Joshua N Adkins

List of Publications by Year
in descending order

146 papers	12,047 citations	34105 52 h-index	28297 105 g-index
151 all docs	151 docs citations	151 times ranked	14878 citing authors

#	Article	IF	Citations
1	The Human Plasma Proteome. Molecular and Cellular Proteomics, 2004, 3, 311-326.	3.8	801
2	Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35â€‰collaborating laboratories and multiple analytical groups, generating a core dataset of 3020â€‰proteins and a publiclyâ€‰available database. Proteomics, 2005, 5, 3226-3245.	2.2	766
3	Toward a Human Blood Serum Proteome. Molecular and Cellular Proteomics, 2002, 1, 947-955.	3.8	705
4	Omic data from evolved <i>E. coli</i> are consistent with computed optimal growth from genomeâ€scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
5	Persister formation in Staphylococcus aureus is associated with ATP depletion. Nature Microbiology, 2016, 1, .	13.3	508
6	DAnTE: a statistical tool for quantitative analysis of -omics data. Bioinformatics, 2008, 24, 1556-1558.	4.1	397
7	Normalization Approaches for Removing Systematic Biases Associated with Mass Spectrometry and Label-Free Proteomics. Journal of Proteome Research, 2006, 5, 277-286.	3.7	375
8	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. Proteomics, 2005, 5, 3475-3490.	2.2	332
9	Utilizing Human Blood Plasma for Proteomic Biomarker Discoveryâ€. Journal of Proteome Research, 2005, 4, 1073-1085.	3.7	288
10	Distance restraints from crosslinking mass spectrometry: Mining a molecular dynamics simulation database to evaluate lysineâ€"lysine distances. Protein Science, 2014, 23, 747-759.	7.6	243
11	In silico method for modelling metabolism and gene product expression at genome scale. Nature Communications, 2012, 3, 929.	12.8	238
12	VIPER: an advanced software package to support high-throughput LC-MS peptide identification. Bioinformatics, 2007, 23, 2021-2023.	4.1	194
13	Decon2LS: An open-source software package for automated processing and visualization of high resolution mass spectrometry data. BMC Bioinformatics, 2009, 10, 87.	2.6	190
14	Whole proteome analysis of post-translational modifications: Applications of mass-spectrometry for proteogenomic annotation. Genome Research, 2007, 17, 1362-1377.	5.5	175
15	Improved Peptide Elution Time Prediction for Reversed-Phase Liquid Chromatography-MS by Incorporating Peptide Sequence Information. Analytical Chemistry, 2006, 78, 5026-5039.	6.5	163
16	High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform. Analytical Chemistry, 2019, 91, 13119-13127.	6.5	156
17	Robust Algorithm for Alignment of Liquid Chromatographyâ^'Mass Spectrometry Analyses in an Accurate Mass and Time Tag Data Analysis Pipeline. Analytical Chemistry, 2006, 78, 7397-7409.	6.5	155
18	MASIC: A software program for fast quantitation and flexible visualization of chromatographic profiles from detected LCâ€"MS(/MS) features. Computational Biology and Chemistry, 2008, 32, 215-217.	2.3	154

