Richard D Smith

List of Publications by Year
in descending order

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1,343 papers	98,343 citations	228 145 h-index	1310 224 g-index
1380 all docs	1380 docs citations	1380 times ranked	69690 citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic responses in mouse models poorly mimic human inflammatory diseases. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3507-3512.	3.3	2,518
2	New developments in biochemical mass spectrometry: electrospray ionization. Analytical Chemistry, 1990, 62, 882-899.	3.2	1,092
3	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	13.5	804
4	A common open representation of mass spectrometry data and its application to proteomics research. Nature Biotechnology, 2004, 22, 1459-1466.	9.4	724
5	Toward a Human Blood Serum Proteome. Molecular and Cellular Proteomics, 2002, 1, 947-955.	2.5	705
6	Omic data from evolved <i>E. coli</i> are consistent with computed optimal growth from genomeâ€scale models. Molecular Systems Biology, 2010, 6, 390.	3.2	615
7	On-line mass spectrometric detection for capillary zone electrophoresis. Analytical Chemistry, 1987, 59, 1230-1232.	3.2	597
8	Responding to global infectious disease outbreaks: Lessons from SARS on the role of risk perception, communication and management. Social Science and Medicine, 2006, 63, 3113-3123.	1.8	593
9	Activated ClpP kills persisters and eradicates a chronic biofilm infection. Nature, 2013, 503, 365-370.	13.7	578
10	Principles and practice of electrospray ionizationâ€"mass spectrometry for large polypeptides and proteins. Mass Spectrometry Reviews, 1991, 10, 359-452.	2.8	565
11	Reversedâ€phase chromatography with multiple fraction concatenation strategy for proteome profiling of human MCF10A cells. Proteomics, 2011, 11, 2019-2026.	1.3	564
12	Comparative Analysis of Proteome and Transcriptome Variation in Mouse. PLoS Genetics, 2011, 7, e1001393.	1.5	548
13	Improved electrospray ionization interface for capillary zone electrophoresis-mass spectrometry. Analytical Chemistry, 1988, 60, 1948-1952.	3.2	525
14	Identification of Proteins in Human Cytomegalovirus (HCMV) Particles: the HCMV Proteome. Journal of Virology, 2004, 78, 10960-10966.	1.5	521
15	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	13.5	498
16	Fundamentals of Traveling Wave Ion Mobility Spectrometry. Analytical Chemistry, 2008, 80, 9689-9699.	3.2	434
17	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	13.5	430
18	An accurate mass tag strategy for quantitative and high-throughput proteome measurements. Proteomics, 2002, 2, 513-523.	1.3	423

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19	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. Cell, 2020, 182, 200-225.e35.	13.5	410
20	Proteomics by FTICR mass spectrometry: Top down and bottom up. Mass Spectrometry Reviews, 2005, 24, 168-200.	2.8	403
21	DAnTE: a statistical tool for quantitative analysis of -omics data. Bioinformatics, 2008, 24, 1556-1558.	1.8	397
22	Human PlasmaN-Glycoproteome Analysis by Immunoaffinity Subtraction, Hydrazide Chemistry, and Mass Spectrometry. Journal of Proteome Research, 2005, 4, 2070-2080.	1.8	394
23	Nanodroplet processing platform for deep and quantitative proteome profiling of 10â€"100 mammalian cells. Nature Communications, 2018, 9, 882.	5.8	384
24	Global analysis of the Deinococcus radiodurans proteome by using accurate mass tags. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11049-11054.	3.3	383
25	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatographyâ€"mass spectrometry. Nature Protocols, 2018, 13, 1632-1661.	5.5	377
26	Capillary zone electrophoresis-mass spectrometry using an electrospray ionization interface. Analytical Chemistry, 1988, 60, 436-441.	3.2	375
27	Normalization Approaches for Removing Systematic Biases Associated with Mass Spectrometry and Label-Free Proteomics. Journal of Proteome Research, 2006, 5, 277-286.	1.8	375
