

Huoming Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

2,528
citations

185998

28
h-index

197535

49
g-index

59
all docs

59
docs citations

59
times ranked

4632
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 genomes from Saudi Arabia implicate nucleocapsid mutations in host response and increased viral load. <i>Nature Communications</i> , 2022, 13, 601.	5.8	40
2	Analysis of the <i>Arabidopsis</i> <i>coilin</i> mutant reveals a positive role of AtCOILIN in plant immunity. <i>Plant Physiology</i> , 2022, 190, 745-761.	2.3	6
3	Narrow Precursor Mass Range for DIA-MS Enhances Protein Identification and Quantification in <i>Arabidopsis</i> . <i>Life</i> , 2021, 11, 982.	1.1	9
4	Probing SWATH-MS as a tool for proteome level quantification in a nonmodel fish. <i>Molecular Ecology Resources</i> , 2020, 20, 1647-1657.	2.2	9
5	Evidence for a role of protein phosphorylation in the maintenance of the cnidarian-algal symbiosis. <i>Molecular Ecology</i> , 2019, 28, 5373-5386.	2.0	7
6	Integrated transcriptomic and proteomic analysis of pathogenic mycobacteria and their <i>esx-1</i> mutants reveal secretion-dependent regulation of ESX-1 substrates and WhiB6 as a transcriptional regulator. <i>PLoS ONE</i> , 2019, 14, e0211003.	1.1	18
7	MAP 4K4 associates with BIK 1 to regulate plant innate immunity. <i>EMBO Reports</i> , 2019, 20, e47965.	2.0	22
8	<i>Arabidopsis</i> proteome and the mass spectral assay library. <i>Scientific Data</i> , 2019, 6, 278.	2.4	39
9	Ubiquitin ligases HUIWE1 and NEDD4 cooperatively control signal-dependent PRC2-Ezh1/2-mediated adaptive stress response pathway in skeletal muscle cells. <i>Epigenetics and Chromatin</i> , 2019, 12, 78.	1.8	16
10	Purification and characterisation of a protease (tamarillin) from tamarillo fruit. <i>Food Chemistry</i> , 2018, 256, 228-234.	4.2	29
11	Comparative proteomics and codon substitution analysis reveal mechanisms of differential resistance to hypoxia in congeneric snails. <i>Journal of Proteomics</i> , 2018, 172, 36-48.	1.2	9
12	The caseinolytic protease complex component CLPC1 in <i>Arabidopsis</i> maintains proteome and RNA homeostasis in chloroplasts. <i>BMC Plant Biology</i> , 2018, 18, 192.	1.6	9
13	Role of G3BP1 in glucocorticoid receptor-mediated microRNA-15b and microRNA-23a biogenesis in endothelial cells. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 3613-3630.	2.4	12
14	Comparative proteome analysis between <i>C. briggsae</i> embryos and larvae reveals a role of chromatin modification proteins in embryonic cell division. <i>Scientific Reports</i> , 2017, 7, 4296.	1.6	2
15	Transcriptome and Proteome Studies Reveal Candidate Attachment Genes during the Development of the Barnacle <i>Amphibalanus Amphitrite</i> . <i>Frontiers in Marine Science</i> , 2016, 3, .	1.2	12
16	Molecular signatures of transgenerational response to ocean acidification in a species of reef fish. <i>Nature Climate Change</i> , 2016, 6, 1014-1018.	8.1	103
17	Quantitative analysis of oyster larval proteome provides new insights into the effects of multiple climate change stressors. <i>Global Change Biology</i> , 2016, 22, 2054-2068.	4.2	70
18	Transcriptome and proteome dynamics in larvae of the barnacle <i>Balanus Amphitrite</i> from the Red Sea. <i>BMC Genomics</i> , 2015, 16, 1063.	1.2	18

