

# Joshua N Adkins

## List of Publications by Year in descending order

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146  
papers

12,047  
citations

34016

52  
h-index

28224

105  
g-index

151  
all docs

151  
docs citations

151  
times ranked

14878  
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic Analysis of Human Lung Development. American Journal of Respiratory and Critical Care Medicine, 2022, 205, 208-218.	2.5	9
2	Preserved and variable spatial 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.	0.7	4
3	The <i>Campylobacter jejuni</i> CiaD effector co-opts the host cell protein IQGAP1 to promote cell entry. Nature Communications, 2021, 12, 1339.	5.8	10
4	Assessment of TMT Labeling Efficiency in Large-Scale Quantitative Proteomics: The Critical Effect of Sample pH. ACS Omega, 2021, 6, 12660-12666.	1.6	11
5	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.	1.8	16
6	High-throughput and high-efficiency sample preparation for single-cell proteomics using a nested nanowell chip. Nature Communications, 2021, 12, 6246.	5.8	76
7	Assessment of the Utility of the Oral Fluid and Plasma Proteomes for Hydrocodone Exposure. Journal of Medical Toxicology, 2020, 16, 49-60.	0.8	2
8	Phloem Exudate Protein Profiles during Drought and Recovery Reveal Abiotic Stress Responses in Tomato Vasculature. International Journal of Molecular Sciences, 2020, 21, 4461.	1.8	13
9	A porcine ligated loop model reveals new insight into the host immune response against <i>Campylobacter jejuni</i> . Gut Microbes, 2020, 12, 1814121.	4.3	7
10	Amylases in the Human Vagina. MSphere, 2020, 5, .	1.3	30
11	High-Throughput Single Cell Proteomics Enabled by Multiplex Isobaric Labeling in a Nanodroplet Sample Preparation Platform. Analytical Chemistry, 2019, 91, 13119-13127.	3.2	156
12	Unified feature association networks through integration of transcriptomic and proteomic data. PLoS Computational Biology, 2019, 15, e1007241.	1.5	7
13	New mass spectrometry technologies contributing towards comprehensive and high throughput omics analyses of single cells. Analyst, The, 2019, 144, 794-807.	1.7	67
14	<i>Campylobacter jejuni</i> Demonstrates Conserved Proteomic and Transcriptomic Responses When Co-cultured With Human INT 407 and Caco-2 Epithelial Cells. Frontiers in Microbiology, 2019, 10, 755.	1.5	19
15	Gut anatomical properties and microbial functional assembly promote lignocellulose deconstruction and colony subsistence of a wood-feeding beetle. Nature Microbiology, 2019, 4, 864-875.	5.9	68
16	Stochastic Variation in Expression of the Tricarboxylic Acid Cycle Produces Persister Cells. MBio, 2019, 10, .	1.8	84
17	Prediction of bacterial E3 ubiquitin ligase effectors using reduced amino acid peptide fingerprinting. PeerJ, 2019, 7, e7055.	0.9	6
18	Multiple mechanisms drive phage infection efficiency in nearly identical hosts. ISME Journal, 2018, 12, 1605-1618.	4.4	48

