

Matthew E Monroe

List of Publications by Year in descending order

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119
papers

10,849
citations

38660

50
h-index

34900

98
g-index

123
all docs

123
docs citations

123
times ranked

14421
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic Time-Warping Correction for Shifts in Ultrahigh Resolving Power Ion Mobility Spectrometry and Structures for Lossless Ion Manipulations. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 996-1007.	1.2	14
2	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	7.7	327
3	A resource of lipidomics and metabolomics data from individuals with undiagnosed diseases. <i>Scientific Data</i> , 2021, 8, 114.	2.4	12
4	Mass spectrometry-based direct detection of multiple types of protein thiol modifications in pancreatic beta cells under endoplasmic reticulum stress. <i>Redox Biology</i> , 2021, 46, 102111.	3.9	27
5	From Prevention to Disease Perturbations: A Multi-Omic Assessment of Exercise and Myocardial Infarctions. <i>Biomolecules</i> , 2021, 11, 40.	1.8	8
6	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. <i>Cell</i> , 2020, 183, 1962-1985.e31.	13.5	177
7	Unveiling molecular signatures of preeclampsia and gestational diabetes mellitus with multi-omics and innovative cheminformatics visualization tools. <i>Molecular Omics</i> , 2020, 16, 521-532.	1.4	16
8	Block Design with Common Reference Samples Enables Robust Large-Scale Label-Free Quantitative Proteome Profiling. <i>Journal of Proteome Research</i> , 2020, 19, 2863-2872.	1.8	10
9	Accurate Identification of Deamidation and Citrullination from Global Shotgun Proteomics Data Using a Dual-Search Delta Score Strategy. <i>Journal of Proteome Research</i> , 2020, 19, 1863-1872.	1.8	16
10	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	13.5	410
11	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	13.5	296
12	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020, 1, 100004.	3.3	46
13	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	13.5	430
14	SLIM Ultrahigh Resolution Ion Mobility Spectrometry Separations of Isotopologues and Isotopomers Reveal Mobility Shifts due to Mass Distribution Changes. <i>Analytical Chemistry</i> , 2019, 91, 11952-11962.	3.2	76
15	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	13.5	498
16	Quality Control Analysis in Real-time (QC-ART): A Tool for Real-time Quality Control Assessment of Mass Spectrometry-based Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1824-1836.	2.5	25
17	MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1012-E1021.	3.3	142
18	A Customizable Flow Injection System for Automated, High Throughput, and Time Sensitive Ion Mobility Spectrometry and Mass Spectrometry Measurements. <i>Analytical Chemistry</i> , 2018, 90, 737-744.	3.2	11