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19	Immunoassay and antibody microarray analysis of the HUPO Plasma Proteome Project reference specimens: Systematic variation between sample types and calibration of mass spectrometry data. Proteomics, 2005, 5, 3278-3291.	2.2	150
20	A statistical framework for protein quantitation in bottom-up MS-based proteomics. Bioinformatics, 2009, 25, 2028-2034.	4.1	149
21	Comprehensive computational design of ordered peptide macrocycles. Science, 2017, 358, 1461-1466.	12.6	146
22	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. Bioinformatics, 2008, 24, 1021-1023.	4.1	143
23	Functional Consequences of Preorganized Helical Structure in the Intrinsically Disordered Cell-Cycle Inhibitor p27Kip1â€. Biochemistry, 2002, 41, 752-759.	2.5	142
24	Modelâ€driven multiâ€omic data analysis elucidates metabolic immunomodulators of macrophage activation. Molecular Systems Biology, 2012, 8, 558.	7.2	142
25	Top-down proteomics reveals a unique protein S-thiolation switch in <i>Salmonella</i> Typhimurium in response to infection-like conditions. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10153-10158.	7.1	140
26	Proteomic Analysis of Salmonella enterica Serovar Typhimurium Isolated from RAW 264.7 Macrophages. Journal of Biological Chemistry, 2006, 281, 29131-29140.	3.4	136
27	The proteome of dissimilatory metal-reducing microorganism Geobacter sulfurreducens under various growth conditions. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 1198-1206.	2.3	128
28	A community effort towards a knowledge-base and mathematical model of the human pathogen Salmonella Typhimurium LT2. BMC Systems Biology, 2011, 5, 8.	3.0	128
29	Proteogenomics: needs and roles to be filled by proteomics in genome annotation. Briefings in Functional Genomics & Proteomics, 2008, 7, 50-62.	3.8	124
30	GIM3E: condition-specific models of cellular metabolism developed from metabolomics and expression data. Bioinformatics, 2013, 29, 2900-2908.	4.1	122
31	Computational Prediction of Type III and IV Secreted Effectors in Gram-Negative Bacteria. Infection and Immunity, 2011, 79, 23-32.	2.2	113
32	Discovery of Novel Secreted Virulence Factors from <i>Salmonella enterica</i> Serovar Typhimurium by Proteomic Analysis of Culture Supernatants. Infection and Immunity, 2011, 79, 33-43.	2.2	112
33	A Systems Biology Approach to Infectious Disease Research: Innovating the Pathogen-Host Research Paradigm. MBio, 2011, 2, e00325-10.	4.1	111
34	Global Systems-Level Analysis of Hfq and SmpB Deletion Mutants in Salmonella: Implications for Virulence and Global Protein Translation. PLoS ONE, 2009, 4, e4809.	2.5	109
35	Phosphoproteome Profiling of Human Skin Fibroblast Cells in Response to Low- and High-Dose Irradiation. Journal of Proteome Research, 2006, 5, 1252-1260.	3.7	108
36	Analysis of the Salmonella typhimurium Proteome through Environmental Response toward Infectious Conditions. Molecular and Cellular Proteomics, 2006, 5, 1450-1461.	3.8	103

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37	Distinct Cerebrospinal Fluid Proteomes Differentiate Post-Treatment Lyme Disease from Chronic Fatigue Syndrome. PLoS ONE, 2011, 6, e17287.	2.5	103
38	The Utility of Accurate Mass and LC Elution Time Information in the Analysis of Complex Proteomes. Journal of the American Society for Mass Spectrometry, 2005, 16, 1239-1249.	2.8	100
39	Normalization of peak intensities in bottom-up MS-based proteomics using singular value decomposition. Bioinformatics, 2009, 25, 2573-2580.	4.1	97
40	Identification of Cross-Linked Peptides after Click-Based Enrichment Using Sequential Collision-Induced Dissociation and Electron Transfer Dissociation Tandem Mass Spectrometry. Analytical Chemistry, 2009, 81, 5524-5532.	6.5	91
41	Differential Label-free Quantitative Proteomic Analysis of Shewanella oneidensis Cultured under Aerobic and Suboxic Conditions by Accurate Mass and Time Tag Approach. Molecular and Cellular Proteomics, 2006, 5, 714-725.	3.8	85
42	Stochastic Variation in Expression of the Tricarboxylic Acid Cycle Produces Persister Cells. MBio, 2019, 10, .	4.1	84
43	A Multi-Omic View of Host-Pathogen-Commensal Interplay in Salmonella-Mediated Intestinal Infection. PLoS ONE, 2013, 8, e67155.	2.5	81
44	Discovery of Salmonella Virulence Factors Translocated via Outer Membrane Vesicles to Murine Macrophages. Infection and Immunity, 2011, 79, 2182-2192.	2.2	77
45	High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip. Nature Communications, 2021, 12, 6246.	12.8	76
46	Comparative Proteomics of Human Monkeypox and Vaccinia Intracellular Mature and Extracellular Enveloped Virions. Journal of Proteome Research, 2008, 7, 960-968.	3.7	75
47	Intrinsic structural disorder and sequence features of the cell cycle inhibitor p57Kip2. Proteins: Structure, Function and Bioinformatics, 2002, 46, 1-7.	2.6	74
48	Comparative Bacterial Proteomics: Analysis of the Core Genome Concept. PLoS ONE, 2008, 3, e1542.	2.5	71
49	Discovery of Novel Glucose-Regulated Proteins in Isolated Human Pancreatic Islets Using LC–MS/MS-Based Proteomics. Journal of Proteome Research, 2012, 11, 3520-3532.	3.7	69
50	Gut anatomical properties and microbial functional assembly promote lignocellulose deconstruction and colony subsistence of a wood-feeding beetle. Nature Microbiology, 2019, 4, 864-875.	13.3	68
51	New mass spectrometry technologies contributing towards comprehensive and high throughput omics analyses of single cells. Analyst, The, 2019, 144, 794-807.	3.5	67
52	Spatial mapping of protein abundances in the mouse brain by voxelation integrated with high-throughput liquid chromatography-mass spectrometry. Genome Research, 2007, 17, 328-336.	5.5	62
53	A proteomic study of the HUPO Plasma Proteome Project's pilot samples using an accurate mass and time tag strategy. Proteomics, 2005, 5, 3454-3466.	2.2	60
54	Xlink-Identifier: An Automated Data Analysis Platform for Confident Identifications of Chemically Cross-Linked Peptides Using Tandem Mass Spectrometry. Journal of Proteome Research, 2011, 10, 923-931.	3.7	55

