

Sheng Zhang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

97 papers	4,582 citations	34 h-index	66 g-index
105 ext. papers	5,931 ext. citations	8 avg, IF	5.34 L-index

#	Paper	IF	Citations
97	Early non-neutralizing, afucosylated antibody responses are associated with COVID-19 severity.. <i>Science Translational Medicine</i> , 2022 , 14, eabm7853	17.5	10
96	Altered succinylation of mitochondrial proteins, APP and tau in Alzheimer's disease.. <i>Nature Communications</i> , 2022 , 13, 159	17.4	3
95	Quantitative proteomics reveals tissue-specific toxic mechanisms for acute hydrogen sulfide-induced injury of diverse organs in pig. <i>Science of the Total Environment</i> , 2022 , 806, 150365	10.2	
94	Oxygen level regulates N-terminal translation elongation of selected proteins through deoxyhypusine hydroxylation. <i>Cell Reports</i> , 2022 , 39, 110855	10.6	1
93	Reduction of the canonical function of a glycolytic enzyme enolase triggers immune responses that further affect metabolism and growth in Arabidopsis. <i>Plant Cell</i> , 2021 ,	11.6	2
92	Vitamin D kinetics in nonpregnant and pregnant women after a single oral dose of trideuterated vitamin D. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2021 , 216, 106034	5.1	0
91	The human brain acetylome reveals that decreased acetylation of mitochondrial proteins associates with Alzheimer's disease. <i>Journal of Neurochemistry</i> , 2021 , 158, 282-296	6	1
90	Divergent early antibody responses define COVID-19 disease trajectories 2021 ,		3
89	Proinflammatory IgG Fc structures in patients with severe COVID-19. <i>Nature Immunology</i> , 2021 , 22, 67-73	19.1	116
88	Comparison of MS, synchronous precursor selection MS, and real-time search MS methodologies for lung proteomes of hydrogen sulfide treated swine. <i>Analytical and Bioanalytical Chemistry</i> , 2021 , 413, 419-429	4.4	1
87	MaMAPK3-MaICE1-MaPOD P7 pathway, a positive regulator of cold tolerance in banana. <i>BMC Plant Biology</i> , 2021 , 21, 97	5.3	4
86	Shotgun scanning glycomutagenesis: A simple and efficient strategy for constructing and characterizing neoglycoproteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	1
85	Aerial ammonia exposure induces the perturbation of the interorgan ammonia disposal and branched-chain amino acid catabolism in growing pigs. <i>Animal Nutrition</i> , 2021 , 7, 947-958	4.8	
84	HIF1 β stabilization in hypoxia is not oxidant-initiated. <i>ELife</i> , 2021 , 10,	8.9	2
83	Maternal Anti-Dengue IgG Fucosylation Predicts Susceptibility to Dengue Disease in Infants. <i>Cell Reports</i> , 2020 , 31, 107642	10.6	14
82	FcRn, but not FcRs, drives maternal-fetal transplacental transport of human IgG antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 12943-12951	11.5	25
81	MaXLinker: Proteome-wide Cross-link Identifications with High Specificity and Sensitivity. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 554-568	7.6	21

80	The proteomic profiling of multiple tissue damage in chickens for a selenium deficiency biomarker discovery. <i>Food and Function</i> , 2020 , 11, 1312-1321	6.1	40
79	Proteomic Analysis and Cell Viability of Nine Amnion, Chorion, Umbilical Cord, and Amniotic Fluid-Derived Products. <i>Cartilage</i> , 2020 , 1947603520976767	3	4
78	The Penium margaritaceum Genome: Hallmarks of the Origins of Land Plants. <i>Cell</i> , 2020 , 181, 1097-1111	6.12	62