28	Temporal Proteome and Lipidome Profiles Reveal Hepatitis C Virus-Associated Reprogramming of Hepatocellular Metabolism and Bioenergetics. PLoS Pathogens, 2010, 6, e1000719.	2.1	361
29	An Interlaboratory Evaluation of Drift Tube Ion Mobilityâ€"Mass Spectrometry Collision Cross Section Measurements. Analytical Chemistry, 2017, 89, 9048-9055.	3.2	361
30	Mass spectrometry-based proteomics: existing capabilities and future directions. Chemical Society Reviews, 2012, 41, 3912.	18.7	351
31	Rapid expansion of supercritical fluid solutions: solute formation of powders, thin films, and fibers. Industrial & Engineering Chemistry Research, 1987, 26, 2298-2306.	1.8	348
32	Phosphoprotein Isotope-Coded Affinity Tag Approach for Isolating and Quantitating Phosphopeptides in Proteome-Wide Analyses. Analytical Chemistry, 2001, 73, 2578-2586.	3.2	348
33	Theory versuspractice: a review of ?willingness-to-pay? in health and health care. Health Economics (United Kingdom), 2001, 10, 39-52.	0.8	340
34	Proteogenomic and metabolomic characterization of human glioblastoma. Cancer Cell, 2021, 39, 509-528.e20.	7.7	327
35	Ischemia in Tumors Induces Early and Sustained Phosphorylation Changes in Stress Kinase Pathways but Does Not Affect Global Protein Levels. Molecular and Cellular Proteomics, 2014, 13, 1690-1704.	2.5	323
36	Probability-Based Evaluation of Peptide and Protein Identifications from Tandem Mass Spectrometry and SEQUEST Analysis:Â The Human Proteome. Journal of Proteome Research, 2005, 4, 53-62.	1.8	320

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37	A Perspective on the Maillard Reaction and the Analysis of Protein Glycation by Mass Spectrometry: Probing the Pathogenesis of Chronic Disease. Journal of Proteome Research, 2009, 8, 754-769.	1.8	319
38	Observations on the solubility of surfactants and related molecules in carbon dioxide at 50Â°C. Journal of Supercritical Fluids, 1990, 3, 51-65.	1.6	317
39	Advances and Challenges in Liquid Chromatography-Mass Spectrometry-based Proteomics Profiling for Clinical Applications. Molecular and Cellular Proteomics, 2006, 5, 1727-1744.	2.5	309
40	Quantitative Analysis of Bacterial and Mammalian Proteomes Using a Combination of Cysteine Affinity Tags and 15N-Metabolic Labeling. Analytical Chemistry, 2001, 73, 2132-2139.	3.2	296
41	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	13.5	296
42	Transport functions dominate the SAR11 metaproteome at low-nutrient extremes in the Sargasso Sea. ISME Journal, 2009, 3, 93-105.	4.4	295
43	The challenge of antimicrobial resistance: What economics can contribute. Science, 2019, 364, .	6.0	292
44	Advances in proteomics data analysis and display using an accurate mass and time tag approach. Mass Spectrometry Reviews, 2006, 25, 450-482.	2.8	291
45	Ultra-High-Efficiency Strong Cation Exchange LC/RPLC/MS/MS for High Dynamic Range Characterization of the Human Plasma Proteome. Analytical Chemistry, 2004, 76, 1134-1144.	3.2	290
46	Utilizing Human Blood Plasma for Proteomic Biomarker Discoveryâ€. Journal of Proteome Research, 2005, 4, 1073-1085.	1.8	288
47	Use of Artificial Neural Networks for the Accurate Prediction of Peptide Liquid Chromatography Elution Times in Proteome Analyses. Analytical Chemistry, 2003, 75, 1039-1048.	3.2	285
48	Solvent-induced conformational changes of polypeptides probed by electrospray-ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 1991, 5, 101-105.	0.7	279
49	Primary sequence information from intact proteins by electrospray ionization tandem mass spectrometry. Science, 1990, 248, 201-204.	6.0	278
50	Tandem mass spectrometry identifies many mouse brain <i>O</i> -GlcNAcylated proteins including EGF domain-specific <i>O</i> -GlcNAc transferase targets. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7280-7285.	3.3	275
51	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31.	13.5	273