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55	Proteomics Analysis of the Causative Agent of Typhoid Fever. Journal of Proteome Research, 2008, 7, 546-557.	3.7	54
56	Proteomic Investigation of the Time Course Responses of RAW 264.7 Macrophages to Infection with <i>Salmonella enterica</i>. Infection and Immunity, 2009, 77, 3227-3233.	2.2	54
57	Phosphate-Containing Polyethylene Glycol Polymers Prevent Lethal Sepsis by Multidrug-Resistant Pathogens. Antimicrobial Agents and Chemotherapy, 2014, 58, 966-977.	3.2	53
58	Salmonella modulates metabolism during growth under conditions that induce expression of virulence genes. Molecular BioSystems, 2013, 9, 1522.	2.9	49
59	Multiple mechanisms drive phage infection efficiency in nearly identical hosts. ISME Journal, 2018, 12, 1605-1618.	9.8	48
60	Proteome-Wide Identification of Proteins and Their Modifications with Decreased Ambiguities and Improved False Discovery Rates Using Unique Sequence Tags. Analytical Chemistry, 2008, 80, 1871-1882.	6.5	46
61	A Statistical Method for Assessing Peptide Identification Confidence in Accurate Mass and Time Tag Proteomics. Analytical Chemistry, 2011, 83, 6135-6140.	6.5	46
62	A multi-pronged search for a common structural motif in the secretion signal of Salmonella enterica serovar Typhimurium type III effector proteins. Molecular BioSystems, 2010, 6, 2448.	2.9	45
63	Identification of Widespread Adenosine Nucleotide Binding in Mycobacterium tuberculosis. Chemistry and Biology, 2013, 20, 123-133.	6.0	45
64	Biomarker Candidate Identification inYersiniapestisUsing Organism-Wide Semiquantitative Proteomics. Journal of Proteome Research, 2006, 5, 3008-3017.	3.7	42
65	Elimination of Systematic Mass Measurement Errors in Liquid Chromatographyâˆ'Mass Spectrometry Based Proteomics Using Regression Models anda PrioriPartial Knowledge of the Sample Content. Analytical Chemistry, 2008, 80, 693-706.	6.5	38
66	An experimentally-supported genome-scale metabolic network reconstruction for Yersinia pestis CO92. BMC Systems Biology, 2011, 5, 163.	3.0	38
67	The Genome Organization of Thermotoga maritima Reflects Its Lifestyle. PLoS Genetics, 2013, 9, e1003485.	3.5	38
68	Linear Discriminant Analysis-Based Estimation of the False Discovery Rate for Phosphopeptide Identifications. Journal of Proteome Research, 2008, 7, 2195-2203.	3.7	37
69	Comparative Phosphoproteomics Reveals Components of Host Cell Invasion and Post-transcriptional Regulation During Francisella Infection. Molecular and Cellular Proteomics, 2013, 12, 3297-3309.	3.8	35
70	Controlling the Response: Predictive Modeling of a Highly Central, Pathogen-Targeted Core Response Module in Macrophage Activation. PLoS ONE, 2011, 6, e14673.	2.5	33
71	A Method to Determine Lysine Acetylation Stoichiometries. International Journal of Proteomics, 2014, 2014, 1-8.	2.0	33
72	Mass Measurement Accuracy in Analyses of Highly Complex Mixtures Based Upon Multidimensional Recalibration. Analytical Chemistry, 2006, 78, 8374-8385.	6.5	32