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19	An algorithm to correct saturated mass spectrometry ion abundances for enhanced quantitation and mass accuracy in omic studies. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 91-99.	0.7	25
20	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography–mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1632-1661.	5.5	377
21	Coupling Front-End Separations, Ion Mobility Spectrometry, and Mass Spectrometry For Enhanced Multidimensional Biological and Environmental Analyses. <i>Annual Review of Analytical Chemistry</i> , 2017, 10, 71-92.	2.8	84
22	Comparing identified and statistically significant lipids and polar metabolites in 15-year old serum and dried blood spot samples for longitudinal studies. <i>Rapid Communications in Mass Spectrometry</i> , 2017, 31, 447-456.	0.7	31
23	SPE-IMS-MS: An automated platform for sub-sixty second surveillance of endogenous metabolites and xenobiotics in biofluids. <i>Clinical Mass Spectrometry</i> , 2016, 2, 1-10.	1.9	63
24	Simultaneous Proteomic Discovery and Targeted Monitoring using Liquid Chromatography, Ion Mobility Spectrometry, and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3694-3705.	2.5	29
25	The fungal cultivar of leaf-cutter ants produces specific enzymes in response to different plant substrates. <i>Molecular Ecology</i> , 2016, 25, 5795-5805.	2.0	37
26	Dinitrogenase-Driven Photobiological Hydrogen Production Combats Oxidative Stress in <i>Cyanothece</i> sp. Strain ATCC 51142. <i>Applied and Environmental Microbiology</i> , 2016, 82, 7227-7235.	1.4	16
27	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	13.5	804
28	Uncovering biologically significant lipid isomers with liquid chromatography, ion mobility spectrometry and mass spectrometry. <i>Analyst, The</i> , 2016, 141, 1649-1659.	1.7	196
29	Enhancing bottom-up and top-down proteomic measurements with ion mobility separations. <i>Proteomics</i> , 2015, 15, 2766-2776.	1.3	54
30	An Optimized Informatics Pipeline for Mass Spectrometry-Based Peptidomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 2002-2008.	1.2	10
31	Correcting systematic bias and instrument measurement drift with mzRefinery. <i>Bioinformatics</i> , 2015, 31, 3838-3840.	1.8	32
32	Muscle Segment Homeobox Genes Direct Embryonic Diapause by Limiting Inflammation in the Uterus*. <i>Journal of Biological Chemistry</i> , 2015, 290, 15337-15349.	1.6	18
33	Enhancing biological analyses with three dimensional field asymmetric ion mobility, low field drift tube ion mobility and mass spectrometry (1/4FAIMS/IMS-MS) separations. <i>Analyst, The</i> , 2015, 140, 6955-6963.	1.7	14
34	Comprehensive Quantitative Analysis of Ovarian and Breast Cancer Tumor Peptidomes. <i>Journal of Proteome Research</i> , 2015, 14, 422-433.	1.8	26
35	Enrichment and Broad Representation of Plant Biomass-Degrading Enzymes in the Specialized Hyphal Swellings of <i>Leucoagaricus gongylophorus</i> , the Fungal Symbiont of Leaf-Cutter Ants. <i>PLoS ONE</i> , 2015, 10, e0134752.	1.1	28
36	High and Low Doses of Ionizing Radiation Induce Different Secretome Profiles in a Human Skin Model. <i>PLoS ONE</i> , 2014, 9, e92332.	1.1	13

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37	Proteome-wide Light/Dark Modulation of Thiol Oxidation in Cyanobacteria Revealed by Quantitative Site-specific Redox Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3270-3285.	2.5	75
38	Advancing the High Throughput Identification of Liver Fibrosis Protein Signatures Using Multiplexed Ion Mobility Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1119-1127.	2.5	51
39	Accounting for Population Variation in Targeted Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 321-323.	1.8	4
40	Detecting and Removing Data Artifacts in Hadamard Transform Ion Mobility-Mass Spectrometry Measurements. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 2020-2027.	1.2	42
41	GlyQ-IQ: Glycomics Quintivariate-Informed Quantification with High-Performance Computing and GlycoGrid 4D Visualization. <i>Analytical Chemistry</i> , 2014, 86, 6268-6276.	3.2	11
42	Signatures for Mass Spectrometry Data Quality. <i>Journal of Proteome Research</i> , 2014, 13, 2215-2222.	1.8	18
43	Basophile: Accurate Fragment Charge State Prediction Improves Peptide Identification Rates. <i>Genomics, Proteomics and Bioinformatics</i> , 2013, 11, 86-95.	3.0	1
44	<i>Leucoagaricus gongylophorus</i> Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3770-3778.	1.4	98
45	STEPS: A grid search methodology for optimized peptide identification filtering of MS/MS database search results. <i>Proteomics</i> , 2013, 13, 766-770.	1.3	18
46	Proteome Analyses of Strains ATCC 51142 and PCC 7822 of the Diazotrophic Cyanobacterium <i>Cyanothece</i> sp. under Culture Conditions Resulting in Enhanced H ₂ Production. <i>Applied and Environmental Microbiology</i> , 2013, 79, 1070-1077.	1.4	26
47	Quantitative site-specific reactivity profiling of S-nitrosylation in mouse skeletal muscle using cysteinyl peptide enrichment coupled with mass spectrometry. <i>Free Radical Biology and Medicine</i> , 2013, 57, 68-78.	1.3	61
48	In-Source Fragmentation and the Sources of Partially Tryptic Peptides in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 910-916.	1.8	51
49	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
50	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
51	Improving N-Glycan Coverage using HPLC-MS with Electrospray Ionization at Subambient Pressure. <i>Analytical Chemistry</i> , 2012, 84, 9208-9213.	3.2	13
52	Detection and Identification of Heme C-Modified Peptides by Histidine Affinity Chromatography, High-Performance Liquid Chromatography-Mass Spectrometry, and Database Searching. <i>Journal of Proteome Research</i> , 2012, 11, 6147-6158.	1.8	9
53	Mapping N-Linked Glycosylation Sites in the Secretome and Whole Cells of <i>Aspergillus niger</i> Using Hydrazide Chemistry and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 143-156.	1.8	62
54	Comparative Omics-Driven Genome Annotation Refinement: Application across <i>Yersinia</i> . <i>PLoS ONE</i> , 2012, 7, e33903.	1.1	30

