List of Publications by Year in descending order

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Χυ ΖΗΛΝΟ

#	Article	IF	CITATIONS
1	Modulation of gut microbiota by berberine and metformin during the treatment of high-fat diet-induced obesity in rats. Scientific Reports, 2015, 5, 14405.	3.3	499
2	Structural Changes of Gut Microbiota during Berberine-Mediated Prevention of Obesity and Insulin Resistance in High-Fat Diet-Fed Rats. PLoS ONE, 2012, 7, e42529.	2.5	435
3	Structural modulation of gut microbiota during alleviation of type 2 diabetes with a Chinese herbal formula. ISME Journal, 2015, 9, 552-562.	9.8	362
4	Quantitative analysis of SARS-CoV-2 RNA from wastewater solids in communities with low COVID-19 incidence and prevalence. Water Research, 2021, 188, 116560.	11.3	297
5	Metaproteomics reveals associations between microbiome and intestinal extracellular vesicle proteins in pediatric inflammatory bowel disease. Nature Communications, 2018, 9, 2873.	12.8	209
6	RapidAIM: a culture- and metaproteomics-based Rapid Assay of Individual Microbiome responses to drugs. Microbiome, 2020, 8, 33.	11.1	209
7	Advancing functional and translational microbiome research using meta-omics approaches. Microbiome, 2019, 7, 154.	11.1	177
8	Gut Microbial Dysbiosis Is Associated with Altered Hepatic Functions and Serum Metabolites in Chronic Hepatitis B Patients. Frontiers in Microbiology, 2017, 8, 2222.	3.5	172
9	Catching a resurgence: Increase in SARS-CoV-2 viral RNA identified in wastewater 48Âh before COVID-19 clinical tests and 96Âh before hospitalizations. Science of the Total Environment, 2021, 770, 145319.	8.0	159
10	MetaPro-IQ: a universal metaproteomic approach to studying human and mouse gut microbiota. Microbiome, 2016, 4, 31.	11.1	154
11	MetaLab: an automated pipeline for metaproteomic data analysis. Microbiome, 2017, 5, 157.	11.1	128
12	Proteogenomic characterization identifies clinically relevant subgroups of intrahepatic cholangiocarcinoma. Cancer Cell, 2022, 40, 70-87.e15.	16.8	120
13	Assessing the impact of protein extraction methods for human gut metaproteomics. Journal of Proteomics, 2018, 180, 120-127.	2.4	115
14	Exosomeâ€mediated effects and applications in inflammatory bowel disease. Biological Reviews, 2020, 95, 1287-1307.	10.4	89
15	Structural changes of gut microbiota in a rat non-alcoholic fatty liver disease model treated with a Chinese herbal formula. Systematic and Applied Microbiology, 2013, 36, 188-196.	2.8	83
16	Deep Metaproteomics Approach for the Study of Human Microbiomes. Analytical Chemistry, 2017, 89, 9407-9415.	6.5	83
17	An in vitro model maintaining taxon-specific functional activities of the gut microbiome. Nature Communications, 2019, 10, 4146.	12.8	70
18	Proteomic analysis of ascending colon biopsies from a paediatric inflammatory bowel disease inception cohort identifies protein biomarkers that differentiate Crohn's disease from UC. Gut, 2017, 66, 1573-1583.	12.1	69