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73	The Influence of Sample Preparation and Replicate Analyses on HeLa Cell Phosphoproteome Coverage. Journal of Proteome Research, 2008, 7, 2215-2221.	3.7	31
74	VESPA: software to facilitate genomic annotation of prokaryotic organisms through integration of proteomic and transcriptomic data. BMC Genomics, 2012, 13, 131.	2.8	31
75	Systems analysis of multiple regulator perturbations allows discovery of virulence factors in Salmonella. BMC Systems Biology, 2011, 5, 100.	3.0	30
76	Comparative Omics-Driven Genome Annotation Refinement: Application across Yersiniae. PLoS ONE, 2012, 7, e33903.	2.5	30
77	Diverse Secreted Effectors Are Required for Salmonella Persistence in a Mouse Infection Model. PLoS ONE, 2013, 8, e70753.	2.5	30
78	ChIP-Seq Analysis of the σE Regulon of Salmonella enterica Serovar Typhimurium Reveals New Genes Implicated in Heat Shock and Oxidative Stress Response. PLoS ONE, 2015, 10, e0138466.	2.5	30
79	Amylases in the Human Vagina. MSphere, 2020, 5, .	2.9	30
80	Dynamic and Differential in Vivo Modifications of the Isoform HMGA1a and HMGA1b Chromatin Proteins. Journal of Biological Chemistry, 2005, 280, 8961-8973.	3.4	29
81	A Computational Strategy to Analyze Label-Free Temporal Bottom-Up Proteomics Data. Journal of Proteome Research, 2008, 7, 2595-2604.	3.7	29
82	Experimental annotation of post-translational features and translated coding regions in the pathogen Salmonella Typhimurium. BMC Genomics, 2011, 12, 433.	2.8	29
83	A multi-omic systems approach to elucidating Yersinia virulence mechanisms. Molecular BioSystems, 2013, 9, 44-54.	2.9	29
84	Rare Earth Elements Alter Redox Balance in Methylomicrobium alcaliphilum 20ZR. Frontiers in Microbiology, 2018, 9, 2735.	3.5	28
85	The food-borne pathogen Campylobacter jejuni responds to the bile salt deoxycholate with countermeasures to reactive oxygen species. Scientific Reports, 2017, 7, 15455.	3.3	27
86	Targeted Protein Degradation by Salmonella under Phagosome-mimicking Culture Conditions Investigated Using Comparative Peptidomics. Molecular and Cellular Proteomics, 2007, 6, 717-727.	3.8	26
87	Cross-linking and mass spectrometry methodologies to facilitate structural biology: finding a path through the maze. Journal of Structural and Functional Genomics, 2013, 14, 77-90.	1.2	25
88	Characterization of Strategies for Obtaining Confident Identifications in Bottom-Up Proteomics Measurements Using Hybrid FTMS Instruments. Analytical Chemistry, 2008, 80, 8514-8525.	6.5	24
89	Mixed-Isotope Labeling with LC-IMS-MS for Characterization of Protein–Protein Interactions by Chemical Cross-Linking. Journal of the American Society for Mass Spectrometry, 2013, 24, 444-449.	2.8	24
90	Analysis of the Salmonella regulatory network suggests involvement of SsrB and H-NS in σE-regulated SPI-2 gene expression. Frontiers in Microbiology, 2015, 6, 27.	3.5	24

