

# Xiangmin Lin

## List of Publications by Year in descending order

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69  
papers

2,605  
citations

136950

32  
h-index

197818

49  
g-index

72  
all docs

72  
docs citations

72  
times ranked

2515  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Lysine Acetylation Modification in the Porin Aha1 of <i>Aeromonas hydrophila</i> Regulates the Uptake of Multidrug Antibiotics. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100248.	3.8	8
2	Quantitative proteomics reveals the antibiotics adaptation mechanism of <i>Aeromonas hydrophila</i> under kanamycin stress. <i>Journal of Proteomics</i> , 2022, 264, 104621.	2.4	2
3	A high-throughput screening approach for bacterial quorum sensing inhibitors (QSIs) against <i>Aeromonas hydrophila</i> infection. <i>Aquaculture</i> , 2022, 560, 738488.	3.5	4
4	Quantitative Proteomics Reveals That the Protein Components of Outer Membrane Vesicles (OMVs) in <i>Aeromonas hydrophila</i> Play Protective Roles in Antibiotic Resistance. <i>Journal of Proteome Research</i> , 2022, 21, 1707-1717.	3.7	2
5	TonB-Dependent Receptors Affect the Spontaneous Oxytetracycline Resistance Evolution in <i>Aeromonas hydrophila</i> . <i>Journal of Proteome Research</i> , 2021, 20, 154-163.	3.7	10
6	Proteomics Analysis Reveals Bacterial Antibiotics Resistance Mechanism Mediated by <i>ahslyA</i> Against Enoxacin in <i>Aeromonas hydrophila</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 699415.	3.5	2
7	Proteomics analysis reveals the importance of transcriptional regulator <i>slyA</i> in regulation of several physiological functions in <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2021, 244, 104275.	2.4	4
8	Profile of protein lysine propionylation in <i>Aeromonas hydrophila</i> and its role in enzymatic regulation. <i>Biochemical and Biophysical Research Communications</i> , 2021, 562, 1-8.	2.1	2
9	Marine Bacterial Secondary Metabolites: A Treasure House for Structurally Unique and Effective Antimicrobial Compounds. <i>Marine Drugs</i> , 2021, 19, 530.	4.6	41
10	Comparative transcriptomic analysis reveals the molecular mechanisms related to oxytetracycline-resistance in strains of <i>Aeromonas hydrophila</i> . <i>Aquaculture Reports</i> , 2021, 21, 100812.	1.7	7
11	Quantitative proteomics reveals the molecular mechanism of <i>Aeromonas hydrophila</i> in enoxacin stress. <i>Journal of Proteomics</i> , 2020, 211, 103561.	2.4	14
12	Acetylome profiling of <i>Vibrio alginolyticus</i> reveals its role in bacterial virulence. <i>Journal of Proteomics</i> , 2020, 211, 103543.	2.4	39
13	The LysR-Type Transcriptional Regulator <i>YeeY</i> Plays Important Roles in the Regulatory of Furazolidone Resistance in <i>Aeromonas hydrophila</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 577376.	3.5	7
14	Editorial: The Molecular Mechanisms of Antibiotic Resistance in Aquatic Pathogens. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 586460.	3.9	1
15	Anti-quorum Sensing and Protective Efficacies of Naringin Against <i>Aeromonas hydrophila</i> Infection in <i>Danio rerio</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 600622.	3.5	13
16	Proteomics analysis reveals the effect of <i>Aeromonas hydrophila</i> sirtuin <i>CobB</i> on biological functions. <i>Journal of Proteomics</i> , 2020, 225, 103848.	2.4	17
17	Soil Sickness in Aged Tea Plantation Is Associated With a Shift in Microbial Communities as a Result of Plant Polyphenol Accumulation in the Tea Gardens. <i>Frontiers in Plant Science</i> , 2020, 11, 601.	3.6	54
18	First Succinylome Profiling of <i>Vibrio alginolyticus</i> Reveals Key Role of Lysine Succinylation in Cellular Metabolism and Virulence. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 626574.	3.9	9

