Jimmy K Eng

List of Publications by Year
in descending order

157	35,165	10070	9605
papers	citations	75	147
		h-index	g-index
161	161	161	34174
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	In Vivo Cross-Linking MS Reveals Conservation in OmpA Linkage to Different Classes of Î²-Lactamase Enzymes. Journal of the American Society for Mass Spectrometry, 2020, 31, 190-195.	1.2	13
2	Systemic Proteome Alterations Linked to Early Stage Pancreatic Cancer in Diabetic Patients. Cancers, 2020, 12, 1534.	1.7	18
3	Full-Featured, Real-Time Database Searching Platform Enables Fast and Accurate Multiplexed Quantitative Proteomics. Journal of Proteome Research, 2020, 19, 2026-2034.	1.8	171
4	Extending Comet for Global Amino Acid Variant and Postâ€Translational Modification Analysis Using the PSI Extended FASTA Format. Proteomics, 2020, 20, e1900362.	1.3	18
5	Predictive proteomic signatures for response of pancreatic cancer patients receiving chemotherapy. Clinical Proteomics, 2019, 16, 31.	1.1	16
6	In Vivo Proteome of *Pseudomonas aeruginosa* in Airways of Cystic Fibrosis Patients. Journal of Proteome Research, 2019, 18, 2601-2612.	1.8	23
7	Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 2019, 18, 2686-2692.	1.8	22
8	A Tandem Mass Spectrometry Sequence Database Search Method for Identification of O-Fucosylated Proteins by Mass Spectrometry. Journal of Proteome Research, 2019, 18, 652-663.	1.8	16
9	Tools for 3D Interactome Visualization. Journal of Proteome Research, 2019, 18, 753-758.	1.8	26
10	Mango: A General Tool for Collision Induced Dissociation-Cleavable Cross-Linked Peptide Identification. Analytical Chemistry, 2018, 90, 6028-6034.	3.2	39
11	Sipros Ensemble improves database searching and filtering for complex metaproteomics. Bioinformatics, 2018, 34, 795-802.	1.8	35
12	Bifunctional Immunity Proteins Protect Bacteria against FtsZ-Targeting ADP-Ribosylating Toxins. Cell, 2018, 175, 1380-1392.e14.	13.5	109
13	Quantitative Proteomics Based on Optimized Data-Independent Acquisition in Plasma Analysis. Journal of Proteome Research, 2017, 16, 665-676.	1.8	39
14	Extracellular Matrix Proteins Mediate HIV-1 gp120 Interactions with Î±$_4$Î²$_7$. Journal of Virology, 2017, 91, .	1.5	8
15	Large-Scale and Targeted Quantitative Cross-Linking MS Using Isotope-Labeled Protein Interaction Reporter (PIR) Cross-Linkers. Journal of Proteome Research, 2017, 16, 720-727.	1.8	38
16	XLinkDB 2.0: integrated, large-scale structural analysis of protein crosslinking data. Bioinformatics, 2016, 32, 2716-2718.	1.8	54
17	Spectral Library Searching To Identify Cross-Linked Peptides. Journal of Proteome Research, 2016, 15, 1725-1731.	1.8	12
18	In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in Acinetobacter baumannii strain AB5075. Nature Communications, 2016, 7, 13414.	5.8	81

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19	In Vivo Conformational Dynamics of Hsp90 and Its Interactors. Cell Chemical Biology, 2016, 23, 716-726.	2.5	73
20	Visualization of Host-Polerovirus Interaction Topologies Using Protein Interaction Reporter Technology. Journal of Virology, 2016, 90, 1973-1987.	1.5	38
21	A General Method for Targeted Quantitative Cross-Linking Mass Spectrometry. PLoS ONE, 2016, 11, e0167547.	1.1	46
22	Research Resource: Androgen Receptor Activity Is Regulated Through the Mobilization of Cell Surface Receptor Networks. Molecular Endocrinology, 2015, 29, 1195-1218.	3.7	8
23	Quantitative interactome analysis reveals a chemoresistant edgotype. Nature Communications, 2015, 6, 7928.	5.8	77
24	Dynamic Proteome Response of Pseudomonas aeruginosa to Tobramycin Antibiotic Treatment. Molecular and Cellular Proteomics, 2015, 14, 2126-2137.	2.5	37
