

Christoph Borchers

List of Publications by Year in descending order

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332
papers

20,357
citations

11608

70
h-index

15218

126
g-index

344
all docs

344
docs citations

344
times ranked

25889
citing authors

#	ARTICLE	IF	CITATIONS
1	Histone demethylation by a family of JmjC domain-containing proteins. <i>Nature</i> , 2006, 439, 811-816.	13.7	1,846
2	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. <i>Nature Biotechnology</i> , 2009, 27, 633-641.	9.4	958
3	Purification and Functional Characterization of a Histone H3-Lysine 4-Specific Methyltransferase. <i>Molecular Cell</i> , 2001, 8, 1207-1217.	4.5	472
4	Multiple Reaction Monitoring-based, Multiplexed, Absolute Quantitation of 45 Proteins in Human Plasma. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1860-1877.	2.5	468
5	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	9.0	452
6	JNK phosphorylates paxillin and regulates cell migration. <i>Nature</i> , 2003, 424, 219-223.	13.7	442
7	Targeting of protein ubiquitination by BTB-Cullin 3-Roc1 ubiquitin ligases. <i>Nature Cell Biology</i> , 2003, 5, 1001-1007.	4.6	390
8	An isotope-labeled chemical derivatization method for the quantitation of short-chain fatty acids in human feces by liquid chromatography-tandem mass spectrometry. <i>Analytica Chimica Acta</i> , 2015, 854, 86-94.	2.6	380
9	Phosphorylation of RNA polymerase II CTD regulates H3 methylation in yeast. <i>Genes and Development</i> , 2003, 17, 654-663.	2.7	363
10	Harmonizing lipidomics: NIST interlaboratory comparison exercise for lipidomics using SRM 1950-Metabolites in Frozen Human Plasma. <i>Journal of Lipid Research</i> , 2017, 58, 2275-2288.	2.0	312
11	A Quantitative Study of the Effects of Chaotropic Agents, Surfactants, and Solvents on the Digestion Efficiency of Human Plasma Proteins by Trypsin. <i>Journal of Proteome Research</i> , 2010, 9, 5422-5437.	1.8	301
12	Adora2b-elicited Per2 stabilization promotes a HIF-dependent metabolic switch crucial for myocardial adaptation to ischemia. <i>Nature Medicine</i> , 2012, 18, 774-782.	15.2	278
13	Architecture of the RNA polymerase II-Mediator core initiation complex. <i>Nature</i> , 2015, 518, 376-380.	13.7	259
14	Effect of Antibiotic Treatment on the Intestinal Metabolome. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 1494-1503.	1.4	258
15	Current trends in quantitative proteomics. <i>Journal of Mass Spectrometry</i> , 2009, 44, 1637-1660.	0.7	219
16	MRM-based multiplexed quantitation of 67 putative cardiovascular disease biomarkers in human plasma. <i>Proteomics</i> , 2012, 12, 1222-1243.	1.3	191
17	A Human Proteome Detection and Quantitation Project. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 883-886.	2.5	186
18	Mass spectrometry based biomarker discovery, verification, and validation - Quality assurance and control of protein biomarker assays. <i>Molecular Oncology</i> , 2014, 8, 840-858.	2.1	178