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19	Bioleaching of arsenic from medicinal realgar by pure and mixed cultures. Process Biochemistry, 2007, 42, 1265-1271.	3.7	65
20	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. Microbiome, 2019, 7, 122.	11.1	65
21	iMetaLab 1.0: a web platform for metaproteomics data analysis. Bioinformatics, 2018, 34, 3954-3956.	4.1	64
22	Perspective and Guidelines for Metaproteomics in Microbiome Studies. Journal of Proteome Research, 2019, 18, 2370-2380.	3.7	63
23	Oxytetracycline stress reconstruct the core microbial community related to nitrogen transformation during composting. Bioresource Technology, 2021, 319, 124142.	9.6	59
24	Targeting the Human Genome–Microbiome Axis for Drug Discovery: Inspirations from Global Systems Biology and Traditional Chinese Medicine. Journal of Proteome Research, 2012, 11, 3509-3519.	3.7	57
25	Bottom-Up Proteomics (2013–2015): Keeping up in the Era of Systems Biology. Analytical Chemistry, 2016, 88, 95-121.	6.5	52
26	Proteomic and Metaproteomic Approaches to Understand Host–Microbe Interactions. Analytical Chemistry, 2018, 90, 86-109.	6.5	44
27	Evaluating in Vitro Culture Medium of Gut Microbiome with Orthogonal Experimental Design and a Metaproteomics Approach. Journal of Proteome Research, 2018, 17, 154-163.	3.7	41
28	<i>In Vitro</i> Metabolic Labeling of Intestinal Microbiota for Quantitative Metaproteomics. Analytical Chemistry, 2016, 88, 6120-6125.	6.5	40
29	<i>Sargassum fusiforme</i> fucoidan modifies gut microbiota and intestinal metabolites during alleviation of hyperglycemia in type 2 diabetic mice. Food and Function, 2021, 12, 3572-3585.	4.6	38
30	The structural alteration of gut microbiota in low-birth-weight mice undergoing accelerated postnatal growth. Scientific Reports, 2016, 6, 27780.	3.3	34
31	Widespread protein lysine acetylation in gut microbiome and its alterations in patients with Crohn's disease. Nature Communications, 2020, 11, 4120.	12.8	32
32	Berberine and its structural analogs have differing effects on functional profiles of individual gut microbiomes. Gut Microbes, 2020, 11, 1348-1361.	9.8	30
33	Metaproteomic and Metabolomic Approaches for Characterizing the Gut Microbiome. Proteomics, 2019, 19, e1800363.	2.2	28
34	Aging Disrupts the Circadian Patterns of Protein Expression in the Murine Hippocampus. Frontiers in Aging Neuroscience, 2019, 11, 368.	3.4	25
35	Open: Mucosal-luminal interface proteomics reveals biomarkers of pediatric inflammatory bowel disease-associated colitis. American Journal of Gastroenterology, 2018, 113, 713-724.	0.4	23
36	MetaLab 2.0 Enables Accurate Post-Translational Modifications Profiling in Metaproteomics. Journal of the American Society for Mass Spectrometry, 2020, 31, 1473-1482.	2.8	21

Xu Zhang

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37	Biological extraction of realgar by <i>Acidithiobacillus ferrooxidans</i> and its <i>in vitro</i> and <i>in vivo</i> antitumor activities. Pharmaceutical Biology, 2010, 48, 40-47.	2.9	16
38	A functional ecological network based on metaproteomics responses of individual gut microbiomes to resistant starches. Computational and Structural Biotechnology Journal, 2020, 18, 3833-3842.	4.1	15
39	Peptide-Centric Approaches Provide an Alternative Perspective To Re-Examine Quantitative Proteomic Data. Analytical Chemistry, 2016, 88, 1973-1978.	6.5	14
40	Chemoenzymatic Method for Glycoproteomic N-Glycan Type Quantitation. Analytical Chemistry, 2020, 92, 1618-1627.	6.5	11
41	Comparative proteomic analysis reveals metabolic variability of probiotic Enterococcus durans during aerobic and anaerobic cultivation. Journal of Proteomics, 2020, 220, 103764.	2.4	8
42	pepFunk: a tool for peptide-centric functional analysis of metaproteomic human gut microbiome studies. Bioinformatics, 2020, 36, 4171-4179.	4.1	7
43	Metaproteomics Reveals Growth Phase-Dependent Responses of an <i>In Vitro</i> Gut Microbiota to Metformin. Journal of the American Society for Mass Spectrometry, 2020, 31, 1448-1458.	2.8	7
44	Evaluating live microbiota biobanking using an <i>ex vivo</i> microbiome assay and metaproteomics. Gut Microbes, 2022, 14, 2035658.	9.8	7
45	iMetaLab Suite: A oneâ€stop toolset for metaproteomics. , 2022, 1, .		7
46	Exploring the Microbiome-Wide Lysine Acetylation, Succinylation, and Propionylation in Human Gut Microbiota. Analytical Chemistry, 2021, 93, 6594-6598.	6.5	6
47	Studying the Temporal Dynamics of the Gut Microbiota Using Metabolic Stable Isotope Labeling and Metaproteomics. Analytical Chemistry, 2020, 92, 15711-15718.	6.5	5
48	Examining the Effects of an Anti-Salmonella Bacteriophage Preparation, BAFASAL®, on Ex-Vivo Human Gut Microbiome Composition and Function Using a Multi-Omics Approach. Viruses, 2021, 13, 1734.	3.3	5
49	Separation and characterization of human microbiomes by metaproteomics. TrAC - Trends in Analytical Chemistry, 2018, 108, 221-230.	11.4	4
50	Differential Lysis Approach Enables Selective Extraction of Taxon-Specific Proteins for Gut Metaproteomics. Analytical Chemistry, 2020, 92, 5379-5386.	6.5	4
51	Elevated colonic microbiota-associated paucimannosidic and truncated N-glycans in pediatric ulcerative colitis. Journal of Proteomics, 2021, 249, 104369.	2.4	4
52	Comprehensive Assessment of Functional Effects of Commonly Used Sugar Substitute Sweeteners on <i>Ex Vivo</i> Human Gut Microbiome. Microbiology Spectrum, 2022, 10, .	3.0	3