25	A Deeper Look into Cometâ€"Implementation and Features. Journal of the American Society for Mass Spectrometry, 2015, 26, 1865-1874.	1.2	175
26	Probing the Protein Interaction Network of Pseudomonas aeruginosa Cells by Chemical Cross-Linking Mass Spectrometry. Structure, 2015, 23, 762-773.	1.6	71
27	Crux: Rapid Open Source Protein Tandem Mass Spectrometry Analysis. Journal of Proteome Research, 2014, 13, 4488-4491.	1.8	130
28	<i>In Vivo</i> Protein Interaction Network Identified with a Novel Real-Time Cross-Linked Peptide Identification Strategy. Journal of Proteome Research, 2013, 12, 1569-1579.	1.8	130
29	Comet: An openâ€source <scp>MS</scp>/<scp>MS</scp> sequence database search tool. Proteomics, 2013, 13, 22-24.	1.3	1,175
30	XLink-DB: Database and Software Tools for Storing and Visualizing Protein Interaction Topology Data. Journal of Proteome Research, 2013, 12, 1989-1995.	1.8	50
31	Protein Interactions, Post-translational Modifications and Topologies in Human Cells. Molecular and Cellular Proteomics, 2013, 12, 1451-1467.	2.5	102
32	Systematic measurement of transcription factor-DNA interactions by targeted mass spectrometry identifies candidate gene regulatory proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3645-3650.	3.3	31
33	Protein Kinase PKN1 Represses Wnt/Î²-Catenin Signaling in Human Melanoma Cells. Journal of Biological Chemistry, 2013, 288, 34658-34670.	1.6	29
34	A Mass Spectrometry Proteomics Data Management Platform. Molecular and Cellular Proteomics, 2012, 11, 824-831.	2.5	31
35	A likelihood-based scoring method for peptide identification using mass spectrometry. Annals of Applied Statistics, 2012, 6, .	0.5	4
36	<i>De Novo</i> Correction of Mass Measurement Error in Low Resolution Tandem MS Spectra for Shotgun Proteomics. Journal of the American Society for Mass Spectrometry, 2012, 23, 2075-2082.	1.2	10

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37	In VivoApplication of Photocleavable Protein Interaction Reporter Technology. Journal of Proteome Research, 2012, 11, 1027-1041.	1.8	29
38	Accurate Peptide Fragment Mass Analysis: Multiplexed Peptide Identification and Quantification. Journal of Proteome Research, 2012, 11, 1621-1632.	1.8	86
39	Cross-linking Measurements of the <i>Potato leafroll virus</i> Reveal Protein Interaction Topologies Required for Virion Stability, Aphid Transmission, and Virus–Plant Interactions. Journal of Proteome Research, 2012, 11, 2968-2981.	1.8	62
40	Sites of ubiquitin attachment in <i>Saccharomyces cerevisiae</i>. Proteomics, 2012, 12, 236-240.	1.3	43
41	iProphet: Multi-level Integrative Analysis of Shotgun Proteomic Data Improves Peptide and Protein Identification Rates and Error Estimates. Molecular and Cellular Proteomics, 2011, 10, M111.007690.	2.5	490
42	Fast Parallel Tandem Mass Spectral Library Searching Using GPU Hardware Acceleration. Journal of Proteome Research, 2011, 10, 2882-2888.	1.8	47
43	The Fasted/Fed Mouse Metabolic Acetylome: N6-Acetylation Differences Suggest Acetylation Coordinates Organ-Specific Fuel Switching. Journal of Proteome Research, 2011, 10, 4134-4149.	1.8	68
44	A Face in the Crowd: Recognizing Peptides Through Database Search. Molecular and Cellular Proteomics, 2011, 10, R111.009522.	2.5	147
45	Microdialysis Combined with Proteomics for Protein Identification in Breast Tumor Microenvironment In Vivo. Cancer Microenvironment, 2011, 4, 61-71.	3.1	13
46	Cross-linking Measurements of In Vivo Protein Complex Topologies. Molecular and Cellular Proteomics, 2011, 10, M110.006841.	2.5	81
47	Installation and Use of LabKey Server for Proteomics. Current Protocols in Bioinformatics, 2011, 36, Unit 13.5..	25.8	3