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19	Individual Variability of Protein Expression in Human Tissues. <i>Journal of Proteome Research</i> , 2018, 17, 3914-3922.	1.8	15
20	Rare Earth Elements Alter Redox Balance in <i>Methylobacterium alcaliphilum</i> 20ZR. <i>Frontiers in Microbiology</i> , 2018, 9, 2735.	1.5	28
21	Comprehensive computational design of ordered peptide macrocycles. <i>Science</i> , 2017, 358, 1461-1466.	6.0	146
22	The food-borne pathogen <i>Campylobacter jejuni</i> responds to the bile salt deoxycholate with countermeasures to reactive oxygen species. <i>Scientific Reports</i> , 2017, 7, 15455.	1.6	27
23	Protein abundances can distinguish between naturally-occurring and laboratory strains of <i>Yersinia pestis</i> , the causative agent of plague. <i>PLoS ONE</i> , 2017, 12, e0183478.	1.1	6
24	Identification of Novel Host Interactors of Effectors Secreted by <i>Salmonella</i> and <i>Citrobacter</i> . <i>MSystems</i> , 2016, 1, .	1.7	22
25	The landscape of viral proteomics and its potential to impact human health. <i>Expert Review of Proteomics</i> , 2016, 13, 579-591.	1.3	9
26	Persister formation in <i>Staphylococcus aureus</i> is associated with ATP depletion. <i>Nature Microbiology</i> , 2016, 1, .	5.9	508
27	Electroporation of Functional Bacterial Effectors into Mammalian Cells. <i>Journal of Visualized Experiments</i> , 2015, , 52296.	0.2	3
28	The Pacific Northwest National Laboratory library of bacterial and archaeal proteomic biodiversity. <i>Scientific Data</i> , 2015, 2, 150041.	2.4	14
29	Multicopy Single-Stranded DNA Directs Intestinal Colonization of Enteric Pathogens. <i>PLoS Genetics</i> , 2015, 11, e1005472.	1.5	22
30	ChIP-Seq Analysis of the $\sigma^E$ Regulon of <i>Salmonella enterica</i> Serovar Typhimurium Reveals New Genes Implicated in Heat Shock and Oxidative Stress Response. <i>PLoS ONE</i> , 2015, 10, e0138466.	1.1	30
31	Global Analysis of <i>Salmonella</i> Alternative Sigma Factor E on Protein Translation. <i>Journal of Proteome Research</i> , 2015, 14, 1716-1726.	1.8	11
32	Analysis of the <i>Salmonella</i> regulatory network suggests involvement of SsrB and H-NS in $\sigma^E$ -regulated SPI-2 gene expression. <i>Frontiers in Microbiology</i> , 2015, 6, 27.	1.5	24
33	Identification of <i>Salmonella</i> Typhimurium Deubiquitinase SseL Substrates by Immunoaffinity Enrichment and Quantitative Proteomic Analysis. <i>Journal of Proteome Research</i> , 2015, 14, 4029-4038.	1.8	11
34	Structural and Functional Characterization of DUF1471 Domains of <i>Salmonella</i> Proteins SrfN, YdgH/SssB, and YahO. <i>PLoS ONE</i> , 2014, 9, e101787.	1.1	13
35	Protein and microRNA biomarkers from lavage, urine, and serum in military personnel evaluated for dyspnea. <i>BMC Medical Genomics</i> , 2014, 7, 58.	0.7	12
36	Phosphate-Containing Polyethylene Glycol Polymers Prevent Lethal Sepsis by Multidrug-Resistant Pathogens. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 966-977.	1.4	53

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37	A Method to Determine Lysine Acetylation Stoichiometries. <i>International Journal of Proteomics</i> , 2014, 2014, 1-8.	2.0	33
38	Distance restraints from crosslinking mass spectrometry: Mining a molecular dynamics simulation database to evaluate lysine-lysine distances. <i>Protein Science</i> , 2014, 23, 747-759.	3.1	243
39	Mixed-Isotope Labeling with LC-IMS-MS for Characterization of Protein-Protein Interactions by Chemical Cross-Linking. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 444-449.	1.2	24
40	New sub-family of lysozyme-like proteins shows no catalytic activity: crystallographic and biochemical study of STM3605 protein from <i>Salmonella Typhimurium</i> . <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 1-10.	1.2	4
41	GIM3E: condition-specific models of cellular metabolism developed from metabolomics and expression data. <i>Bioinformatics</i> , 2013, 29, 2900-2908.	1.8	122
42	Top-down proteomics reveals a unique protein S-thiolation switch in <i>Salmonella Typhimurium</i> in response to infection-like conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10153-10158.	3.3	140
43	Identification of Widespread Adenosine Nucleotide Binding in <i>Mycobacterium tuberculosis</i> . <i>Chemistry and Biology</i> , 2013, 20, 123-133.	6.2	45
44	A multi-omic systems approach to elucidating <i>Yersinia</i> virulence mechanisms. <i>Molecular BioSystems</i> , 2013, 9, 44-54.	2.9	29
45	<i>Salmonella</i> modulates metabolism during growth under conditions that induce expression of virulence genes. <i>Molecular BioSystems</i> , 2013, 9, 1522.	2.9	49
46	Evaluation of Selected Binding Domains for the Analysis of Ubiquitinated Proteomes. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1214-1223.	1.2	7
47	Cross-linking and mass spectrometry methodologies to facilitate structural biology: finding a path through the maze. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 77-90.	1.2	25
48	A Semiautomated Framework for Integrating Expert Knowledge into Disease Marker Identification. <i>Disease Markers</i> , 2013, 35, 513-523.	0.6	3
49	The Genome Organization of <i>Thermotoga maritima</i> Reflects Its Lifestyle. <i>PLoS Genetics</i> , 2013, 9, e1003485.	1.5	38
50	Comparative Phosphoproteomics Reveals Components of Host Cell Invasion and Post-transcriptional Regulation During <i>Francisella</i> Infection. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3297-3309.	2.5	35
51	RNA Type III Secretion Signals That Require Hfq. <i>Journal of Bacteriology</i> , 2013, 195, 2119-2125.	1.0	18
52	Multi-omic Data Integration Links Deleted in Breast Cancer 1 (DBC1) Degradation to Chromatin Remodeling in Inflammatory Response. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2136-2147.	2.5	3
53	Diverse Secreted Effectors Are Required for <i>Salmonella</i> Persistence in a Mouse Infection Model. <i>PLoS ONE</i> , 2013, 8, e70753.	1.1	30
54	A Multi-Omic View of Host-Pathogen-Commensal Interplay in <i>Salmonella</i> -Mediated Intestinal Infection. <i>PLoS ONE</i> , 2013, 8, e67155.	1.1	81