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19	Hydrogen/Deuterium Exchange Mass Spectrometry with Top-Down Electron Capture Dissociation for Characterizing Structural Transitions of a 17 kDa Protein. <i>Journal of the American Chemical Society</i> , 2009, 131, 12801-12808.	6.6	174
20	Crosslinking combined with mass spectrometry for structural proteomics. <i>Mass Spectrometry Reviews</i> , 2010, 29, 862-876.	2.8	172
21	Diet and specific microbial exposure trigger features of environmental enteropathy in a novel murine model. <i>Nature Communications</i> , 2015, 6, 7806.	5.8	172
22	Reduced Insulin Production Relieves Endoplasmic Reticulum Stress and Induces β Cell Proliferation. <i>Cell Metabolism</i> , 2016, 23, 179-193.	7.2	160
23	Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2357-2374.	2.5	153
24	HIF1A Reduces Acute Lung Injury by Optimizing Carbohydrate Metabolism in the Alveolar Epithelium. <i>PLoS Biology</i> , 2013, 11, e1001665.	2.6	138
25	Towards high-throughput metabolomics using ultrahigh-field Fourier transform ion cyclotron resonance mass spectrometry. <i>Metabolomics</i> , 2008, 4, 128-140.	1.4	136
26	SISCAPA Peptide Enrichment on Magnetic Beads Using an In-line Bead Trap Device. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 995-1005.	2.5	134
27	Multiplexed quantification of 63 proteins in human urine by multiple reaction monitoring-based mass spectrometry for discovery of potential bladder cancer biomarkers. <i>Journal of Proteomics</i> , 2012, 75, 3529-3545.	1.2	134
28	Metabolic Profiling of Bile Acids in Human and Mouse Blood by LC-MS/MS in Combination with Phospholipid-Depletion Solid-Phase Extraction. <i>Analytical Chemistry</i> , 2015, 87, 1127-1136.	3.2	134
29	Molecular Characterization of Surface Topology in Protein Tertiary Structures by Amino-Acylation and Mass Spectrometric Peptide Mapping. <i>Bioconjugate Chemistry</i> , 1994, 5, 583-590.	1.8	127
30	Regulation of the Cytoplasmic Quality Control Protein Degradation Pathway by BAG2. <i>Journal of Biological Chemistry</i> , 2005, 280, 38673-38681.	1.6	123
31	Advances in multiplexed MRM-based protein biomarker quantitation toward clinical utility. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 917-926.	1.1	123
32	Direct MALDI-MS/MS of Phosphopeptides Affinity-Bound to Immobilized Metal Ion Affinity Chromatography Beads. <i>Analytical Chemistry</i> , 2002, 74, 3429-3433.	3.2	118
33	PeptidePicker: A scientific workflow with web interface for selecting appropriate peptides for targeted proteomics experiments. <i>Journal of Proteomics</i> , 2014, 106, 151-161.	1.2	117
34	An integrated genomic, proteomic and biochemical analysis of (+)- α - β -carene biosynthesis in Sitka spruce (<i>Picea sitchensis</i>) genotypes that are resistant or susceptible to white pine weevil. <i>Plant Journal</i> , 2011, 65, 936-948.	2.8	116
35	An Isotopically Coded CID-cleavable Biotinylated Cross-linker for Structural Proteomics. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S8.	2.5	113
36	Electron Capture Dissociation of Electrosprayed Protein Ions for Spatially Resolved Hydrogen Exchange Measurements. <i>Journal of the American Chemical Society</i> , 2008, 130, 11574-11575.	6.6	111