52	Effect of reducing disulfide-containing proteins on electrospray ionization mass spectra. Analytical Chemistry, 1990, 62, 693-698.	3.2	272
53	Observation of the Noncovalent Quaternary Associations of Proteins by Electrospray Ionization Mass Spectrometry. Journal of the American Chemical Society, 1994, 116, 5271-5278.	6.6	270
54	Utility of Accurate Mass Tags for Proteome-Wide Protein Identification. Analytical Chemistry, 2000, 72, 3349-3354.	3.2	269

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55	High-Efficiency Nanoscale Liquid Chromatography Coupled On-Line with Mass Spectrometry Using Nanoelectrospray Ionization for Proteomics. Analytical Chemistry, 2002, 74, 4235-4249.	3.2	267
56	Synechococcus elongatus UTEX 2973, a fast growing cyanobacterial chassis for biosynthesis using light and CO2. Scientific Reports, 2015, 5, 8132.	1.6	265
57	The observation of non-covalent interactions in solution by electrospray ionization mass spectrometry: Promise, pitfalls and prognosis. Biological Mass Spectrometry, 1993, 22, 493-501.	0.5	263
58	High-pH reversed-phase chromatography with fraction concatenation for 2D proteomic analysis. Expert Review of Proteomics, 2012, 9, 129-134.	1.3	260
59	Normalization and missing value imputation for label-free LC-MS analysis. BMC Bioinformatics, 2012, 13, S5.	1.2	259
60	Tandem mass spectrometry of very large molecules. 2. Dissociation of multiply charged proline-containing proteins from electrospray ionization. Analytical Chemistry, 1993, 65, 425-438.	3.2	252
61	An IMSâˆ'IMS Analogue of MSâˆ'MS. Analytical Chemistry, 2006, 78, 4161-4174.	3.2	251
62	Mechanisms of Severe Acute Respiratory Syndrome Coronavirus-Induced Acute Lung Injury. MBio, 2013, 4, .	1.8	251
63	Peptide and protein analysis by electrospray ionization-mass spectrometry and capillary electrophoresis-mass spectrometry. Analytical Biochemistry, 1989, 179, 404-412.	1.1	247
64	Pathogenic Influenza Viruses and Coronaviruses Utilize Similar and Contrasting Approaches To Control Interferon-Stimulated Gene Responses. MBio, 2014, 5, e01174-14.	1.8	246
65	High-Sensitivity Ion Mobility Spectrometry/Mass Spectrometry Using Electrodynamic Ion Funnel Interfaces. Analytical Chemistry, 2005, 77, 3330-3339.	3.2	244
66	Connecting Genomic Alterations to Cancer Biology with Proteomics: The NCI Clinical Proteomic Tumor Analysis Consortium. Cancer Discovery, 2013, 3, 1108-1112.	7.7	243
67	Extraction of metal ions from liquid and solid materials by supercritical carbon dioxide. Analytical Chemistry, 1992, 64, 2875-2878.	3.2	240
68	Probing Proteomes Using Capillary Isoelectric Focusing-Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 1999, 71, 2076-2084.	3.2	239
69	A novel ion funnel for focusing ions at elevated pressure using electrospray ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 1997, 11, 1813-1817.	0.7	238
70	In silico method for modelling metabolism and gene product expression at genome scale. Nature Communications, 2012, 3, 929.	5.8	238
71	Collisional activation and collision-activated dissociation of large multiply charged polypeptides and proteins produced by electrospray ionization. Journal of the American Society for Mass Spectrometry, 1990, 1, 53-65.	1.2	236
72	Binding MOAD (Mother Of All Databases). Proteins: Structure, Function and Bioinformatics, 2005, 60, 333-340.	1.5	236

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73	Proteogenomic characterization of pancreatic ductal adenocarcinoma. Cell, 2021, 184, 5031-5052.e26.	13.5	236
74	Chemically Etched Open Tubular and Monolithic Emitters for Nanoelectrospray Ionization Mass Spectrometry. Analytical Chemistry, 2006, 78, 7796-7801.	3.2	233
75	Charge competition and the linear dynamic range of detection in electrospray ionization mass spectrometry. Journal of the American Society for Mass Spectrometry, 2004, 15, 1416-1423.	1.2	230