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55	A Comprehensive Subcellular Proteomic Survey of <i>Salmonella</i> Grown under Phagosome-Mimicking versus Standard Laboratory Conditions. <i>International Journal of Proteomics</i> , 2012, 2012, 1-12.	2.0	20
56	Model-driven multi-omic data analysis elucidates metabolic immunomodulators of macrophage activation. <i>Molecular Systems Biology</i> , 2012, 8, 558.	3.2	142
57	Discovery of Novel Glucose-Regulated Proteins in Isolated Human Pancreatic Islets Using LC-MS/MS-Based Proteomics. <i>Journal of Proteome Research</i> , 2012, 11, 3520-3532.	1.8	69
58	VESPA: software to facilitate genomic annotation of prokaryotic organisms through integration of proteomic and transcriptomic data. <i>BMC Genomics</i> , 2012, 13, 131.	1.2	31
59	Studying <i>Salmonellae</i> and <i>Yersiniae</i> Host-Pathogen Interactions Using Integrated Omics and Modeling. <i>Current Topics in Microbiology and Immunology</i> , 2012, 363, 21-41.	0.7	10
60	In silico method for modelling metabolism and gene product expression at genome scale. <i>Nature Communications</i> , 2012, 3, 929.	5.8	238
61	Comparative Omics-Driven Genome Annotation Refinement: Application across <i>Yersiniae</i> . <i>PLoS ONE</i> , 2012, 7, e33903.	1.1	30
62	A Statistical Method for Assessing Peptide Identification Confidence in Accurate Mass and Time Tag Proteomics. <i>Analytical Chemistry</i> , 2011, 83, 6135-6140.	3.2	46
63	Xlink-Identifier: An Automated Data Analysis Platform for Confident Identifications of Chemically Cross-Linked Peptides Using Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 923-931.	1.8	55
64	Technologies and Approaches to Elucidate and Model the Virulence Program of <i>Salmonella</i> . <i>Frontiers in Microbiology</i> , 2011, 2, 121.	1.5	18
65	Controlling the Response: Predictive Modeling of a Highly Central, Pathogen-Targeted Core Response Module in Macrophage Activation. <i>PLoS ONE</i> , 2011, 6, e14673.	1.1	33
66	Experimental annotation of post-translational features and translated coding regions in the pathogen <i>Salmonella Typhimurium</i> . <i>BMC Genomics</i> , 2011, 12, 433.	1.2	29
67	Systems analysis of multiple regulator perturbations allows discovery of virulence factors in <i>Salmonella</i> . <i>BMC Systems Biology</i> , 2011, 5, 100.	3.0	30
68	An experimentally-supported genome-scale metabolic network reconstruction for <i>Yersinia pestis</i> CO92. <i>BMC Systems Biology</i> , 2011, 5, 163.	3.0	38
69	A community effort towards a knowledge-base and mathematical model of the human pathogen <i>Salmonella Typhimurium</i> LT2. <i>BMC Systems Biology</i> , 2011, 5, 8.	3.0	128
70	A Systems Biology Approach to Infectious Disease Research: Innovating the Pathogen-Host Research Paradigm. <i>MBio</i> , 2011, 2, e00325-10.	1.8	111
71	Discovery of Novel Secreted Virulence Factors from <i>Salmonella enterica</i> Serovar <i>Typhimurium</i> by Proteomic Analysis of Culture Supernatants. <i>Infection and Immunity</i> , 2011, 79, 33-43.	1.0	112
72	Computational Prediction of Type III and IV Secreted Effectors in Gram-Negative Bacteria. <i>Infection and Immunity</i> , 2011, 79, 23-32.	1.0	113