48	Androgen-Sensitive Microsomal Signaling Networks Coupled to the Proliferation and Differentiation of Human Prostate Cancer Cells. Genes and Cancer, 2011, 2, 956-978.	0.6	12
49	Index-ion Triggered MS2 Ion Quantification: A Novel Proteomics Approach for Reproducible Detection and Quantification of Targeted Proteins in Complex Mixtures. Molecular and Cellular Proteomics, 2011, 10, M110.005611.	2.5	26
50	A guided tour of the Trans–Proteomic Pipeline. Proteomics, 2010, 10, 1150-1159.	1.3	710
51	Trans–Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. Proteomics, 2010, 10, 1190-1195.	1.3	39
52	Quantitative analysis of the secretome of TGFâ€Î² signalingâ€deficient mammary fibroblasts. Proteomics, 2010, 10, 2458-2470.	1.3	37
53	Differential Protein Expression Profiles in Estrogen Receptor-Positive and -Negative Breast Cancer Tissues Using Label-Free Quantitative Proteomics. Genes and Cancer, 2010, 1, 251-271.	0.6	38
54	ChromEval: A Software Application for the Rapid Evaluation of HPLC System Performance in Proteomic Applications. Analytical Chemistry, 2010, 82, 5060-5068.	3.2	1

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55	A Photocleavable and Mass Spectrometry Identifiable Cross-Linker for Protein Interaction Studies. Analytical Chemistry, 2010, 82, 3556-3566.	3.2	49
56	Precursor Charge State Prediction for Electron Transfer Dissociation Tandem Mass Spectra. Journal of Proteome Research, 2010, 9, 5438-5444.	1.8	9
57	Characterizing the connectivity of poly-ubiquitin chains by selected reaction monitoring mass spectrometry. Molecular BioSystems, 2010, 6, 2004.	2.9	35
58	Proteomics data repositories. Proteomics, 2009, 9, 4653-4663.	1.3	39
59	Quantitative Phosphoproteomic Analysis of T Cell Receptor Signaling Reveals System-Wide Modulation of Protein-Protein Interactions. Science Signaling, 2009, 2, ra46.	1.6	330
60	Proteomic Analyses Using <i>Grifola frondosa</i> Metalloendoprotease Lys-N. Journal of Proteome Research, 2009, 8, 1415-1422.	1.8	29
61	Analysis of RP-HPLC Loading Conditions for Maximizing Peptide Identifications in Shotgun Proteomics. Journal of Proteome Research, 2009, 8, 4161-4168.	1.8	12
62	MaRiMba: A Software Application for Spectral Library-Based MRM Transition List Assembly. Journal of Proteome Research, 2009, 8, 4396-4405.	1.8	80
63	Building consensus spectral libraries for peptide identification in proteomics. Nature Methods, 2008, 5, 873-875.	9.0	255
64	A Fast SEQUEST Cross Correlation Algorithm. Journal of Proteome Research, 2008, 7, 4598-4602.	1.8	214
65	The Standard Protein Mix Database: A Diverse Data Set To Assist in the Production of Improved Peptide and Protein Identification Software Tools. Journal of Proteome Research, 2008, 7, 96-103.	1.8	156
66	Quantification of the Compositional Information Provided by Immonium Ions on a Quadrupole-Time-of-Flight Mass Spectrometer. Analytical Chemistry, 2008, 80, 5596-5606.	3.2	40
67	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. Molecular and Cellular Proteomics, 2008, 7, 1389-1396.	2.5	472
68	MRMer, an Interactive Open Source and Cross-platform System for Data Extraction and Visualization of Multiple Reaction Monitoring Experiments. Molecular and Cellular Proteomics, 2008, 7, 2270-2278.	2.5	80
69	Global Survey of Human T Leukemic Cells by Integrating Proteomics and Transcriptomics Profiling. Molecular and Cellular Proteomics, 2007, 6, 1343-1353.	2.5	31
70	Identification of Putative Androgen Receptor Interaction Protein Modules. Molecular and Cellular Proteomics, 2007, 6, 252-271.	2.5	51
71	Proteomics Analysis of Human Coronary Atherosclerotic Plaque. Molecular and Cellular Proteomics, 2007, 6, 1088-1102.	2.5	149