76	Clustering Millions of Tandem Mass Spectra. Journal of Proteome Research, 2008, 7, 113-122.	1.8	230
77	Collisional effects on the charge distribution of ions from large molecules, formed by electrospray-ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 1988, 2, 207-210.	0.7	227
78	Automated 20 kpsi RPLC-MS and MS/MS with Chromatographic Peak Capacities of 1000â˜'1500 and Capabilities in Proteomics and Metabolomics. Analytical Chemistry, 2005, 77, 3090-3100.	3.2	227
79	Enrichment of Integral Membrane Proteins for Proteomic Analysis Using Liquid Chromatographyâ˜'Tandem Mass Spectrometry. Journal of Proteome Research, 2002, 1, 351-360.	1.8	226
80	An Ion Funnel Interface for Improved Ion Focusing and Sensitivity Using Electrospray Ionization Mass Spectrometry. Analytical Chemistry, 1998, 70, 4111-4119.	3.2	223
81	Statistical Characterization of the Charge State and Residue Dependence of Low-Energy CID Peptide Dissociation Patterns. Analytical Chemistry, 2005, 77, 5800-5813.	3.2	219
82	Does Trypsin Cut Before Proline?. Journal of Proteome Research, 2008, 7, 300-305.	1.8	217
83	The ion funnel: Theory, implementations, and applications. Mass Spectrometry Reviews, 2010, 29, 294-312.	2.8	217
84	Review, Evaluation, and Discussion of the Challenges of Missing Value Imputation for Mass Spectrometry-Based Label-Free Global Proteomics. Journal of Proteome Research, 2015, 14, 1993-2001.	1.8	217
85	Packed Capillary Reversed-Phase Liquid Chromatography with High-Performance Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry for Proteomics. Analytical Chemistry, 2001, 73, 1766-1775.	3.2	214
86	Antibody-free, targeted mass-spectrometric approach for quantification of proteins at low picogram per milliliter levels in human plasma/serum. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15395-15400.	3.3	211
87	Ionization and transmission efficiency in an electrospray ionizationâ€"mass spectrometry interface. Journal of the American Society for Mass Spectrometry, 2007, 18, 1582-1590.	1.2	210
88	High Throughput Proteome-Wide Precision Measurements of Protein Expression Using Mass Spectrometry. Journal of the American Chemical Society, 1999, 121, 7949-7950.	6.6	209
89	Precautionary Behavior in Response to Perceived Threat of Pandemic Influenza. Emerging Infectious Diseases, 2007, 13, 1307-1313.	2.0	209
90	Tandem mass spectrometry of very large molecules: serum albumin sequence information from multiply charged ions formed by electrospray ionization. Analytical Chemistry, 1991, 63, 2488-2499.	3.2	198

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91	Evaluation of Multiprotein Immunoaffinity Subtraction for Plasma Proteomics and Candidate Biomarker Discovery Using Mass Spectrometry. Molecular and Cellular Proteomics, 2006, 5, 2167-2174.	2.5	197
92	Uncovering biologically significant lipid isomers with liquid chromatography, ion mobility spectrometry and mass spectrometry. Analyst, The, 2016, 141, 1649-1659.	1.7	196
93	Generation of Multiple Electrosprays Using Microfabricated Emitter Arrays for Improved Mass Spectrometric Sensitivity. Analytical Chemistry, 2001, 73, 1658-1663.	3.2	195
94	VIPER: an advanced software package to support high-throughput LC-MS peptide identification. Bioinformatics, 2007, 23, 2021-2023.	1.8	194
95	Decon2LS: An open-source software package for automated processing and visualization of high resolution mass spectrometry data. BMC Bioinformatics, 2009, 10, 87.	1.2	190
96	Using Electrospray Ionization FTICR Mass Spectrometry To Study Competitive Binding of Inhibitors to Carbonic Anhydrase. Journal of the American Chemical Society, 1995, 117, 8859-8860.	6.6	189
97	High-Throughput Proteomics Using High-Efficiency Multiple-Capillary Liquid Chromatography with On-Line High-Performance ESI FTICR Mass Spectrometry. Analytical Chemistry, 2001, 73, 3011-3021.	3.2	189