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73	Discovery of Salmonella Virulence Factors Translocated via Outer Membrane Vesicles to Murine Macrophages. <i>Infection and Immunity</i> , 2011, 79, 2182-2192.	1.0	77
74	Distinct Cerebrospinal Fluid Proteomes Differentiate Post-Treatment Lyme Disease from Chronic Fatigue Syndrome. <i>PLoS ONE</i> , 2011, 6, e17287.	1.1	103
75	Proteomic biomarkers in plasma that differentiate rapid and slow decline in lung function in adult cigarette smokers with chronic obstructive pulmonary disease (COPD). <i>Analytical and Bioanalytical Chemistry</i> , 2010, 397, 1809-1819.	1.9	19
76	Characterization of Macaque Pulmonary Fluid Proteome during Monkeypox Infection. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2760-2771.	2.5	16
77	Applications in Data-Intensive Computing. <i>Advances in Computers</i> , 2010, , 1-70.	1.2	1
78	Omic data from evolved <i>E. coli</i> are consistent with computed optimal growth from genome-scale models. <i>Molecular Systems Biology</i> , 2010, 6, 390.	3.2	615
79	Using support vector machine for improving protein-protein interaction prediction utilizing domain interactions. , 2010, , .		0
80	Integrated Post-Experiment Monoisotopic Mass Refinement: An Integrated Approach to Accurately Assign Monoisotopic Precursor Masses to Tandem Mass Spectrometric Data. <i>Analytical Chemistry</i> , 2010, 82, 8510-8518.	3.2	21
81	A multi-pronged search for a common structural motif in the secretion signal of Salmonella enterica serovar Typhimurium type III effector proteins. <i>Molecular BioSystems</i> , 2010, 6, 2448.	2.9	45
82	Performing Comparative Peptidomics Analyses of Salmonella from Different Growth Conditions. <i>Methods in Molecular Biology</i> , 2010, 615, 13-27.	0.4	3
83	Omics.pnl.gov: A Portal for the Distribution and Sharing of Multi-Disciplinary Pan-Omics Information. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 001-004.	0.4	9
84	Proteome of Salmonella Enterica Serotype Typhimurium Grown in a Low Mg <sup>2+</sup> /pH Medium. <i>Journal of Proteomics and Bioinformatics</i> , 2009, 02, 388-397.	0.4	21
85	Normalization of peak intensities in bottom-up MS-based proteomics using singular value decomposition. <i>Bioinformatics</i> , 2009, 25, 2573-2580.	1.8	97
86	Proteomic Investigation of the Time Course Responses of RAW 264.7 Macrophages to Infection with <i>Salmonella enterica</i> . <i>Infection and Immunity</i> , 2009, 77, 3227-3233.	1.0	54
87	Decon2LS: An open-source software package for automated processing and visualization of high resolution mass spectrometry data. <i>BMC Bioinformatics</i> , 2009, 10, 87.	1.2	190
88	A Method for Investigating Protein-Protein Interactions Related to <i>Salmonella</i> Typhimurium Pathogenesis. <i>Journal of Proteome Research</i> , 2009, 8, 1504-1514.	1.8	22
89	A statistical framework for protein quantitation in bottom-up MS-based proteomics. <i>Bioinformatics</i> , 2009, 25, 2028-2034.	1.8	149
90	Identification of Cross-Linked Peptides after Click-Based Enrichment Using Sequential Collision-Induced Dissociation and Electron Transfer Dissociation Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5524-5532.	3.2	91