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37	Defects in myosin VB are associated with a spectrum of previously undiagnosed low β -glutamyltransferase cholestasis. <i>Hepatology</i> , 2017, 65, 1655-1669.	3.6	107
38	Recent advancements in matrix-assisted laser desorption/ionization mass spectrometry imaging. <i>Current Opinion in Biotechnology</i> , 2017, 43, 62-69.	3.3	107
39	Targeted proteomics using selected reaction monitoring reveals the induction of specific terpene synthases in a multi-level study of methyl jasmonate-treated Norway spruce (<i>Picea abies</i>). <i>Plant Journal</i> , 2009, 60, 1015-1030.	2.8	106
40	Impact of <i>Salmonella</i> Infection on Host Hormone Metabolism Revealed by Metabolomics. <i>Infection and Immunity</i> , 2011, 79, 1759-1769.	1.0	104
41	Chemical fingerprinting of naphthenic acids and oil sands process waters – A review of analytical methods for environmental samples. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2013, 48, 1145-1163.	0.9	103
42	Metabolomic analysis of key central carbon metabolism carboxylic acids as their β -nitrophenylhydrazones by UPLC/ESI-MS. <i>Electrophoresis</i> , 2013, 34, 2891-2900.	1.3	100
43	Design, Implementation and Multisite Evaluation of a System Suitability Protocol for the Quantitative Assessment of Instrument Performance in Liquid Chromatography-Multiple Reaction Monitoring-MS (LC-MRM-MS). <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2623-2639.	2.5	100
44	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
45	The dimerization motif of cytosolic sulfotransferases. <i>FEBS Letters</i> , 2001, 490, 39-43.	1.3	99
46	Discovery of a small-molecule HIV-1 integrase inhibitor-binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 10080-10085.	3.3	98
47	Mass-spectrometry-based clinical proteomics – a review and prospective. <i>Analyst, The</i> , 2010, 135, 1830.	1.7	98
48	A Systems-Biology Analysis of Feedback Inhibition in the Sho1 Osmotic-Stress-Response Pathway. <i>Current Biology</i> , 2007, 17, 659-667.	1.8	97
49	Isotopically Coded Cleavable Cross-linker for Studying Protein-Protein Interaction and Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1167-1179.	2.5	94
50	The first pilot project of the consortium for top-down proteomics: A status report. <i>Proteomics</i> , 2014, 14, 1130-1140.	1.3	90
51	Mass-Spectrometric Detection of SARS-CoV-2 Virus in Scrapings of the Epithelium of the Nasopharynx of Infected Patients via Nucleocapsid N Protein. <i>Journal of Proteome Research</i> , 2020, 19, 4393-4397.	1.8	87
52	Phosphorylation of Stem-Loop Binding Protein (SLBP) on Two Threonines Triggers Degradation of SLBP, the Sole Cell Cycle-Regulated Factor Required for Regulation of Histone mRNA Processing, at the End of S Phase. <i>Molecular and Cellular Biology</i> , 2003, 23, 1590-1601.	1.1	85
53	Proteomic Signatures in Plasma during Early Acute Renal Allograft Rejection. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1954-1967.	2.5	85
54	Structure of EspB from the ESX-1 Type VII Secretion System and Insights into its Export Mechanism. <i>Structure</i> , 2015, 23, 571-583.	1.6	85

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55	Direct interaction with filamins modulates the stability and plasma membrane expression of CFTR. <i>Journal of Clinical Investigation</i> , 2007, 117, 364-374.	3.9	85
56	Comparison of standard- and nano-flow liquid chromatography platforms for MRM-based quantitation of putative plasma biomarker proteins. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 1089-1101.	1.9	83
57	<i>Mycobacterium leprae</i> intracellular survival relies on cholesterol accumulation in infected macrophages: a potential target for new drugs for leprosy treatment. <i>Cellular Microbiology</i> , 2014, 16, 797-815.	1.1	83
58	Targeted and Untargeted Proteomics Approaches in Biomarker Development. <i>Proteomics</i> , 2020, 20, e1900029.	1.3	83
59	Multiplexed Quantitation of Endogenous Proteins in Dried Blood Spots by Multiple Reaction Monitoring - Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 781-791.	2.5	81
60	Multiple Reaction Monitoring Enables Precise Quantification of 97 Proteins in Dried Blood Spots. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3094-3104.	2.5	81
61	Solving protein structures using short-distance cross-linking constraints as a guide for discrete molecular dynamics simulations. <i>Science Advances</i> , 2017, 3, e1700479.	4.7	80
62	Identification of In-Gel Digested Proteins by Complementary Peptide Mass Fingerprinting and Tandem Mass Spectrometry Data Obtained on an Electrospray Ionization Quadrupole Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2000, 72, 1163-1168.	3.2	78
63	Phosphorylation of paxillin by p38MAPK is involved in the neurite extension of PC-12 cells. <i>Journal of Cell Biology</i> , 2004, 164, 593-602.	2.3	78
64	Characterizing Short-Lived Protein Folding Intermediates by Top-Down Hydrogen Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 8591-8597.	3.2	78
65	Preliminary comparison of precursor scans and liquid chromatography-tandem mass spectrometry on a hybrid quadrupole time-of-flight mass spectrometer. <i>Journal of Chromatography A</i> , 1999, 854, 119-130.	1.8	77
66	An immunoaffinity tandem mass spectrometry (iMALDI) assay for detection of <i>Francisella tularensis</i> . <i>Analytica Chimica Acta</i> , 2007, 605, 70-79.	2.6	75
67	Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: The Amsterdam Principles. <i>Journal of Proteome Research</i> , 2009, 8, 3689-3692.	1.8	75
68	The Tetratricopeptide Repeat Domain and a C-terminal Region Control the Activity of Ser/Thr Protein Phosphatase 5. <i>Journal of Biological Chemistry</i> , 1999, 274, 23666-23672.	1.6	73
69	Identification of two small regulatory RNAs linked to virulence in <i>Brucella abortus</i> 2308. <i>Molecular Microbiology</i> , 2012, 85, 345-360.	1.2	73
70	Hydroxyflavones as a New Family of Matrices for MALDI Tissue Imaging. <i>Analytical Chemistry</i> , 2013, 85, 7566-7573.	3.2	72
71	Current trends in quantitative proteomics - an update. <i>Journal of Mass Spectrometry</i> , 2017, 52, 319-341.	0.7	70
72	Towards the development of an immuno MALDI (iMALDI) mass spectrometry assay for the diagnosis of hypertension. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1680-1686.	1.2	69