98	Characterization of the human blood plasma proteome. Proteomics, 2005, 5, 4034-4045.	1.3	189
99	Ultrasensitive Proteomics Using High-Efficiency On-Line Micro-SPE-NanoLC-NanoESI MS and MS/MS. Analytical Chemistry, 2004, 76, 144-154.	3.2	188
100	High Throughput Quantitative Analysis of Serum Proteins Using Glycopeptide Capture and Liquid Chromatography Mass Spectrometry. Molecular and Cellular Proteomics, 2005, 4, 144-155.	2.5	187
101	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometryâ€"Based Assays. Clinical Chemistry, 2016, 62, 48-69.	1.5	187
102	Solubility of fluorinated metal diethyldithiocarbamates in Supercritical carbon dioxide. Journal of Supercritical Fluids, 1991, 4, 194-198.	1.6	186
103	Advancing the sensitivity of selected reaction monitoringâ€based targeted quantitative proteomics. Proteomics, 2012, 12, 1074-1092.	1.3	186
104	Proteomic Analysis of Single Mammalian Cells Enabled by Microfluidic Nanodroplet Sample Preparation and Ultrasensitive NanoLCâ€MS. Angewandte Chemie - International Edition, 2018, 57, 12370-12374.	7.2	186
105	New mass spectrometric methods for the study of noncovalent associations of biopolymers. Chemical Society Reviews, 1997, 26, 191.	18.7	183
106	Design and Implementation of a New Electrodynamic Ion Funnel. Analytical Chemistry, 2000, 72, 2247-2255.	3.2	183
107	Enhanced Detection of Low Abundance Human Plasma Proteins Using a Tandem IgY12-SuperMix Immunoaffinity Separation Strategy. Molecular and Cellular Proteomics, 2008, 7, 1963-1973.	2.5	183
108	Establishing the Proteome of Normal Human Cerebrospinal Fluid. PLoS ONE, 2010, 5, e10980.	1.1	183

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109	Stable isotope-coded proteomic mass spectrometry. Current Opinion in Biotechnology, 2003, 14, 101-109.	3.3	182
110	Integrative Analysis of the Mitochondrial Proteome in Yeast. PLoS Biology, 2004, 2, e160.	2.6	181
111	Combining capillary electrophoresis with mass spectrometry for applications in proteomics. Electrophoresis, 2005, 26, 1291-1305.	1.3	180
112	SerpinB1 Promotes Pancreatic Î² Cell Proliferation. Cell Metabolism, 2016, 23, 194-205.	7.2	177
113	Integrated Proteogenomic Characterization across Major Histological Types of Pediatric Brain Cancer. Cell, 2020, 183, 1962-1985.e31.	13.5	177
114	Direct mass spectrometric analysis of intact proteins of the yeast large ribosomal subunit using capillary LC/FTICR. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 5942-5947.	3.3	176
115	Sheathless capillary electrophoresis-electrospray ionization mass spectrometry using 10 Î¼m I.D. capillaries: Analyses of tryptic digests of cytochrome c. Journal of Chromatography A, 1994, 659, 217-222.	1.8	175
116	Whole proteome analysis of post-translational modifications: Applications of mass-spectrometry for proteogenomic annotation. Genome Research, 2007, 17, 1362-1377.	2.4	175
117	Advances in targeted proteomics and applications to biomedical research. Proteomics, 2016, 16, 2160-2182.	1.3	175
118	Probing qualitative conformation differences of multiply protonated gas-phase proteins via hydrogen/deuterium isotopic exchange with water-d2. Journal of the American Chemical Society, 1992, 114, 5897-5898.	6.6	174
119	Small volume and low flow-rate electrospray lonization mass spectrometry of aqueous samples. Rapid Communications in Mass Spectrometry, 1993, 7, 1017-1021.	0.7	172
120	Liquid Chromatography-Mass Spectrometry-based Quantitative Proteomics. Journal of Biological Chemistry, 2011, 286, 25443-25449.	1.6	171
121	A proteogenomic portrait of lung squamous cell carcinoma. Cell, 2021, 184, 4348-4371.e40.	13.5	170
122	Clinical microfluidics for neutrophil genomics and proteomics. Nature Medicine, 2010, 16, 1042-1047.	15.2	168
123	Observation of a small oligonucleotide duplex by electrospray ionization mass spectrometry. Journal of the American Chemical Society, 1993, 115, 803-804.	6.6	167