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91	An Architecture for Real Time Data Acquisition and Online Signal Processing for High Throughput Tandem Mass Spectrometry. , 2009, , .		1
92	Global Systems-Level Analysis of Hfq and SmpB Deletion Mutants in Salmonella: Implications for Virulence and Global Protein Translation. PLoS ONE, 2009, 4, e4809.	1.1	109
93	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.	1.2	14
94	MASIC: A software program for fast quantitation and flexible visualization of chromatographic profiles from detected LC-MS(/MS) features. Computational Biology and Chemistry, 2008, 32, 215-217.	1.1	154
95	Elimination of Systematic Mass Measurement Errors in Liquid Chromatography-Mass Spectrometry Based Proteomics Using Regression Models and a Priori Partial Knowledge of the Sample Content. Analytical Chemistry, 2008, 80, 693-706.	3.2	38
96	Characterization of Strategies for Obtaining Confident Identifications in Bottom-Up Proteomics Measurements Using Hybrid FTMS Instruments. Analytical Chemistry, 2008, 80, 8514-8525.	3.2	24
97	Linear Discriminant Analysis-Based Estimation of the False Discovery Rate for Phosphopeptide Identifications. Journal of Proteome Research, 2008, 7, 2195-2203.	1.8	37
98	A Computational Strategy to Analyze Label-Free Temporal Bottom-Up Proteomics Data. Journal of Proteome Research, 2008, 7, 2595-2604.	1.8	29
99	Proteomics Analysis of the Causative Agent of Typhoid Fever. Journal of Proteome Research, 2008, 7, 546-557.	1.8	54
100	The Influence of Sample Preparation and Replicate Analyses on HeLa Cell Phosphoproteome Coverage. Journal of Proteome Research, 2008, 7, 2215-2221.	1.8	31
101	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.	3.2	46
102	Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step <sup>18</sup> O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography. Journal of Proteome Research, 2008, 7, 4215-4224.	1.8	16
103	Comparative Proteomics of Human Monkeypox and Vaccinia Intracellular Mature and Extracellular Enveloped Virions. Journal of Proteome Research, 2008, 7, 960-968.	1.8	75
104	DAnTE: a statistical tool for quantitative analysis of -omics data. Bioinformatics, 2008, 24, 1556-1558.	1.8	397
105	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. Bioinformatics, 2008, 24, 1021-1023.	1.8	143
106	Proteogenomics: needs and roles to be filled by proteomics in genome annotation. Briefings in Functional Genomics & Proteomics, 2008, 7, 50-62.	3.8	124
107	Use of high-throughput mass spectrometry to elucidate host-pathogen interactions in Salmonella. Future Microbiology, 2008, 3, 625-634.	1.0	8
108	Comparative Bacterial Proteomics: Analysis of the Core Genome Concept. PLoS ONE, 2008, 3, e1542.	1.1	71

