

Huoming Zhang

List of Publications by Year in descending order

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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	Hypoxic Tumor Cell Modulates Its Microenvironment to Enhance Angiogenic and Metastatic Potential by Secretion of Proteins and Exosomes. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1085-1099.	2.5	459
2	Local Atherosclerotic Plaques Are a Source of Prognostic Biomarkers for Adverse Cardiovascular Events. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010, 30, 612-619.	1.1	108
3	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
4	Simultaneous Characterization of Glyco- and Phosphoproteomes of Mouse Brain Membrane Proteome with Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 635-647.	2.5	90
5	Identification of Novel Functional Differences in Monocyte Subsets Using Proteomic and Transcriptomic Methods. <i>Journal of Proteome Research</i> , 2009, 8, 4028-4038.	1.8	89
6	A Comparative Study of Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) versus SCX-IMAC-Based Methods for Phosphopeptide Isolation/Enrichment. <i>Journal of Proteome Research</i> , 2008, 7, 4869-4877.	1.8	88
7	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
8	Identification of redox-sensitive cysteines in the Arabidopsis proteome using OxiTRAQ, a quantitative redox proteomics method. <i>Proteomics</i> , 2014, 14, 750-762.	1.3	81
9	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
10	Circulating Haptoglobin Is an Independent Prognostic Factor in the Sera of Patients with Epithelial Ovarian Cancer. <i>Neoplasia</i> , 2007, 9, 1-7.	2.3	72
11	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
12	Hybridization of Pulsed-Q Dissociation and Collision-Activated Dissociation in Linear Ion Trap Mass Spectrometer for iTRAQ Quantitation. <i>Journal of Proteome Research</i> , 2008, 7, 4831-4840.	1.8	63
13	Phenotyping of an <i>in Vitro</i> Model of Ischemic Penumbra by iTRAQ-Based Shotgun Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 472-484.	1.8	63
14	Differential recovery of membrane proteins after extraction by aqueous methanol and trifluoroethanol. <i>Proteomics</i> , 2007, 7, 1654-1663.	1.3	56
15	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
16	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
17	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
18	Rapid transcriptome and proteome profiling of a non-model marine invertebrate, <i>Bugula neritina</i> . <i>Proteomics</i> , 2010, 10, 2972-2981.	1.3	46

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19	Butenolide Inhibits Marine Fouling by Altering the Primary Metabolism of Three Target Organisms. ACS Chemical Biology, 2012, 7, 1049-1058.	1.6	46
20	Study of monocyte membrane proteome perturbation during lipopolysaccharide-induced tolerance using iTRAQ-based quantitative proteomic approach. Proteomics, 2010, 10, 2780-2789.	1.3	45
21	The Putative E3 Ubiquitin Ligase ECERIFERUM9 Regulates Abscisic Acid Biosynthesis and Response during Seed Germination and Postgermination Growth in Arabidopsis. Plant Physiology, 2014, 165, 1255-1268.	2.3	42
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). Environmental Science & Technology, 2015, 49, 1851-1859.	4.6	41
23	Proteomic identification of early salicylate- and flg22-responsive redox-sensitive proteins in Arabidopsis. Scientific Reports, 2015, 5, 8625.	1.6	41
24	SARS-CoV-2 genomes from Saudi Arabia implicate nucleocapsid mutations in host response and increased viral load. Nature Communications, 2022, 13, 601.	5.8	40
25	Arabidopsis proteome and the mass spectral assay library. Scientific Data, 2019, 6, 278.	2.4	39
26	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
27	Quantitative Proteomics Study of Larval Settlement in the Barnacle Balanus amphitrite. PLoS ONE, 2014, 9, e88744.	1.1	35
28	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). Aquatic Toxicology, 2014, 157, 47-56.	1.9	29
29	Purification and characterisation of a protease (tamarillin) from tamarillo fruit. Food Chemistry, 2018, 256, 228-234.	4.2	29
30	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
31	Quantitative proteomics reveals differential biological processes in healthy neonatal cord neutrophils and adult neutrophils. Proteomics, 2014, 14, 1688-1697.	1.3	22
32	MAP 4K4 associates with BIK 1 to regulate plant innate immunity. EMBO Reports, 2019, 20, e47965.	2.0	22
33	iTRAQ-based quantitative proteomic analysis reveals acute hypo-osmotic responsive proteins in the gills of the Japanese eel (<i>Anguilla japonica</i>). Journal of Proteomics, 2014, 105, 133-143.	1.2	21
34	The Arabidopsis gene DIG6 encodes a large 60S subunit nuclear export GTPase 1 that is involved in ribosome biogenesis and affects multiple auxin-regulated development processes. Journal of Experimental Botany, 2015, 66, 6863-6875.	2.4	21
35	One-Step Procedure for Peptide Extraction from In-Gel Digestion Sample for Mass Spectrometric Analysis. Analytical Chemistry, 2008, 80, 9797-9805.	3.2	19
36	Transcriptome and proteome dynamics in larvae of the barnacle Balanus Amphitrite from the Red Sea. BMC Genomics, 2015, 16, 1063.	1.2	18