72	Installation and Use of the Computational Proteomics Analysis System (CPAS). , 2007, Chapter 13, Unit 13.5.		2

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73	Integrated Pipeline for Mass Spectrometry-Based Discovery and Confirmation of Biomarkers Demonstrated in a Mouse Model of Breast Cancer. Journal of Proteome Research, 2007, 6, 3962-3975.	1.8	171
74	An integrated chemical, mass spectrometric and computational strategy for (quantitative) phosphoproteomics: application to Drosophila melanogaster Kc167 cells. Molecular BioSystems, 2007, 3, 275.	2.9	76
75	Contribution of Protein Fractionation to Depth of Analysis of the Serum and Plasma Proteomes. Journal of Proteome Research, 2007, 6, 3558-3565.	1.8	153
76	A Platform for Accurate Mass and Time Analyses of Mass Spectrometry Data. Journal of Proteome Research, 2007, 6, 2685-2694.	1.8	76
77	Development and validation of a spectral library searching method for peptide identification from MS/MS. Proteomics, 2007, 7, 655-667.	1.3	487
78	A combined dataset of human cerebrospinal fluid proteins identified by multi-dimensional chromatography and tandem mass spectrometry. Proteomics, 2007, 7, 469-473.	1.3	111
79	Direct cancer tissue proteomics: a method to identify candidate cancer biomarkers from formalin-fixed paraffin-embedded archival tissues. Oncogene, 2007, 26, 65-76.	2.6	129
80	Head-to-Head Comparison of Serum Fractionation Techniques. Journal of Proteome Research, 2007, 6, 828-836.	1.8	152
81	Analysis of the Saccharomyces cerevisiae proteome with PeptideAtlas. Genome Biology, 2006, 7, R106.	13.9	60
82	UniPep--a database for human N-linked glycosites: a resource for biomarker discovery. Genome Biology, 2006, 7, R73.	13.9	101
83	Characterization of Proteome of Human Cerebrospinal Fluid. International Review of Neurobiology, 2006, 73, 29-98.	0.9	28
84	Computational Proteomics Analysis System (CPAS):Â An Extensible, Open-Source Analytic System for Evaluating and Publishing Proteomic Data and High Throughput Biological ExperimentsJ. Proteome Res.2006,5, 112â˜˜121.. Journal of Proteome Research, 2006, 5, 1024-1024.	1.8	4
85	Computational Proteomics Analysis System (CPAS):â€‰ An Extensible, Open-Source Analytic System for Evaluating and Publishing Proteomic Data and High Throughput Biological Experiments. Journal of Proteome Research, 2006, 5, 112-121.	1.8	204
86	Quality Control Metrics for LCâ˜˜MS Feature Detection Tools Demonstrated onSaccharomycescerevisiaeProteomic Profiles. Journal of Proteome Research, 2006, 5, 1527-1534.	1.8	31
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88	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. , 2006, , 1-35.		4
89	Challenges in deriving high-confidence protein identifications from data gathered by a HUPO plasma proteome collaborative study. Nature Biotechnology, 2006, 24, 333-338.	9.4	309
90	General framework for developing and evaluating database scoring algorithms using the TANDEM search engine. Bioinformatics, 2006, 22, 2830-2832.	1.8	209

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91	A suite of algorithms for the comprehensive analysis of complex protein mixtures using high-resolution LC-MS. Bioinformatics, 2006, 22, 1902-1909.	1.8	250
92	The PeptideAtlas project. Nucleic Acids Research, 2006, 34, D655-D658.	6.5	733
93	Systematic Characterization of Nuclear Proteome during Apoptosis. Molecular and Cellular Proteomics, 2006, 5, 1131-1145.	2.5	62
94	Quantitative proteomics of cerebrospinal fluid from patients with Alzheimer disease. Journal of Alzheimer's Disease, 2005, 7, 125-133.	1.2	160
95	Protein Identification Using TurboSEQUEST. Current Protocols in Bioinformatics, 2005, 10, Unit 13.3.	25.8	18