77	Both gut microbiota and cytokines act to atherosclerosis in ApoE ^{-/-} mice. <i>Microbial Pathogenesis</i> , 2020 , 138, 103827	3.8	10
76	Heat treatment of bovine colostrum: I. Effects on bacterial and somatic cell counts, immunoglobulin, insulin, and IGF-I concentrations, as well as the colostrum proteome. <i>Journal of Dairy Science</i> , 2020 , 103, 9368-9383	4	12
75	Heat treatment of bovine colostrum: II. Effects on calf serum immunoglobulin, insulin, and IGF-I concentrations, and the serum proteome. <i>Journal of Dairy Science</i> , 2020 , 103, 9384-9406	4	7
74	Challenges and Opportunities in Clinical Applications of Blood-Based Proteomics in Cancer. <i>Cancers</i> , 2020 , 12,	6.6	20
73	Secreted sphingomyelins modulate low mammary cancer incidence observed in certain mammals. <i>Scientific Reports</i> , 2020 , 10, 20580	4.9	0
72	Proteomics insights into the effects of MSTN on muscle glucose and lipid metabolism in genetically edited cattle. <i>General and Comparative Endocrinology</i> , 2020 , 291, 113237	3	16
71	Host-induced gene silencing of Foc TR4 ERG6/11 genes exhibits superior resistance to Fusarium wilt of banana. <i>Plant Biotechnology Journal</i> , 2020 , 18, 11-13	11.6	23
70	Proteomic characterization of outer membrane vesicles from gut mucosa-derived fusobacterium nucleatum. <i>Journal of Proteomics</i> , 2019 , 195, 125-137	3.9	21
69	Integrated proteomic and metabolomic analysis suggests high rates of glycolysis are likely required to support high carotenoid accumulation in banana pulp. <i>Food Chemistry</i> , 2019 , 297, 125016	8.5	11
68	Mapping and Profiling Lipid Distribution in a 3D Model of Breast Cancer Progression. <i>ACS Central Science</i> , 2019 , 5, 768-780	16.8	19
67	Serum Proteomics on the Basis of Discovery of Predictive Biomarkers of Response to Androgen Deprivation Therapy in Advanced Prostate Cancer. <i>Clinical Genitourinary Cancer</i> , 2019 , 17, 248-253.e7	3.3	7
66	Structure and chemistry of lysinoalanine crosslinking in the spirochaete flagella hook. <i>Nature Chemical Biology</i> , 2019 , 15, 959-965	11.7	7
65	Overexpression of a CPYC-Type Glutaredoxin, , Causes Abnormal Embryos and an Increased Grain Weight in Rice. <i>Frontiers in Plant Science</i> , 2019 , 10, 848	6.2	4
64	Atmospheric Ammonia Affects Myofiber Development and Lipid Metabolism in Growing Pig Muscle. <i>Animals</i> , 2019 , 10,	3.1	7
63	Adaption of Roots to Nitrogen Deficiency Revealed by 3D Quantification and Proteomic Analysis. <i>Plant Physiology</i> , 2019 , 179, 329-347	6.6	38

62	Evaluation of six sample preparation procedures for qualitative and quantitative proteomics analysis of milk fat globule membrane. <i>Electrophoresis</i> , 2018 , 39, 2332-2339	3.6	25
61	Ube2V2 Is a Rosetta Stone Bridging Redox and Ubiquitin Codes, Coordinating DNA Damage Responses. <i>ACS Central Science</i> , 2018 , 4, 246-259	16.8	33
60	Cerebral ischemia induces the aggregation of proteins linked to neurodegenerative diseases. <i>Scientific Reports</i> , 2018 , 8, 2701	4.9	38
59	Probing the molecular regulation of lipopolysaccharide stress in piglet liver by comparative proteomics analysis. <i>Electrophoresis</i> , 2018 , 39, 2321-2331	3.6	5
58	Estrogen receptor beta modulates permeability transition in brain mitochondria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018 , 1859, 423-433	4.6	23
57	Early Cold-Induced Peroxidases and Aquaporins Are Associated With High Cold Tolerance in Dajiao (spp. <i>Dajiao</i>). <i>Frontiers in Plant Science</i> , 2018 , 9, 282	6.2	14