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109	Optimization of proteomic sample preparation procedures for comprehensive protein characterization of pathogenic systems. <i>Journal of Biomolecular Techniques</i> , 2008, 19, 285-95.	0.8	15
110	Targeted Protein Degradation by Salmonella under Phagosome-mimicking Culture Conditions Investigated Using Comparative Peptidomics. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 717-727.	2.5	26
111	VIPER: an advanced software package to support high-throughput LC-MS peptide identification. <i>Bioinformatics</i> , 2007, 23, 2021-2023.	1.8	194
112	PQudâ€™a visual analysis platform for proteomic data exploration of microbial organisms. <i>Bioinformatics</i> , 2007, 23, 1705-1707.	1.8	2
113	Spatial mapping of protein abundances in the mouse brain by voxelation integrated with high-throughput liquid chromatography-mass spectrometry. <i>Genome Research</i> , 2007, 17, 328-336.	2.4	62
114	Applying a Targeted Label-Free Approach Using LCâ€™MS AMT Tags to Evaluate Changes in Protein Phosphorylation Following Phosphatase Inhibition. <i>Journal of Proteome Research</i> , 2007, 6, 4489-4497.	1.8	22
115	Whole proteome analysis of post-translational modifications: Applications of mass-spectrometry for proteogenomic annotation. <i>Genome Research</i> , 2007, 17, 1362-1377.	2.4	175
116	Robust Algorithm for Alignment of Liquid Chromatographyâ€™Mass Spectrometry Analyses in an Accurate Mass and Time Tag Data Analysis Pipeline. <i>Analytical Chemistry</i> , 2006, 78, 7397-7409.	3.2	155
117	Normalization Approaches for Removing Systematic Biases Associated with Mass Spectrometry and Label-Free Proteomics. <i>Journal of Proteome Research</i> , 2006, 5, 277-286.	1.8	375
118	Biomarker Candidate Identification in <i>Yersinia pestis</i> Using Organism-Wide Semiquantitative Proteomics. <i>Journal of Proteome Research</i> , 2006, 5, 3008-3017.	1.8	42
119	Mass Measurement Accuracy in Analyses of Highly Complex Mixtures Based Upon Multidimensional Recalibration. <i>Analytical Chemistry</i> , 2006, 78, 8374-8385.	3.2	32
120	Phosphoproteome Profiling of Human Skin Fibroblast Cells in Response to Low- and High-Dose Irradiation. <i>Journal of Proteome Research</i> , 2006, 5, 1252-1260.	1.8	108
121	Improved Peptide Elution Time Prediction for Reversed-Phase Liquid Chromatography-MS by Incorporating Peptide Sequence Information. <i>Analytical Chemistry</i> , 2006, 78, 5026-5039.	3.2	163
122	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. , 2006, , 289-315.		0
123	The proteome of dissimilatory metal-reducing microorganism <i>Geobacter sulfurreducens</i> under various growth conditions. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1198-1206.	1.1	128
124	Differential Label-free Quantitative Proteomic Analysis of <i>Shewanella oneidensis</i> Cultured under Aerobic and Suboxic Conditions by Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 714-725.	2.5	85
125	Analysis of the <i>Salmonella typhimurium</i> Proteome through Environmental Response toward Infectious Conditions. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1450-1461.	2.5	103
126	Proteomic Analysis of <i>Salmonella enterica</i> Serovar Typhimurium Isolated from RAW 264.7 Macrophages. <i>Journal of Biological Chemistry</i> , 2006, 281, 29131-29140.	1.6	136



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127	THE CHALLENGE OF PROTEOMIC DATA, FROM MOLECULAR SIGNALS TO BIOLOGICAL NETWORKS AND DISEASE: SESSION INTRODUCTION. , 2005, , .		0
128	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.	1.2	100
129	A proteomic approach to characterize protein shedding. Proteomics, 2005, 5, 123-131.	1.3	17
130	Identification of shed proteins from chinese hamster ovary cells: Application of statistical confidence using human and mouse protein databases. Proteomics, 2005, 5, 1815-1826.	1.3	15
131	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.	1.3	150
132	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.	1.3	60
133	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. Proteomics, 2005, 5, 3475-3490.	1.3	332
134	Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database. Proteomics, 2005, 5, 3226-3245.	1.3	766
135	Dynamic and Differential in Vivo Modifications of the Isoform HMGA1a and HMGA1b Chromatin Proteins. Journal of Biological Chemistry, 2005, 280, 8961-8973.	1.6	29
136	Utilizing Human Blood Plasma for Proteomic Biomarker Discovery. Journal of Proteome Research, 2005, 4, 1073-1085.	1.8	288
137	Simple Protein Complex Purification and Identification Method for High-Throughput Mapping of Protein Interaction Networks. Journal of Proteome Research, 2005, 4, 268-274.	1.8	17
138	Characterization of Plasma Membrane Proteins from Ovarian Cancer Cells Using Mass Spectrometry. Disease Markers, 2004, 19, 219-228.	0.6	8
139	The Human Plasma Proteome. Molecular and Cellular Proteomics, 2004, 3, 311-326.	2.5	801
140	Functional Consequences of Preorganized Helical Structure in the Intrinsically Disordered Cell-Cycle Inhibitor p27Kip1. Biochemistry, 2002, 41, 752-759.	1.2	142
141	Intrinsic structural disorder and sequence features of the cell cycle inhibitor p57Kip2. Proteins: Structure, Function and Bioinformatics, 2002, 46, 1-7.	1.5	74
142	Toward a Human Blood Serum Proteome. Molecular and Cellular Proteomics, 2002, 1, 947-955.	2.5	705
143	Transcriptional activity of the TFIIA four-helix bundle in vivo. Proteins: Structure, Function and Bioinformatics, 2001, 43, 227-232.	1.5	6
144	Stoichiometry of Cyclin A-Cyclin-Dependent Kinase 2 Inhibition by p21Cip1/Waf1. Biochemistry, 2000, 39, 13925-13930.	1.2	23

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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