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73	Detecting post-translational modification signatures as potential biomarkers in clinical mass spectrometry. <i>Expert Review of Proteomics</i> , 2018, 15, 515-535.	1.3	69
74	Development of MRM-Based Assays for the Absolute Quantitation of Plasma Proteins. <i>Methods in Molecular Biology</i> , 2013, 1023, 53-82.	0.4	68
75	Assay Development for the Determination of Phosphorylation Stoichiometry Using Multiple Reaction Monitoring Methods with and without Phosphatase Treatment: Application to Breast Cancer Signaling Pathways. <i>Analytical Chemistry</i> , 2010, 82, 5610-5620.	3.2	66
76	Standardized Protocols for Quality Control of MRM-based Plasma Proteomic Workflows. <i>Journal of Proteome Research</i> , 2013, 12, 222-233.	1.8	66
77	Multiplexed MRM-based quantitation of candidate cancer biomarker proteins in undepleted and non-enriched human plasma. <i>Proteomics</i> , 2013, 13, 2202-2215.	1.3	66
78	Analysis of Disease-Associated Protein Expression Using Quantitative Proteomics—Fibulin-5 Is Expressed in Association with Hepatic Fibrosis. <i>Journal of Proteome Research</i> , 2015, 14, 2278-2286.	1.8	66
79	Photoaffinity labeling combined with mass spectrometric approaches as a tool for structural proteomics. <i>Expert Review of Proteomics</i> , 2006, 3, 399-408.	1.3	65
80	Structure and Dynamics of Small Soluble A β (1-40) Oligomers Studied by Top-Down Hydrogen Exchange Mass Spectrometry. <i>Biochemistry</i> , 2012, 51, 3694-3703.	1.2	64
81	A Unique Morphological Phenotype in Chemoresistant Triple-Negative Breast Cancer Reveals Metabolic Reprogramming and PLIN4 Expression as a Molecular Vulnerability. <i>Molecular Cancer Research</i> , 2019, 17, 2492-2507.	1.5	63
82	Conformer-Specific Hydrogen Exchange Analysis of A β (1-42) Oligomers by Top-Down Electron Capture Dissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 5386-5393.	3.2	62
83	Mass spectrometry-based technologies for high-throughput metabolomics. <i>Bioanalysis</i> , 2009, 1, 1665-1684.	0.6	60
84	MRM for the verification of cancer biomarker proteins: recent applications to human plasma and serum. <i>Expert Review of Proteomics</i> , 2014, 11, 137-148.	1.3	60
85	MeCP2 binds to nucleosome free (linker DNA) regions and to H3K9/H3K27 methylated nucleosomes in the brain. <i>Nucleic Acids Research</i> , 2012, 40, 2884-2897.	6.5	57
86	The Effect of Pre-Analytical Variability on the Measurement of MRM-MS-Based Mid- to High-Abundance Plasma Protein Biomarkers and a Panel of Cytokines. <i>PLoS ONE</i> , 2012, 7, e38290.	1.1	57
87	Development of an immuno tandem mass spectrometry (iMALDI) assay for EGFR diagnosis. <i>Proteomics - Clinical Applications</i> , 2007, 1, 1651-1659.	0.8	56
88	Comprehensive Imaging of Porcine Adrenal Gland Lipids by MALDI-FTMS Using Quercetin as a Matrix. <i>Analytical Chemistry</i> , 2014, 86, 638-646.	3.2	56
89	BiPS, a Photocleavable, Isotopically Coded, Fluorescent Cross-linker for Structural Proteomics. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 273-286.	2.5	55
90	ICC-CLASS: isotopically-coded cleavable crosslinking analysis software suite. <i>BMC Bioinformatics</i> , 2010, 11, 64.	1.2	55