56	The Secretome and N-Glycosylation Profiles of the Charophycean Green Alga, <i>Penium margaritaceum</i> , Resemble Those of Embryophytes. <i>Proteomes</i> , 2018 , 6,	4.6	9
55	OsNOA1 functions in a threshold-dependent manner to regulate chloroplast proteins in rice at lower temperatures. <i>BMC Plant Biology</i> , 2018 , 18, 44	5.3	6
54	Parallel comparative proteomics and phosphoproteomics reveal that cattle regulates phosphorylation of key enzymes in glycogen metabolism and glycolysis pathway. <i>Oncotarget</i> , 2018 , 9, 11352-11370	3.3	23
53	IRE1/XBP1 controls T cell function in ovarian cancer by regulating mitochondrial activity. <i>Nature</i> , 2018 , 562, 423-428	50.4	139
52	Akt3 is a privileged first responder in isozyme-specific electrophile response. <i>Nature Chemical Biology</i> , 2017 , 13, 333-338	11.7	39
51	Comparative Phosphoproteomics Reveals an Important Role of MKK2 in Banana (<i>Musa</i> spp.) Cold Signal Network. <i>Scientific Reports</i> , 2017 , 7, 40852	4.9	18
50	Identification and characterization of glycation adducts on osteocalcin. <i>Analytical Biochemistry</i> , 2017 , 525, 46-53	3.1	28
49	Multi-omics analyses of red blood cell reveal antioxidation mechanisms associated with hemolytic toxicity of gossypol. <i>Oncotarget</i> , 2017 , 8, 103693-103709	3.3	5
48	Proteomic analysis reveals dynamic regulation of fruit development and sugar and acid accumulation in apple. <i>Journal of Experimental Botany</i> , 2016 , 67, 5145-57	7	58
47	Use of a stable-isotope-labeled reporter peptide and antioxidants for reliable quantification of methionine oxidation in a monoclonal antibody by liquid chromatography/mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2016 , 30, 1734-1742	2.2	3
46	Spirochaete flagella hook proteins self-catalyse a lysinoalanine covalent crosslink for motility. <i>Nature Microbiology</i> , 2016 , 1, 16134	26.6	17
45	Single Mutations in the VP2 300 Loop Region of the Three-Fold Spike of the Carnivore Parvovirus Capsid Can Determine Host Range. <i>Journal of Virology</i> , 2016 , 90, 753-67	6.6	43

44	Application of wide selected-ion monitoring data-independent acquisition to identify tomato fruit proteins regulated by the CUTIN DEFICIENT2 transcription factor. <i>Proteomics</i> , 2016 , 16, 2081-94	4.8	19
43	Metabolomics-assisted proteomics identifies succinylation and SIRT5 as important regulators of cardiac function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 4320-5	11.5	169
42	Proteomic analysis of conidia germination in <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> tropical race 4 reveals new targets in ergosterol biosynthesis pathway for controlling <i>Fusarium</i> wilt of banana. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 7189-207	5.7	29
41	Physiological and proteome analysis suggest critical roles for the photosynthetic system for high water-use efficiency under drought stress in <i>Malus</i> . <i>Plant Science</i> , 2015 , 236, 44-60	5.3	52
40	Alpha-ketoglutarate dehydrogenase complex-dependent succinylation of proteins in neurons and neuronal cell lines. <i>Journal of Neurochemistry</i> , 2015 , 134, 86-96	6	68
39	The ubiquitin ligase HERC3 attenuates NF- κ B-dependent transcription independently of its enzymatic activity by delivering the RelA subunit for degradation. <i>Nucleic Acids Research</i> , 2015 , 43, 9889-904	20.1	16