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55	Proteome and computational analyses reveal new insights into the mechanisms of hepatitis C virus-mediated liver disease posttransplantation. <i>Hepatology</i> , 2012, 56, 28-38.	3.6	39
56	Tandem mass spectrometry identifies many mouse brain <i>O</i> -GlcNAcylated proteins including EGF domain-specific <i>O</i> -GlcNAc transferase targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7280-7285.	3.3	275
57	Identification of <i>c</i> -Type Heme-Containing Peptides Using Nonactivated Immobilized Metal Affinity Chromatography Resin Enrichment and Higher-Energy Collisional Dissociation. <i>Analytical Chemistry</i> , 2011, 83, 7260-7268.	3.2	5
58	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
59	Comprehensive Identification of Glycated Peptides and Their Glycation Motifs in Plasma and Erythrocytes of Control and Diabetic Subjects. <i>Journal of Proteome Research</i> , 2011, 10, 3076-3088.	1.8	92
60	Spectral archives: extending spectral libraries to analyze both identified and unidentified spectra. <i>Nature Methods</i> , 2011, 8, 587-591.	9.0	86
61	Reversed-phase chromatography with multiple fraction concatenation strategy for proteome profiling of human MCF10A cells. <i>Proteomics</i> , 2011, 11, 2019-2026.	1.3	564
62	An efficient data format for mass spectrometry-based proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1784-1788.	1.2	16
63	Phosphoproteomics Profiling of Human Skin Fibroblast Cells Reveals Pathways and Proteins Affected by Low Doses of Ionizing Radiation. <i>PLoS ONE</i> , 2010, 5, e14152.	1.1	21
64	Endogenous 3,4-Dihydroxyphenylalanine and Dopaquinone Modifications on Protein Tyrosine. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1199-1208.	2.5	23
65	DtaRefinery, a Software Tool for Elimination of Systematic Errors from Parent Ion Mass Measurements in Tandem Mass Spectra Data Sets. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 486-496.	2.5	54
66	Quantitative Analysis of Cell Surface Membrane Proteins Using Membrane-Impermeable Chemical Probe Coupled with ¹⁸ O Labeling. <i>Journal of Proteome Research</i> , 2010, 9, 2160-2169.	1.8	19
67	Plasma Proteome Response to Severe Burn Injury Revealed by ¹⁸ O-Labeled <i>Universal</i> Reference-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 4779-4789.	1.8	54
68	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
69	Improved LC-MS/MS Spectral Counting Statistics by Recovering Low-Scoring Spectra Matched to Confidently Identified Peptide Sequences. <i>Journal of Proteome Research</i> , 2010, 9, 5698-5704.	1.8	47
70	Novel Ser/Thr Protein Phosphatase 5 (PP5) Regulated Targets during DNA Damage Identified by Proteomics Analysis. <i>Journal of Proteome Research</i> , 2010, 9, 945-953.	1.8	18
71	Region-Specific Protein Abundance Changes in the Brain of MPTP-Induced Parkinson's Disease Mouse Model. <i>Journal of Proteome Research</i> , 2010, 9, 1496-1509.	1.8	69
72	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ¹⁸ O-Labeled <i>Universal</i> Reference Sample. <i>Journal of Proteome Research</i> , 2009, 8, 290-299.	1.8	59