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91	Stoichiometry of Cyclin Aˆ Cyclin-Dependent Kinase 2 Inhibition by p21Cip1/Waf1â€. Biochemistry, 2000, 39, 13925-13930.	2.5	23
92	Applying a Targeted Label-Free Approach Using LCâˆ'MS AMT Tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition. Journal of Proteome Research, 2007, 6, 4489-4497.	3.7	22
93	A Method for Investigating Proteinâˆ'Protein Interactions Related to <i>Salmonella</i> Typhimurium Pathogenesis. Journal of Proteome Research, 2009, 8, 1504-1514.	3.7	22
94	Multicopy Single-Stranded DNA Directs Intestinal Colonization of Enteric Pathogens. PLoS Genetics, 2015, 11, e1005472.	3.5	22
95	Identification of Novel Host Interactors of Effectors Secreted by <i>Salmonella</i> and <i>Citrobacter</i>. MSystems, 2016, 1, .	3.8	22
96	Proteome of Salmonella Enterica Serotype Typhimurium Grown in a Low Mg2+/pH Medium. Journal of Proteomics and Bioinformatics, 2009, 02, 388-397.	0.4	21
97	Integrated Post-Experiment Monoisotopic Mass Refinement: An Integrated Approach to Accurately Assign Monoisotopic Precursor Masses to Tandem Mass Spectrometric Data. Analytical Chemistry, 2010, 82, 8510-8518.	6.5	21
98	A Comprehensive Subcellular Proteomic Survey of <i>Salmonella</i> Grown under Phagosome-Mimicking versus Standard Laboratory Conditions. International Journal of Proteomics, 2012, 2012, 1-12.	2.0	20
99	Proteomic biomarkers in plasma that differentiate rapid and slow decline in lung function in adult cigarette smokers with chronic obstructive pulmonary disease (COPD). Analytical and Bioanalytical Chemistry, 2010, 397, 1809-1819.	3.7	19
100	Campylobacter jejuni Demonstrates Conserved Proteomic and Transcriptomic Responses When Co-cultured With Human INT 407 and Caco-2 Epithelial Cells. Frontiers in Microbiology, 2019, 10, 755.	3.5	19
101	Technologies and Approaches to Elucidate and Model the Virulence Program of Salmonella. Frontiers in Microbiology, 2011, 2, 121.	3.5	18
102	RNA Type III Secretion Signals That Require Hfq. Journal of Bacteriology, 2013, 195, 2119-2125.	2.2	18
103	A proteomic approach to characterize protein shedding. Proteomics, 2005, 5, 123-131.	2.2	17
104	Simple Protein Complex Purification and Identification Method for High-Throughput Mapping of Protein Interaction Networks. Journal of Proteome Research, 2005, 4, 268-274.	3.7	17
105	Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step ¹⁸O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography. Journal of Proteome Research, 2008, 7, 4215-4224.	3.7	16
106	Characterization of Macaque Pulmonary Fluid Proteome during Monkeypox Infection. Molecular and Cellular Proteomics, 2010, 9, 2760-2771.	3.8	16
107	Accumulation of Succinyl Coenzyme A Perturbs the Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) Succinylome and Is Associated with Increased Susceptibility to Beta-Lactam Antibiotics. MBio, 2021, 12, e0053021.	4.1	16
108	Identification of shed proteins from chinese hamster ovary cells: Application of statistical confidence using human and mouse protein databases. Proteomics, 2005, 5, 1815-1826.	2.2	15

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109	Individual Variability of Protein Expression in Human Tissues. Journal of Proteome Research, 2018, 17, 3914-3922.	3.7	15
110	Optimization of proteomic sample preparation procedures for comprehensive protein characterization of pathogenic systems. Journal of Biomolecular Techniques, 2008, 19, 285-95.	1.5	15
111	Characterization of the mouse bronchoalveolar lavage proteome by micro-capillary LC–FTICR mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2008, 864, 95-101.	2.3	14
112	The Pacific Northwest National Laboratory library of bacterial and archaeal proteomic biodiversity. Scientific Data, 2015, 2, 150041.	5.3	14
113	Structural and Functional Characterization of DUF1471 Domains of Salmonella Proteins SrfN, YdgH/SssB, and YahO. PLoS ONE, 2014, 9, e101787.	2.5	13
114	Phloem Exudate Protein Profiles during Drought and Recovery Reveal Abiotic Stress Responses in Tomato Vasculature. International Journal of Molecular Sciences, 2020, 21, 4461.	4.1	13
115	Protein and microRNA biomarkers from lavage, urine, and serum in military personnel evaluated for dyspnea. BMC Medical Genomics, 2014, 7, 58.	1.5	12
116	Global Analysis of *Salmonella* Alternative Sigma Factor E on Protein Translation. Journal of Proteome Research, 2015, 14, 1716-1726.	3.7	11
117	Identification of *Salmonella* Typhimurium Deubiquitinase SseL Substrates by Immunoaffinity Enrichment and Quantitative Proteomic Analysis. Journal of Proteome Research, 2015, 14, 4029-4038.	3.7	11
118	Assessment of TMT Labeling Efficiency in Large-Scale Quantitative Proteomics: The Critical Effect of Sample pH. ACS Omega, 2021, 6, 12660-12666.	3.5	11
119	Studying Salmonellae and Yersiniae Host–Pathogen Interactions Using Integrated ʻOmics and Modeling. Current Topics in Microbiology and Immunology, 2012, 363, 21-41.	1.1	10
120	The Campylobacter jejuni CiaD effector co-opts the host cell protein IQGAP1 to promote cell entry. Nature Communications, 2021, 12, 1339.	12.8	10
121	The landscape of viral proteomics and its potential to impact human health. Expert Review of Proteomics, 2016, 13, 579-591.	3.0	9
122	Omics.pnl.gov: A Portal for the Distribution and Sharing of Multi-Disciplinary Pan-Omics Information. Journal of Proteomics and Bioinformatics, 2010, 03, 001-004.	0.4	9
123	Proteomic Analysis of Human Lung Development. American Journal of Respiratory and Critical Care Medicine, 2022, 205, 208-218.	5.6	9
124	Characterization of Plasma Membrane Proteins from Ovarian Cancer Cells Using Mass Spectrometry. Disease Markers, 2004, 19, 219-228.	1.3	8
125	Use of high-throughput mass spectrometry to elucidate host–pathogen interactions in Salmonella. Future Microbiology, 2008, 3, 625-634.	2.0	8
126	Evaluation of Selected Binding Domains for the Analysis of Ubiquitinated Proteomes. Journal of the American Society for Mass Spectrometry, 2013, 24, 1214-1223.	2.8	7