38	Label-free Quantitative Analysis of Changes in Broiler Liver Proteins under Heat Stress using SWATH-MS Technology. <i>Scientific Reports</i> , 2015 , 5, 15119	4.9	28
37	Substitute sweeteners: diverse bacterial oligosaccharyltransferases with unique N-glycosylation site preferences. <i>Scientific Reports</i> , 2015 , 5, 15237	4.9	31
36	In planta processing and glycosylation of a nematode CLAVATA3/ENDOSPERM SURROUNDING REGION-like effector and its interaction with a host CLAVATA2-like receptor to promote parasitism. <i>Plant Physiology</i> , 2015 , 167, 262-72	6.6	40
35	Comparative transcriptomics analysis reveals difference of key gene expression between banana and plantain in response to cold stress. <i>BMC Genomics</i> , 2015 , 16, 446	4.5	66
34	ER Stress Sensor XBP1 Controls Anti-tumor Immunity by Disrupting Dendritic Cell Homeostasis. <i>Cell</i> , 2015 , 161, 1527-38	56.2	427
33	The Cysteine-rich Domain of the DHHC3 Palmitoyltransferase Is Palmitoylated and Contains Tightly Bound Zinc. <i>Journal of Biological Chemistry</i> , 2015 , 290, 29259-69	5.4	36
32	Engineered oligosaccharyltransferases with greatly relaxed acceptor-site specificity. <i>Nature Chemical Biology</i> , 2014 , 10, 816-22	11.7	45
31	A comparative study of lectin affinity based plant N-glycoproteome profiling using tomato fruit as a model. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 566-79	7.6	43
30	Melatonin regulates proteomic changes during leaf senescence in <i>Malus hupehensis</i> . <i>Journal of Pineal Research</i> , 2014 , 57, 291-307	10.4	59
29	Proteomic comparison of historic and recently emerged hypervirulent <i>Clostridium difficile</i> strains. <i>Journal of Proteome Research</i> , 2013 , 12, 1151-61	5.6	32
28	Identification of ADP-ribosylation sites of CD38 mutants by precursor ion scanning mass spectrometry. <i>Analytical Biochemistry</i> , 2013 , 433, 218-26	3.1	5
27	A workflow for large-scale empirical identification of cell wall N-linked glycoproteins of tomato (<i>Solanum lycopersicum</i>) fruit by tandem mass spectrometry. <i>Electrophoresis</i> , 2013 , 34, 2417-31	3.6	14

26	Aryl hydrocarbon receptor activation by dioxin targets phosphoenolpyruvate carboxykinase (PEPCK) for ADP-ribosylation via 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD)-inducible poly(ADP-ribose) polymerase (TiPARP). <i>Journal of Biological Chemistry</i> , 2013 , 288, 21514-25	5.4	24
25	Temporal differential proteomes of <i>Clostridium difficile</i> in the pig ileal-ligated loop model. <i>PLoS ONE</i> , 2012 , 7, e45608	3.7	12
24	Impact of Whole Genome Protein Analysis on Gene Discovery of Disease Models 2012 , 471-530		0
23	Enabling proteomic studies with RNA-Seq: The proteome of tomato pollen as a test case. <i>Proteomics</i> , 2012 , 12, 761-74	4.8	56
22	Comparative characterization of the glycosylation profiles of an influenza hemagglutinin produced in plant and insect hosts. <i>Proteomics</i> , 2012 , 12, 1269-88	4.8	38
21	Analytical technologies for identification and characterization of the plant N-glycoproteome. <i>Frontiers in Plant Science</i> , 2012 , 3, 150	6.2	18
20	Quantitative proteomic analysis reveals that antioxidation mechanisms contribute to cold tolerance in plantain (<i>Musa paradisiaca</i> L.; ABB Group) seedlings. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1853-69	7.6	80
19	Sirt5 is a NAD-dependent protein lysine demalonylase and desuccinylase. <i>Science</i> , 2011 , 334, 806-9	33.3	924