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73	Combined Pulsed-Q Dissociation and Electron Transfer Dissociation for Identification and Quantification of iTRAQ-Labeled Phosphopeptides. <i>Analytical Chemistry</i> , 2009, 81, 4137-4143.	3.2	30
74	An Extensive Survey of Tyrosine Phosphorylation Revealing New Sites in Human Mammary Epithelial Cells. <i>Journal of Proteome Research</i> , 2009, 8, 3852-3861.	1.8	51
75	Application of the accurate mass and time tag approach in studies of the human blood lipidome. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2008, 871, 243-252.	1.2	36
76	MASIC: A software program for fast quantitation and flexible visualization of chromatographic profiles from detected LC-MS/MS features. <i>Computational Biology and Chemistry</i> , 2008, 32, 215-217.	1.1	154
77	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. <i>Analytical Chemistry</i> , 2008, 80, 693-706.	3.2	38
78	Characterization of the Mouse Pancreatic Islet Proteome and Comparative Analysis with Other Mouse Tissues. <i>Journal of Proteome Research</i> , 2008, 7, 3114-3126.	1.8	47
79	Rapid Sample Processing for LC-MS-Based Quantitative Proteomics Using High Intensity Focused Ultrasound. <i>Journal of Proteome Research</i> , 2008, 7, 3860-3867.	1.8	40
80	Characterization of Strategies for Obtaining Confident Identifications in Bottom-Up Proteomics Measurements Using Hybrid FTMS Instruments. <i>Analytical Chemistry</i> , 2008, 80, 8514-8525.	3.2	24
81	Linear Discriminant Analysis-Based Estimation of the False Discovery Rate for Phosphopeptide Identifications. <i>Journal of Proteome Research</i> , 2008, 7, 2195-2203.	1.8	37
82	The Influence of Sample Preparation and Replicate Analyses on HeLa Cell Phosphoproteome Coverage. <i>Journal of Proteome Research</i> , 2008, 7, 2215-2221.	1.8	31
83	Application of Proteomics in the Discovery of Candidate Protein Biomarkers in a Diabetes Autoantibody Standardization Program Sample Subset. <i>Journal of Proteome Research</i> , 2008, 7, 698-707.	1.8	58
84	Quantitative Phosphoproteome Analysis of Lysophosphatidic Acid Induced Chemotaxis Applying Dual-Step ¹⁸ O Labeling Coupled with Immobilized Metal-Ion Affinity Chromatography. <i>Journal of Proteome Research</i> , 2008, 7, 4215-4224.	1.8	16
85	Comparative Proteomics of Human Monkeypox and Vaccinia Intracellular Mature and Extracellular Enveloped Virions. <i>Journal of Proteome Research</i> , 2008, 7, 960-968.	1.8	75
86	High Sensitivity Proteomics Assisted Discovery of a Novel Operon Involved in the Assembly of Photosystem II, a Membrane Protein Complex. <i>Journal of Biological Chemistry</i> , 2008, 283, 27829-27837.	1.6	39
87	Comparative Bacterial Proteomics: Analysis of the Core Genome Concept. <i>PLoS ONE</i> , 2008, 3, e1542.	1.1	71
88	Quantitative Analysis of Human Immunodeficiency Virus Type 1-Infected CD4 + Cell Proteome: Dysregulated Cell Cycle Progression and Nuclear Transport Coincide with Robust Virus Production. <i>Journal of Virology</i> , 2007, 81, 7571-7583.	1.5	84
89	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
90	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