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127	Unified feature association networks through integration of transcriptomic and proteomic data. PLoS Computational Biology, 2019, 15, e1007241.	3.2	7
128	A porcine ligated loop model reveals new insight into the host immune response against<i>Campylobacter jejuni</i>. Gut Microbes, 2020, 12, 1814121.	9.8	7
129	Transcriptional activity of the TFIIA four-helix bundle in vivo. Proteins: Structure, Function and Bioinformatics, 2001, 43, 227-232.	2.6	6
130	Protein abundances can distinguish between naturally-occurring and laboratory strains of Yersinia pestis, the causative agent of plague. PLoS ONE, 2017, 12, e0183478.	2.5	6
131	Prediction of bacterial E3 ubiquitin ligase effectors using reduced amino acid peptide fingerprinting. PeerJ, 2019, 7, e7055.	2.0	6
132	New sub-family of lysozyme-like proteins shows no catalytic activity: crystallographic and biochemical study of STM3605 protein from Salmonella Typhimurium. Journal of Structural and Functional Genomics, 2013, 14, 1-10.	1.2	4
133	Preserved and variable spatialâ€chemical changes of lipids across tomato leaves in response to central vein wounding reveals potential origin of linolenic acid in signal transduction cascade. Plant-Environment Interactions, 2021, 2, 28-35.	1.5	4
134	A Semiautomated Framework for Integrating Expert Knowledge into Disease Marker Identification. Disease Markers, 2013, 35, 513-523.	1.3	3
135	Multi-omic Data Integration Links Deleted in Breast Cancer 1 (DBC1) Degradation to Chromatin Remodeling in Inflammatory Response. Molecular and Cellular Proteomics, 2013, 12, 2136-2147.	3.8	3
136	Electroporation of Functional Bacterial Effectors into Mammalian Cells. Journal of Visualized Experiments, 2015, , 52296.	0.3	3
137	Performing Comparative Peptidomics Analyses of Salmonella from Different Growth Conditions. Methods in Molecular Biology, 2010, 615, 13-27.	0.9	3
138	PQuadâ€"a visual analysis platform for proteomic data exploration of microbial organisms. Bioinformatics, 2007, 23, 1705-1707.	4.1	2
139	Assessment of the Utility of the Oral Fluid and Plasma Proteomes for Hydrocodone Exposure. Journal of Medical Toxicology, 2020, 16, 49-60.	1.5	2
140	An Architecture for Real Time Data Acquisition and Online Signal Processing for High Throughput Tandem Mass Spectrometry. , 2009, , .		1
141	Applications in Data-Intensive Computing. Advances in Computers, 2010, , 1-70.	1.6	1
142	THE CHALLENGE OF PROTEOMIC DATA, FROM MOLECULAR SIGNALS TO BIOLOGICAL NETWORKS AND DISEASE: SESSION INTRODUCTION. , 2005, , .		0
143	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. , 2006, , 289-315.		0
144	Using support vector machine for improving protein-protein interaction prediction utilizing domain interactions. , 2010, , .		0

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145	Immunoassay and antibody microarray analysis of the HUPO Plasma Proteome Project reference specimens: Systematic variation between sample types and calibration of mass spectrometry data. , 0, , 91-113.		0
146	A proteomic study of the HUPO Plasma Proteome Project's pilot samples using an accurate mass and time tag strategy. , 0, , 249-271.		0