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19	Proteomic Changes Associated with Successive Reproductive Periods in Male Polychaetous Nearthes arenaceodontata. <i>Scientific Reports</i> , 2015, 5, 13561.	1.6	2
20	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. <i>Scientific Reports</i> , 2015, 5, 15443.	1.6	78
21	Selective phosphorylation during early macrophage differentiation. <i>Proteomics</i> , 2015, 15, 3731-3743.	1.3	6
22	Hepatic Proteomic Responses in Marine Medaka (<i>Oryzias melastigma</i>) Chronically Exposed to Antifouling Compound Butenolide [5-octylfuran-2(5H)-one] or 4,5-Dichloro-2-n-Octyl-4-Isothiazolin-3-One (DCOIT). <i>Environmental Science & Technology</i> , 2015, 49, 1851-1859.	4.6	41
23	Proteomic identification of early salicylate- and flg22-responsive redox-sensitive proteins in <i>Arabidopsis</i> . <i>Scientific Reports</i> , 2015, 5, 8625.	1.6	41
24	Proteomic analysis of exosomes from nasopharyngeal carcinoma cell identifies intercellular transfer of angiogenic proteins. <i>International Journal of Cancer</i> , 2015, 137, 1830-1841.	2.3	84
25	The <i>Arabidopsis</i> gene DIG6 encodes a large 60S subunit nuclear export GTPase 1 that is involved in ribosome biogenesis and affects multiple auxin-regulated development processes. <i>Journal of Experimental Botany</i> , 2015, 66, 6863-6875.	2.4	21
26	Data for transcriptomic and iTRAQ proteomic analysis of <i>Anguilla japonica</i> gills in response to osmotic stress. <i>Data in Brief</i> , 2015, 3, 120-125.	0.5	2
27	Quantitative Proteomics Study of Larval Settlement in the Barnacle <i>Balanus amphitrite</i> . <i>PLoS ONE</i> , 2014, 9, e88744.	1.1	35
28	Quantitative proteomics reveals differential biological processes in healthy neonatal cord neutrophils and adult neutrophils. <i>Proteomics</i> , 2014, 14, 1688-1697.	1.3	22
29	Identification of redox-sensitive cysteines in the <i>Arabidopsis</i> proteome using OxiTRAQ, a quantitative redox proteomics method. <i>Proteomics</i> , 2014, 14, 750-762.	1.3	81
30	Proteomic changes in brain tissues of marine medaka (<i>Oryzias melastigma</i>) after chronic exposure to two antifouling compounds: Butenolide and 4,5-dichloro-2-n-octyl-4-isothiazolin-3-one (DCOIT). <i>Aquatic Toxicology</i> , 2014, 157, 47-56.	1.9	29
31	Proteomic profiling during the pre-competent to competent transition of the biofouling polychaete <i>Hydroides elegans</i> . <i>Biofouling</i> , 2014, 30, 921-928.	0.8	2
32	iTRAQ-based quantitative proteomic analysis reveals acute hypo-osmotic responsive proteins in the gills of the Japanese eel (<i>Anguilla japonica</i>). <i>Journal of Proteomics</i> , 2014, 105, 133-143.	1.2	21
33	The Putative E3 Ubiquitin Ligase ECERIFERUM9 Regulates Abscisic Acid Biosynthesis and Response during Seed Germination and Postgermination Growth in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2014, 165, 1255-1268.	2.3	42
34	Transcriptomic and iTRAQ proteomic approaches reveal novel short-term hyperosmotic stress responsive proteins in the gill of the Japanese eel (<i>Anguilla japonica</i>). <i>Journal of Proteomics</i> , 2013, 89, 81-94.	1.2	47
35	Understanding the Regulation of Estivation in a Freshwater Snail through iTRAQ-Based Comparative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 5271-5280.	1.8	47
36	First Proteome of the Egg Perivitelline Fluid of a Freshwater Gastropod with Aerial Oviposition. <i>Journal of Proteome Research</i> , 2012, 11, 4240-4248.	1.8	54

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37	Butenolide Inhibits Marine Fouling by Altering the Primary Metabolism of Three Target Organisms. ACS Chemical Biology, 2012, 7, 1049-1058.	1.6	46
38	Quantitative Proteomics Identify Molecular Targets That Are Crucial in Larval Settlement and Metamorphosis of <i>Bugula neritina</i> . Journal of Proteome Research, 2011, 10, 349-360.	1.8	22
39	Comparative proteome analysis of 3T3-L1 adipocyte differentiation using iTRAQ-coupled 2D LC-MS/MS. Journal of Cellular Biochemistry, 2011, 112, 3002-3014.	1.2	38
40	Dependency on de novo protein synthesis and proteomic changes during metamorphosis of the marine bryozoan <i>Bugula neritina</i> . Proteome Science, 2010, 8, 25.	0.7	15
41	Rapid transcriptome and proteome profiling of a non-model marine invertebrate, <i>Bugula neritina</i> . Proteomics, 2010, 10, 2972-2981.	1.3	46
42	Study of monocyte membrane proteome perturbation during lipopolysaccharide-induced tolerance using iTRAQ-based quantitative proteomic approach. Proteomics, 2010, 10, 2780-2789.	1.3	45
43	Hypoxic Tumor Cell Modulates Its Microenvironment to Enhance Angiogenic and Metastatic Potential by Secretion of Proteins and Exosomes. Molecular and Cellular Proteomics, 2010, 9, 1085-1099.	2.5	459
44	Local Atherosclerotic Plaques Are a Source of Prognostic Biomarkers for Adverse Cardiovascular Events. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 612-619.	1.1	108
45	Simultaneous Characterization of Glyco- and Phosphoproteomes of Mouse Brain Membrane Proteome with Electrostatic Repulsion Hydrophilic Interaction Chromatography. Molecular and Cellular Proteomics, 2010, 9, 635-647.	2.5	90
46	Phenotyping of an <i>In Vitro</i> Model of Ischemic Penumbra by iTRAQ-Based Shotgun Quantitative Proteomics. Journal of Proteome Research, 2010, 9, 472-484.	1.8	63
47	Identification of Novel Functional Differences in Monocyte Subsets Using Proteomic and Transcriptomic Methods. Journal of Proteome Research, 2009, 8, 4028-4038.	1.8	89
48	One-Step Procedure for Peptide Extraction from In-Gel Digestion Sample for Mass Spectrometric Analysis. Analytical Chemistry, 2008, 80, 9797-9805.	3.2	19
49	A Comparative Study of Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) versus SCX-IMAC-Based Methods for Phosphopeptide Isolation/Enrichment. Journal of Proteome Research, 2008, 7, 4869-4877.	1.8	88
50	Hybridization of Pulsed-Q Dissociation and Collision-Activated Dissociation in Linear Ion Trap Mass Spectrometer for iTRAQ Quantitation. Journal of Proteome Research, 2008, 7, 4831-4840.	1.8	63
51	Circulating Haptoglobin Is an Independent Prognostic Factor in the Sera of Patients with Epithelial Ovarian Cancer. Neoplasia, 2007, 9, 1-7.	2.3	72
52	Differential recovery of membrane proteins after extraction by aqueous methanol and trifluoroethanol. Proteomics, 2007, 7, 1654-1663.	1.3	56