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91	Applying a Targeted Label-Free Approach Using LC-MS/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
92	Robust Algorithm for Alignment of Liquid Chromatography-Mass Spectrometry Analyses in an Accurate Mass and Time Tag Data Analysis Pipeline. <i>Analytical Chemistry</i> , 2006, 78, 7397-7409.	3.2	155
93	Estimating probabilities of peptide database identifications to LC-FTICR-MS observations. <i>Proteome Science</i> , 2006, 4, 1.	0.7	27
94	Mass Measurement Accuracy in Analyses of Highly Complex Mixtures Based Upon Multidimensional Recalibration. <i>Analytical Chemistry</i> , 2006, 78, 8374-8385.	3.2	32
95	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
96	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
97	Confirmation of the expression of a large set of conserved hypothetical proteins in <i>Shewanella oneidensis</i> MR-1. <i>Journal of Microbiological Methods</i> , 2006, 66, 223-233.	0.7	24
98	Comparison of aerobic and photosynthetic <i>Rhodobacter sphaeroides</i> 2.4.1 proteomes. <i>Journal of Microbiological Methods</i> , 2006, 67, 424-436.	0.7	39
99	Proteomic approaches to bacterial differentiation. <i>Journal of Microbiological Methods</i> , 2006, 67, 473-486.	0.7	23
100	PRISM: A data management system for high-throughput proteomics. <i>Proteomics</i> , 2006, 6, 1783-1790.	1.3	69
101	Advances in proteomics data analysis and display using an accurate mass and time tag approach. <i>Mass Spectrometry Reviews</i> , 2006, 25, 450-482.	2.8	291
102	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
103	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	2.5	142
104	AMT tag approach to proteomic characterization of <i>Deinococcus radiodurans</i> and <i>Shewanella oneidensis</i> . <i>Methods of Biochemical Analysis</i> , 2006, 49, 113-34.	0.2	9
105	The Utility of Accurate Mass and LC Elution Time Information in the Analysis of Complex Proteomes. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 1239-1249.	1.2	100
106	Ultra-sensitive, high throughput and quantitative proteomics measurements. <i>International Journal of Mass Spectrometry</i> , 2005, 240, 195-212.	0.7	17
107	Comparative proteome analyses of human plasma following <i>in vivo</i> lipopolysaccharide administration using multidimensional separations coupled with tandem mass spectrometry. <i>Proteomics</i> , 2005, 5, 572-584.	1.3	125
108	Improved proteome coverage by using high efficiency cysteinyl peptide enrichment: The human mammary epithelial cell proteome. <i>Proteomics</i> , 2005, 5, 1263-1273.	1.3	65

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109	Identification of shed proteins from chinese hamster ovary cells: Application of statistical confidence using human and mouse protein databases. <i>Proteomics</i> , 2005, 5, 1815-1826.	1.3	15
110	Global detection and characterization of hypothetical proteins in <i>Shewanella oneidensis</i> MR-1 using LC-MS based proteomics. <i>Proteomics</i> , 2005, 5, 3120-3130.	1.3	52
111	A proteomic study of the HUPO Plasma Proteome Project's pilot samples using an accurate mass and time tag strategy. <i>Proteomics</i> , 2005, 5, 3454-3466.	1.3	60
112	Quantitative Proteome Analysis of Human Plasma following in Vivo Lipopolysaccharide Administration Using 16O/18O Labeling and the Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 700-709.	2.5	156
113	Probability-Based Evaluation of Peptide and Protein Identifications from Tandem Mass Spectrometry and SEQUEST Analysis: The Human Proteome. <i>Journal of Proteome Research</i> , 2005, 4, 53-62.	1.8	320
114	Human Plasma N-Glycoproteome Analysis by Immunoaffinity Subtraction, Hydrazide Chemistry, and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2005, 4, 2070-2080.	1.8	394
115	Global Whole-Cell FTICR Mass Spectrometric Proteomics Analysis of the Heat Shock Response in the Radioresistant Bacterium <i>Deinococcus radiodurans</i> . <i>Journal of Proteome Research</i> , 2005, 4, 709-718.	1.8	30
116	Identification of Proteins in Human Cytomegalovirus (HCMV) Particles: the HCMV Proteome. <i>Journal of Virology</i> , 2004, 78, 10960-10966.	1.5	521
117	Validation of <i>Shewanella oneidensis</i> MR-1 Small Proteins by AMT Tag-Based Proteome Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2004, 8, 239-254.	1.0	45
118	Integrative Analysis of the Mitochondrial Proteome in Yeast. <i>PLoS Biology</i> , 2004, 2, e160.	2.6	181
119	Multidimensional Proteome Analysis of Human Mammary Epithelial Cells. <i>Journal of Proteome Research</i> , 2004, 3, 68-75.	1.8	91