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37	Integrated transcriptomic and proteomic analysis of pathogenic mycobacteria and their esx-1 mutants reveal secretion-dependent regulation of ESX-1 substrates and WhiB6 as a transcriptional regulator. PLoS ONE, 2019, 14, e0211003.	1.1	18
38	Ubiquitin ligases HUWE1 and NEDD4 cooperatively control signal-dependent PRC2-Ezh1/2-mediated adaptive stress response pathway in skeletal muscle cells. Epigenetics and Chromatin, 2019, 12, 78.	1.8	16
39	Dependency on de novo protein synthesis and proteomic changes during metamorphosis of the marine bryozoan Bugula neritina. Proteome Science, 2010, 8, 25.	0.7	15
40	Transcriptome and Proteome Studies Reveal Candidate Attachment Genes during the Development of the Barnacle Amphibalanus Amphitrite. Frontiers in Marine Science, 2016, 3, .	1.2	12
41	Role of G3BP1 in glucocorticoid receptor-mediated microRNA-15b and microRNA-23a biogenesis in endothelial cells. Cellular and Molecular Life Sciences, 2017, 74, 3613-3630.	2.4	12
42	Comparative proteomics and codon substitution analysis reveal mechanisms of differential resistance to hypoxia in congeneric snails. Journal of Proteomics, 2018, 172, 36-48.	1.2	9
43	The caseinolytic protease complex component CLPC1 in Arabidopsis maintains proteome and RNA homeostasis in chloroplasts. BMC Plant Biology, 2018, 18, 192.	1.6	9
44	Probing SWATH-MS as a tool for proteome level quantification in a nonmodel fish. Molecular Ecology Resources, 2020, 20, 1647-1657.	2.2	9
45	Narrow Precursor Mass Range for DIA-MS Enhances Protein Identification and Quantification in Arabidopsis. Life, 2021, 11, 982.	1.1	9
46	Evidence for a role of protein phosphorylation in the maintenance of the cnidarian-algal symbiosis. Molecular Ecology, 2019, 28, 5373-5386.	2.0	7
47	Selective phosphorylation during early macrophage differentiation. Proteomics, 2015, 15, 3731-3743.	1.3	6
48	Analysis of the Arabidopsis <i>coilin</i> mutant reveals a positive role of AtCOILIN in plant immunity. Plant Physiology, 2022, 190, 745-761.	2.3	6
49	Proteomic profiling during the pre-competent to competent transition of the biofouling polychaete <i>Hydroides elegans</i> . Biofouling, 2014, 30, 921-928.	0.8	2
50	Proteomic Changes Associated with Successive Reproductive Periods in Male Polychaetous Neanthes arenaceodentata. Scientific Reports, 2015, 5, 13561.	1.6	2
51	Data for transcriptomic and iTRAQ proteomic analysis of <i>Anguilla japonica</i> gills in response to osmotic stress. Data in Brief, 2015, 3, 120-125.	0.5	2
52	Comparative proteome analysis between <i>C. briggsae</i> embryos and larvae reveals a role of chromatin modification proteins in embryonic cell division. Scientific Reports, 2017, 7, 4296.	1.6	2