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91	Method and platform standardization in MRM-based quantitative plasma proteomics. <i>Journal of Proteomics</i> , 2013, 95, 66-76.	1.2	55
92	Conformational ensemble of native α -synuclein in solution as determined by short-distance crosslinking constraint-guided discrete molecular dynamics simulations. <i>PLoS Computational Biology</i> , 2019, 15, e1006859.	1.5	55
93	Dietary patterns and ethnicity are associated with distinct plasma proteomic groups. <i>American Journal of Clinical Nutrition</i> , 2012, 95, 352-361.	2.2	54
94	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3415-3431.	1.8	53
95	Enteric Helminths Promote Salmonella Coinfection by Altering the Intestinal Metabolome. <i>Journal of Infectious Diseases</i> , 2017, 215, 1245-1254.	1.9	53
96	Mnd2 and Swm1 Are Core Subunits of the <i>Saccharomyces cerevisiae</i> Anaphase-promoting Complex. <i>Journal of Biological Chemistry</i> , 2003, 278, 16698-16705.	1.6	52
97	Molecular Characterization of a Conformational Epitope of Hen Egg White Lysozyme by Differential Chemical Modification of Immune Complexes and Mass Spectrometric Peptide Mapping. <i>Bioconjugate Chemistry</i> , 1998, 9, 236-241.	1.8	51
98	Heterogeneous Nuclear Ribonuclear Protein U Associates with YAP and Regulates Its Co-activation of Bax Transcription. <i>Journal of Biological Chemistry</i> , 2004, 279, 26300-26306.	1.6	51
99	DNA binding by yeast Mlh1 and Pms1: implications for DNA mismatch repair. <i>Nucleic Acids Research</i> , 2003, 31, 2025-2034.	6.5	50
100	A comparison of MS/MS-based, stable isotope-labeled, quantitation performance on ESI-quadrupole TOF and MALDI-TOF/TOF mass spectrometers. <i>Proteomics</i> , 2009, 9, 3328-3340.	1.3	50
101	MeCP2-E1 isoform is a dynamically expressed, weakly DNA-bound protein with different protein and DNA interactions compared to MeCP2-E2. <i>Epigenetics and Chromatin</i> , 2019, 12, 63.	1.8	50
102	Comprehensive Analysis of Oil Sands Processed Water by Direct-Infusion Fourier-Transform Ion Cyclotron Resonance Mass Spectrometry with and without Offline UHPLC Sample Prefractionation. <i>Environmental Science & Technology</i> , 2013, 47, 4471-4479.	4.6	49
103	Metabolome analysis of 20 taxonomically related benzylisoquinoline alkaloid-producing plants. <i>BMC Plant Biology</i> , 2015, 15, 220.	1.6	49
104	3' End Processing of <i>Drosophila melanogaster</i> Histone Pre-mRNAs: Requirement for Phosphorylated <i>Drosophila</i> Stem-Loop Binding Protein and Coevolution of the Histone Pre-mRNA Processing System. <i>Molecular and Cellular Biology</i> , 2002, 22, 6648-6660.	1.1	48
105	Metabolomics: towards understanding host-microbe interactions. <i>Future Microbiology</i> , 2010, 5, 153-161.	1.0	48
106	Quantitation of Spatially-Localized Proteins in Tissue Samples using MALDI-MRM Imaging. <i>Analytical Chemistry</i> , 2012, 84, 3514-3522.	3.2	48
107	Protein unfolding as a switch from self-recognition to high-affinity client binding. <i>Nature Communications</i> , 2016, 7, 10357.	5.8	48
108	Super Spy variants implicate flexibility in chaperone action. <i>ELife</i> , 2014, 3, e01584.	2.8	48