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19	Comparative metabolomics shows the metabolic profiles fluctuate in multi-drug resistant <i>Escherichia coli</i> strains. <i>Journal of Proteomics</i> , 2019, 207, 103468.	2.4	27
20	Four LysR-type transcriptional regulator family proteins (LTTRs) involved in antibiotic resistance in <i>Aeromonas hydrophila</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 127.	3.6	12
21	Long-Term Monoculture Negatively Regulates Fungal Community Composition and Abundance of Tea Orchards. <i>Agronomy</i> , 2019, 9, 466.	3.0	43
22	The characteristics of antibiotic resistance and phenotypes in 29 outer membrane protein mutant strains in <i>Aeromonas hydrophila</i> . <i>Environmental Microbiology</i> , 2019, 21, 4614-4628.	3.8	31
23	Comprehensive analysis of the lysine acetylome in <i>Aeromonas hydrophila</i> reveals cross-talk between lysine acetylation and succinylation in LuxS. <i>Emerging Microbes and Infections</i> , 2019, 8, 1229-1239.	6.5	27
24	Comparative Extracellular Proteomics of <i>Aeromonas hydrophila</i> Reveals Iron-Regulated Secreted Proteins as Potential Vaccine Candidates. <i>Frontiers in Immunology</i> , 2019, 10, 256.	4.8	54
25	An integrated quantitative proteomic and metabolomics approach to reveal the negative regulation mechanism of LamB in antibiotics resistance. <i>Journal of Proteomics</i> , 2019, 194, 148-159.	2.4	29
26	SWATH based quantitative proteomics analysis reveals Hfq2 play an important role on pleiotropic physiological functions in <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2019, 195, 1-10.	2.4	14
27	Integrated Succinylome and Metabolome Profiling Reveals Crucial Role of S-Ribosylhomocysteine Lyase in Quorum Sensing and Metabolism of <i>Aeromonas hydrophila</i> *. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 200-215.	3.8	45
28	Effect of <i>hfq2</i> gene in <i>Aeromonas hydrophila</i> on biofilm formation. <i>Chinese Science Bulletin</i> , 2019, 64, 1506-1514.	0.7	0
29	The depressed central carbon and energy metabolisms is associated to the acquisition of levofloxacin resistance in <i>Vibrio alginolyticus</i> . <i>Journal of Proteomics</i> , 2018, 181, 83-91.	2.4	57
30	Proteomic Analysis of Alterations in <i>Aeromonas hydrophila</i> Outer Membrane Proteins in Response to Oxytetracycline Stress. <i>Microbial Drug Resistance</i> , 2018, 24, 1067-1074.	2.0	9
31	Reprint of: Quantitative proteomic analysis reveals that chemotaxis is involved in chlortetracycline resistance of <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2018, 180, 138-146.	2.4	12
32	Identification of ethanol tolerant outer membrane proteome reveals OmpC-dependent mechanism in a manner of EnvZ/OmpR regulation in <i>Escherichia coli</i> . <i>Journal of Proteomics</i> , 2018, 179, 92-99.	2.4	10
33	Systematically integrated metabolomic-proteomic studies of <i>Escherichia coli</i> under ciprofloxacin stress. <i>Journal of Proteomics</i> , 2018, 179, 61-70.	2.4	34
34	Quantitative proteomic analysis reveals that chemotaxis is involved in chlortetracycline resistance of <i>Aeromonas hydrophila</i> . <i>Journal of Proteomics</i> , 2018, 172, 143-151.	2.4	27
35	Quantitative Proteomics Reveals Antibiotics Resistance Function of Outer Membrane Proteins in <i>Aeromonas hydrophila</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 390.	3.9	21
36	In-Silico Prediction and Modeling of the Quorum Sensing LuxS Protein and Inhibition of AI-2 Biosynthesis in <i>Aeromonas hydrophila</i> . <i>Molecules</i> , 2018, 23, 2627.	3.8	18

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37	Identification and efficacy of glycine, serine and threonine metabolism in potentiating kanamycin-mediated killing of <i>Edwardsiella piscicida</i> . <i>Journal of Proteomics</i> , 2018, 183, 34-44.	2.4	53
38	Alanine Enhances Aminoglycosides-Induced ROS Production as Revealed by Proteomic Analysis. <i>Frontiers in Microbiology</i> , 2018, 9, 29.	3.5	77
39	The protective efficacy of four iron-related recombinant proteins and their single-walled carbon nanotube encapsulated counterparts against <i>Aeromonas hydrophila</i> infection in zebrafish. <i>Fish and Shellfish Immunology</i> , 2018, 82, 50-59.	3.6	27
40	Global protein expression profile response of planktonic <i>Aeromonas hydrophila</i> exposed to chlortetracycline. <i>World Journal of Microbiology and Biotechnology</i> , 2017, 33, 68.	3.6	36
41	Quantitative proteomic analysis of iron-regulated outer membrane proteins in <i>Aeromonas hydrophila</i> as potential vaccine candidates. <i>Fish and Shellfish Immunology</i> , 2017, 68, 1-9.	3.6	24
42	Quantitative proteomic analysis of <i>Edwardsiella tarda</i> in response to oxytetracycline stress in biofilm. <i>Journal of Proteomics</i> , 2017, 150, 141-148.	2.4	37
43	C-Terminal Domain of Hemocyanin, a Major Antimicrobial Protein from <i>Litopenaeus vannamei</i> : Structural Homology with Immunoglobulins and Molecular Diversity. <i>Frontiers in Immunology</i> , 2017, 8, 611.	4.8	72
44	Proteomic Analysis Reveals That Metabolic Flows Affect the Susceptibility of <i>Aeromonas hydrophila</i> to Antibiotics. <i>Scientific Reports</i> , 2016, 6, 39413.	3.3	44
45	Proteomics Analysis Reveals a Potential Antibiotic Cocktail Therapy Strategy for <i>Aeromonas hydrophila</i> Infection in Biofilm. <i>Journal of Proteome Research</i> , 2016, 15, 1810-1820.	3.7	105
46	Quantitative proteomic analysis of cell envelope preparations under iron starvation stress in <i>Aeromonas hydrophila</i> . <i>BMC Microbiology</i> , 2016, 16, 161.	3.3	13
47	Quantitative proteomics study on Lsi1 in regulation of rice ( <i>Oryza sativa</i> L.) cold resistance. <i>Plant Growth Regulation</i> , 2016, 78, 307-323.	3.4	31
48	Outer membrane proteomics of kanamycin-resistant <i>Escherichia coli</i> identified MipA as a novel antibiotic resistance-related protein. <i>FEMS Microbiology Letters</i> , 2015, 362, .	1.8	39
49	An Integrated Quantitative and Targeted Proteomics Reveals Fitness Mechanisms of <i>Aeromonas hydrophila</i> under Oxytetracycline Stress. <i>Journal of Proteome Research</i> , 2015, 14, 1515-1525.	3.7	52
50	Cerebrospinal Fluid Peptides as Potential Parkinson Disease Biomarkers: A Staged Pipeline for Discovery and Validation*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 544-555.	3.8	51
51	Proteomic profiling in MPTP monkey model for early Parkinson disease biomarker discovery. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 779-787.	2.3	25
52	Metaproteomic analysis of bacterial communities in marine mudflat aquaculture sediment. <i>World Journal of Microbiology and Biotechnology</i> , 2015, 31, 1397-1408.	3.6	7
53	Decreased expression of LamB and Odp1 complex is crucial for antibiotic resistance in <i>Escherichia coli</i> . <i>Journal of Proteomics</i> , 2014, 98, 244-253.	2.4	64
54	Fluctuation of multiple metabolic pathways is required for <i>Escherichia coli</i> in response to chlortetracycline stress. <i>Molecular BioSystems</i> , 2014, 10, 901-908.	2.9	64