18	Evaluation of different multidimensional LC-MS/MS pipelines for isobaric tags for relative and absolute quantitation (iTRAQ)-based proteomic analysis of potato tubers in response to cold storage. <i>Journal of Proteome Research</i> , 2011 , 10, 4647-60	5.6	93
17	Production of secretory and extracellular N-linked glycoproteins in <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2011 , 77, 871-81	4.8	93
16	Ao38, a new cell line from eggs of the black witch moth, <i>Ascalapha odorata</i> (Lepidoptera: Noctuidae), is permissive for AcMNPV infection and produces high levels of recombinant proteins. <i>BMC Biotechnology</i> , 2010 , 10, 50	3.5	34
15	Signaling to the apical membrane and to the paracellular pathway: changes in the cytosolic proteome of <i>Aedes</i> Malpighian tubules. <i>Journal of Experimental Biology</i> , 2009 , 212, 329-40	3	22
14	Physiological and proteomic responses of two contrasting <i>Populus cathayana</i> populations to drought stress. <i>Physiologia Plantarum</i> , 2009 , 136, 150-68	4.6	118
13	Absolute quantification of Dehalococcoides proteins: enzyme bioindicators of chlorinated ethene dehalorespiration. <i>Environmental Microbiology</i> , 2009 , 11, 2687-97	5.2	41
12	Development of an integrated approach for evaluation of 2-D gel image analysis: impact of multiple proteins in single spots on comparative proteomics in conventional 2-D gel/MALDI workflow. <i>Electrophoresis</i> , 2007 , 28, 2080-94	3.6	75
11	Characterization of protein glycosylation using chip-based nanoelectrospray with precursor ion scanning quadrupole linear ion trap mass spectrometry. <i>Journal of Biomolecular Techniques</i> , 2005 , 16, 209-19	1.1	13
10	Chip-based nanoelectrospray mass spectrometry for protein characterization. <i>Expert Review of Proteomics</i> , 2004 , 1, 449-68	4.2	41
9	Characterization of protein glycosylation using chip-based infusion nanoelectrospray linear ion trap tandem mass spectrometry. <i>Journal of Biomolecular Techniques</i> , 2004 , 15, 120-33	1.1	21

8	Automated chip-based nanoelectrospray-mass spectrometry for rapid identification of proteins separated by two-dimensional gel electrophoresis. <i>Electrophoresis</i> , 2003 , 24, 3620-32	3.6	80
7	A fully automated nanoelectrospray tandem mass spectrometric method for analysis of Caco-2 samples. <i>Rapid Communications in Mass Spectrometry</i> , 2003 , 17, 1573-8	2.2	69
6	Quantitative determination of noncovalent binding interactions using automated nanoelectrospray mass spectrometry. <i>Analytical Chemistry</i> , 2003 , 75, 3010-8	7.8	141
5	Characterization of a fully automated nanoelectrospray system with mass spectrometric detection for proteomic analyses. <i>Journal of Biomolecular Techniques</i> , 2002 , 13, 72-84	1.1	25
4	Role of Four Conserved Active-Site Aspartic Acid Residues in <i>Thermobifida fusca</i> Endoglucanase Cel6A. <i>ACS Symposium Series</i> , 2000 , 28-38	0.4	
3	Probing the catalytic mechanism of prephenate dehydratase by site-directed mutagenesis of the <i>Escherichia coli</i> P-protein dehydratase domain. <i>Biochemistry</i> , 2000 , 39, 4722-8	3.2	33
2	A fully integrated monolithic microchip electrospray device for mass spectrometry. <i>Analytical Chemistry</i> , 2000 , 72, 4058-63	7.8	268
1	Regulation of phenylalanine biosynthesis. Studies on the mechanism of phenylalanine binding and feedback inhibition in the <i>Escherichia coli</i> P-protein. <i>Biochemistry</i> , 1999 , 38, 12212-7	3.2	42