124	MPLEx: a Robust and Universal Protocol for Single-Sample Integrative Proteomic, Metabolomic, and Lipidomic Analyses. MSystems, 2016, 1, .	1.7	166
125	Microfabricated isoelectric focusing device for direct electrospray ionization-mass spectrometry. Electrophoresis, 2000, 21, 191-197.	1.3	165
126	Pyroptosis by caspase11/4â€gasderminâ€D pathway in alcoholic hepatitis in mice and patients. Hepatology, 2018, 67, 1737-1753.	3.6	165

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127	Proteomics based on high-efficiency capillary separations. Electrophoresis, 2002, 23, 3106-3124.	1.3	164
128	Improved Peptide Elution Time Prediction for Reversed-Phase Liquid Chromatography-MS by Incorporating Peptide Sequence Information. Analytical Chemistry, 2006, 78, 5026-5039.	3.2	163
129	A Microfabricated Dialysis Device for Sample Cleanup in Electrospray Ionization Mass Spectrometry. Analytical Chemistry, 1998, 70, 3553-3556.	3.2	162
130	Sources of Technical Variability in Quantitative LCâ€“MS Proteomics: Human Brain Tissue Sample Analysis. Journal of Proteome Research, 2013, 12, 2128-2137.	1.8	162
131	Serpentine Ultralong Path with Extended Routing (SUPER) High Resolution Traveling Wave Ion Mobility-MS using Structures for Lossless Ion Manipulations. Analytical Chemistry, 2017, 89, 4628-4634.	3.2	162
132	Development and Evaluation of a Micro- and Nanoscale Proteomic Sample Preparation Method. Journal of Proteome Research, 2005, 4, 2397-2403.	1.8	161
133	The trace element chemistry of coal during combustion and the emissions from coal-fired plants. Progress in Energy and Combustion Science, 1980, 6, 53-119.	15.8	160
134	Zeptomole-Sensitivity Electrospray Ionizationâ˘'Fourier Transform Ion Cyclotron Resonance Mass Spectrometry of Proteins. Analytical Chemistry, 2000, 72, 2271-2279.	3.2	160
135	Phosphoprotein Isotope-Coded Affinity Tags:Â Application to the Enrichment and Identification of Low-Abundance Phosphoproteins. Analytical Chemistry, 2002, 74, 607-616.	3.2	160
136	High-Resolution Field Asymmetric Waveform Ion Mobility Spectrometry Using New Planar Geometry Analyzers. Analytical Chemistry, 2006, 78, 3706-3714.	3.2	159
137	The economy-wide impact of pandemic influenza on the UK: a computable general equilibrium modelling experiment. BMJ: British Medical Journal, 2009, 339, b4571-b4571.	2.4	159
138	An Integrated Microfabricated Device for Dual Microdialysis and On-Line ESI-Ion Trap Mass Spectrometry for Analysis of Complex Biological Samples. Analytical Chemistry, 1999, 71, 1485-1490.	3.2	156
139	Quantitative Proteome Analysis of Human Plasma following in Vivo Lipopolysaccharide Administration Using 16O/18O Labeling and the Accurate Mass and Time Tag Approach. Molecular and Cellular Proteomics, 2005, 4, 700-709.	2.5	156
140	What errors do peer reviewers detect, and does training improve their ability to detect them?. Journal of the Royal Society of Medicine, 2008, 101, 507-514.	1.1	156
141	A structural examination and collision cross section database for over 500 metabolites and xenobiotics using drift tube ion mobility spectrometry. Chemical Science, 2017, 8, 7724-7736.	3.7	156
142	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
143	Proteomic analyses using an accurate mass and time tag strategy. BioTechniques, 2004, 37, 621-639.	0.8	155
144	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.	3.2	155

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145	Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008, 26, 164-167.	9.4	155
146	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.	1.1	154
147	Trade in health-related services. Lancet, The, 2009, 373, 593-601.	6.3	154
148	Analytical supercritical fluid extraction of adsorbent materials. Analytical Chemistry, 1987, 59, 38-44.	3.2	153
149	Proteome analyses using accurate mass and elution time peptide tags with capillary LC time-of-flight mass spectrometry. Journal of the American Society for Mass Spectrometry, 2003, 14, 980-991.	1.2	152