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55	Phosphorylated $\alpha$ -Synuclein in Parkinson's Disease. <i>Science Translational Medicine</i> , 2012, 4, 121ra20.	12.4	223
56	DJ-1 isoforms in whole blood as potential biomarkers of Parkinson disease. <i>Scientific Reports</i> , 2012, 2, 954.	3.3	90
57	Differential regulation of OmpC and OmpF by AtpB in <i>Escherichia coli</i> exposed to nalidixic acid and chlortetracycline. <i>Journal of Proteomics</i> , 2012, 75, 5898-5910.	2.4	34
58	Characterization of Outer Membrane Proteins of <i>Escherichia coli</i> in Response to Phenol Stress. <i>Current Microbiology</i> , 2011, 62, 777-783.	2.2	25
59	A Novel Negative Regulation Mechanism of Bacterial Outer Membrane Proteins in Response to Antibiotic Resistance. <i>Journal of Proteome Research</i> , 2010, 9, 5952-5959.	3.7	63
60	From Proteome to Genome for Functional Characterization of pH-Dependent Outer Membrane Proteins in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2009, 8, 1059-1070.	3.7	25
61	Downregulation of Tsx and OmpW and Upregulation of OmpX Are Required for Iron Homeostasis in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2008, 7, 1235-1243.	3.7	37
62	Proteomic Analysis of Nalidixic Acid Resistance in <i>Escherichia coli</i> : Identification and Functional Characterization of OM Proteins. <i>Journal of Proteome Research</i> , 2008, 7, 2399-2405.	3.7	63
63	Identification and Network of Outer Membrane Proteins Regulating Streptomycin Resistance in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2008, 7, 4040-4049.	3.7	58
64	Identification and Antibody-Therapeutic Targeting of Chloramphenicol-Resistant Outer Membrane Proteins in <i>Escherichia coli</i> . <i>Journal of Proteome Research</i> , 2007, 6, 3628-3636.	3.7	62
65	OmpW and OmpV Are Required for NaCl Regulation in <i>Photobacterium damsela</i> . <i>Journal of Proteome Research</i> , 2006, 5, 2250-2257.	3.7	43
66	Systematic Identification of the Subproteome of <i>Escherichia coli</i> Cell Envelope Reveals the Interaction Network of Membrane Proteins and Membrane-Associated Peripheral Proteins. <i>Journal of Proteome Research</i> , 2006, 5, 3268-3276.	3.7	46
67	Analysis of outer membrane proteome of <i>Escherichia coli</i> related to resistance to ampicillin and tetracycline. <i>Proteomics</i> , 2006, 6, 462-473.	2.2	113
68	Proteomic analysis on the expression of outer membrane proteins of <i>Vibrio alginolyticus</i> at different sodium concentrations. <i>Proteomics</i> , 2005, 5, 3142-3152.	2.2	112
69	Proteomic Analysis of the Sarcosine-Insoluble Outer Membrane Fraction of <i>Pseudomonas aeruginosa</i> Responding to Ampicillin, Kanamycin, and Tetracycline Resistance. <i>Journal of Proteome Research</i> , 2005, 4, 2257-2265.	3.7	84