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109	Isotopically-coded short-range hetero-bifunctional photo-reactive crosslinkers for studying protein structure. <i>Journal of Proteomics</i> , 2015, 118, 12-20.	1.2	47
110	Combined top-down and bottom-up proteomics identifies a phosphorylation site in stem-loop-binding proteins that contributes to high-affinity RNA binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3094-3099.	3.3	46
111	Use of Proteinase K Nonspecific Digestion for Selective and Comprehensive Identification of Interpeptide Cross-links: Application to Prion Proteins. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013524-1-M111.013524-13.	2.5	46
112	Novel Neutrophil-Derived Proteins in Bronchoalveolar Lavage Fluid Indicate an Exaggerated Inflammatory Response in Pediatric Cystic Fibrosis Patients. <i>Clinical Chemistry</i> , 2007, 53, 1782-1791.	1.5	45
113	Analysis of Selected Sugars and Sugar Phosphates in Mouse Heart Tissue by Reductive Amination and Liquid Chromatography-Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 5965-5973.	3.2	45
114	Precise quantitation of 136 urinary proteins by LC/MRM-MS using stable isotope labeled peptides as internal standards for biomarker discovery and/or verification studies. <i>Methods</i> , 2015, 81, 24-33.	1.9	45
115	Characterization and Diagnostic Application of <i>Trypanosoma cruzi</i> Trypomastigote Excreted-Secreted Antigens Shed in Extracellular Vesicles Released from Infected Mammalian Cells. <i>Journal of Clinical Microbiology</i> , 2017, 55, 744-758.	1.8	45
116	Mass Spectrometry-Based Structural Proteomics. <i>European Journal of Mass Spectrometry</i> , 2012, 18, 251-267.	0.5	44
117	Dithranol as a MALDI Matrix for Tissue Imaging of Lipids by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 8391-8398.	3.2	44
118	Identification and Validation of Potential New Biomarkers for Prostate Cancer Diagnosis and Prognosis Using 2D-DIGE and MS. <i>BioMed Research International</i> , 2015, 2015, 1-23.	0.9	44
119	Phosphatase-Directed Phosphorylation-Site Determination: A Synthesis of Methods for the Detection and Identification of Phosphopeptides. <i>Journal of Proteome Research</i> , 2005, 4, 1628-1635.	1.8	43
120	Metabolic Signatures of Triatomine Vectors of <i>Trypanosoma cruzi</i> Unveiled by Metabolomics. <i>PLoS ONE</i> , 2013, 8, e77283.	1.1	43
121	Enhanced sensitivity and multiplexing with 2D LC/MRM-MS and labeled standards for deeper and more comprehensive protein quantitation. <i>Journal of Proteomics</i> , 2014, 106, 113-124.	1.2	43
122	Subzero Temperature Chromatography and Top-Down Mass Spectrometry for Protein Higher-Order Structure Characterization: Method Validation and Application to Therapeutic Antibodies. <i>Journal of the American Chemical Society</i> , 2014, 136, 13065-13071.	6.6	43
123	Electrospray ionization tandem mass spectrometry of model peptides reveals diagnostic fragment ions for protein ubiquitination. <i>Rapid Communications in Mass Spectrometry</i> , 2005, 19, 429-437.	0.7	42
124	Model of the Mediator middle module based on protein cross-linking. <i>Nucleic Acids Research</i> , 2013, 41, 9266-9273.	6.5	42
125	Characterization of a discontinuous epitope of the human immunodeficiency virus (HIV) core protein p24 by epitope excision and differential chemical modification followed by mass spectrometric peptide mapping analysis. <i>Protein Science</i> , 2000, 9, 487-496.	3.1	41
126	Metabonomics Reveals Drastic Changes in Anti-Inflammatory/Pro-Resolving Polyunsaturated Fatty Acids-Derived Lipid Mediators in Leprosy Disease. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2381.	1.3	41