150	Head-to-Head Comparison of Serum Fractionation Techniques. Journal of Proteome Research, 2007, 6, 828-836.	1.8	152
151	Ultrasensitive and Quantitative Analyses from Combined Separationsâˆ’Mass Spectrometry for the Characterization of Proteomes. Accounts of Chemical Research, 2004, 37, 269-278.	7.6	151
152	Characterization of supercritical fluid solvents using solvatochromic shifts. The Journal of Physical Chemistry, 1986, 90, 3022-3026.	2.9	150
153	Preservation of non-covalent associations in electrospray ionization mass spectrometry: Multiply charged polypeptide and protein dimers. Organic Mass Spectrometry, 1992, 27, 811-821.	1.3	150
154	Screening Derivatized Peptide Libraries for Tight Binding Inhibitors to Carbonic Anhydrase II by Electrospray Ionization-Mass Spectrometry. Journal of Medicinal Chemistry, 1996, 39, 1949-1955.	2.9	150
155	CPTAC Assay Portal: a repository of targeted proteomic assays. Nature Methods, 2014, 11, 703-704.	9.0	150
156	Creating nanocavities of tunable sizes: Hollow helices. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11583-11588.	3.3	149
157	A statistical framework for protein quantitation in bottom-up MS-based proteomics. Bioinformatics, 2009, 25, 2028-2034.	1.8	149
158	Construction of the contingent valuation market in health care:a critical assessment. Health Economics (United Kingdom), 2003, 12, 609-628.	0.8	148
159	Enrichment and Analysis of Nonenzymatically Glycated Peptides:Â Boronate Affinity Chromatography Coupled with Electron-Transfer Dissociation Mass Spectrometry. Journal of Proteome Research, 2007, 6, 2323-2330.	1.8	147
160	Trapping, Detection, and Mass Determination of Coliphage T4 DNA Ions by Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 1995, 67, 1159-1163.	3.2	146
161	Transition-Metal-Mediated Rational Design and Self-Assembly of Chiral, Nanoscale Supramolecular Polyhedra with UniqueTSymmetryâ€. Organometallics, 1997, 16, 3094-3096.	1.1	146
162	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. Molecular and Cellular Proteomics, 2015, 14, 2301-2307.	2.5	146

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163	Free 25-Hydroxyvitamin D: Impact of Vitamin D Binding Protein Assays on Racial-Genotypic Associations. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 2226-2234.	1.8	145
164	The genome of <i>Cyanothece</i> 51142, a unicellular diazotrophic cyanobacterium important in the marine nitrogen cycle. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15094-15099.	3.3	144
165	Trapping, detection and reaction of very large single molecular ions by mass spectrometry. Nature, 1994, 369, 137-139.	13.7	143
166	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. Bioinformatics, 2008, 24, 1021-1023.	1.8	143
167	Proteome analysis using selective incorporation of isotopically labeled amino acids. Journal of the American Society for Mass Spectrometry, 2000, 11, 78-82.	1.2	142
168	High-Throughput Comparative Proteome Analysis Using a Quantitative Cysteinyl-peptide Enrichment Technology. Analytical Chemistry, 2004, 76, 5345-5353.	3.2	142
169	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. Molecular and Cellular Proteomics, 2006, 5, 1899-1913.	2.5	142
170	Binding MOAD, a high-quality protein ligand database. Nucleic Acids Research, 2007, 36, D674-D678.	6.5	142
171	Modelâ€driven multiâ€omic data analysis elucidates metabolic immunomodulators of macrophage activation. Molecular Systems Biology, 2012, 8, 558.	3.2	142
172	MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1012-E1021.	3.3	142
173	Capillary Electrophoresis/Mass Spectrometry. Analytical Chemistry, 1993, 65, 574A-584A.	3.2	141
174	Perspective:Â A Program to Improve Protein Biomarker Discovery for Cancerâ€. Journal of Proteome Research, 2005, 4, 1104-1109.	1.8	141
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