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127	The Deubiquitinase Activity of the Salmonella Pathogenicity Island 2 Effector, SseL, Prevents Accumulation of Cellular Lipid Droplets. <i>Infection and Immunity</i> , 2011, 79, 4392-4400.	1.0	40
128	Multiple Reaction Monitoring (MRM). <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 378-378.	5.1	40
129	Comparison of Proteins in Whole Blood and Dried Blood Spot Samples by LC/MS/MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1338-1345.	1.2	40
130	Computational Biomarker Pipeline from Discovery to Clinical Implementation: Plasma Proteomic Biomarkers for Cardiac Transplantation. <i>PLoS Computational Biology</i> , 2013, 9, e1002963.	1.5	40
131	Multiplexed MRM with Internal Standards for Cerebrospinal Fluid Candidate Protein Biomarker Quantitation. <i>Journal of Proteome Research</i> , 2014, 13, 3733-3747.	1.8	40
132	Identification of Components of Protein Complexes Using a Fluorescent Photo-Cross-Linker and Mass Spectrometry. <i>Analytical Chemistry</i> , 2002, 74, 1939-1945.	3.2	39
133	Insight into the Structure of the "Unstructured" Tau Protein. <i>Structure</i> , 2019, 27, 1710-1715.e4.	1.6	39
134	Characterization of the Noncovalent Complex of Human Immunodeficiency Virus Glycoprotein 120 with Its Cellular Receptor CD4 by Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. <i>Biochemistry</i> , 1999, 38, 11734-11740.	1.2	38
135	Development of a Protein Chip: A MS-Based Method for Quantitation of Protein Expression and Modification Levels Using an Immunoaffinity Approach. <i>Analytical Chemistry</i> , 2004, 76, 4082-4092.	3.2	37
136	Absolute Quantitation of Proteins in Human Blood by Multiplexed Multiple Reaction Monitoring Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 1000, 167-189.	0.4	37
137	Microfluidic-Mass Spectrometry Interfaces for Translational Proteomics. <i>Trends in Biotechnology</i> , 2017, 35, 954-970.	4.9	37
138	Matrix coating assisted by an electric field (MCAEF) for enhanced tissue imaging by MALDI-MS. <i>Chemical Science</i> , 2015, 6, 729-738.	3.7	36
139	Top-Down Hydrogen-Deuterium Exchange Analysis of Protein Structures Using Ultraviolet Photodissociation. <i>Analytical Chemistry</i> , 2018, 90, 3079-3082.	3.2	36
140	Characterization of the Dexniguldipine Binding Site in the Multidrug Resistance-Related Transport Protein P-Glycoprotein by Photoaffinity Labeling and Mass Spectrometry. <i>Molecular Pharmacology</i> , 2002, 61, 1366-1376.	1.0	35
141	Identification of <i>Leishmania</i> specific protein phosphorylation sites by LC-ESI-MS/MS and comparative genomics analyses. <i>Proteomics</i> , 2010, 10, 3868-3883.	1.3	35
142	Pre-analytical and analytical variability in absolute quantitative MRM-based plasma proteomic studies. <i>Bioanalysis</i> , 2013, 5, 2837-2856.	0.6	35
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