96	Tutorial on tandem mass spectrometry database searching. , 2005, , .		0
97	Quantitative phosphoproteome analysis using a dendrimer conjugation chemistry and tandem mass spectrometry. Nature Methods, 2005, 2, 591-598.	9.0	302
98	Proteomic analysis of synaptosomes using isotope-coded affinity tags and mass spectrometry. Proteomics, 2005, 5, 2531-2541.	1.3	117
99	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
100	Human Plasma PeptideAtlas. Proteomics, 2005, 5, 3497-3500.	1.3	132
101	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
102	An alternative sampling algorithm for use in liquid chromatography/tandem mass spectrometry experiments. Rapid Communications in Mass Spectrometry, 2005, 19, 589-596.	0.7	13
103	Tandem mass spectrometry database searching. , 2005, , .		0
104	The Pseudomonas aeruginosa Proteome during Anaerobic Growth. Journal of Bacteriology, 2005, 187, 8185-8190.	1.0	75
105	High Throughput Proteome Screening for Biomarker Detection. Molecular and Cellular Proteomics, 2005, 4, 182-190.	2.5	124
106	A uniform proteomics MS/MS analysis platform utilizing open XML file formats. Molecular Systems Biology, 2005, 1, 2005.0017.	3.2	620
107	Quantitative proteomic analysis of age-related changes in human cerebrospinal fluid. Neurobiology of Aging, 2005, 26, 207-227.	1.5	162
108	Pancreatic Cancer Proteome: The Proteins That Underlie Invasion, Metastasis, and Immunologic Escape. Gastroenterology, 2005, 129, 1187-1197.	0.6	185

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109	Investigation of Neutral Loss during Collision-Induced Dissociation of Peptide Ions. Analytical Chemistry, 2005, 77, 4870-4882.	3.2	51
110	Proteomic Analysis of the Intestinal Epithelial Cell Response to Enteropathogenic Escherichia coli. Journal of Biological Chemistry, 2004, 279, 20127-20136.	1.6	76
111	Integrated Genomic and Proteomic Analyses of Gene Expression in Mammalian Cells. Molecular and Cellular Proteomics, 2004, 3, 960-969.	2.5	689
112	A common open representation of mass spectrometry data and its application to proteomics research. Nature Biotechnology, 2004, 22, 1459-1466.	9.4	724
113	Identification of TFB5, a new component of general transcription and DNA repair factor IIH. Nature Genetics, 2004, 36, 707-713.	9.4	147
114	A Tool To Visualize and Evaluate Data Obtained by Liquid Chromatography-Electrospray Ionization-Mass Spectrometry. Analytical Chemistry, 2004, 76, 3856-3860.	3.2	88
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117	Lipid Raft Proteins and Their Identification in T Lymphocytes. Sub-Cellular Biochemistry, 2004, 37, 121-152.	1.0	19
118	Initial Proteome Analysis of Model Microorganism Haemophilus influenzae Strain Rd KW20. Journal of Bacteriology, 2003, 185, 4593-4602.	1.0	66
119	Proteomic analysis of Pseudomonas aeruginosa grown under magnesium limitation. Journal of the American Society for Mass Spectrometry, 2003, 14, 742-751.	1.2	79
120	Identification of 2D-gel proteins: A comparison of MALDI/TOF peptide mass mapping to Î¼ LC-ESI tandem mass spectrometry. Journal of the American Society for Mass Spectrometry, 2003, 14, 957-970.	1.2	117
121	The study of macromolecular complexes by quantitative proteomics. Nature Genetics, 2003, 33, 349-355.	9.4	350
122	Identification of androgen-coregulated protein networks from the microsomes of human prostate cancer cells. Genome Biology, 2003, 5, R4.	13.9	40
123	The Application of New Software Tools to Quantitative Protein Profiling Via Isotope-coded Affinity Tag (ICAT) and Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2003, 2, 428-442.	2.5	89
124	PROTEOME-3D: An Interactive Bioinformatics Tool for Large-Scale Data Exploration and Knowledge Discovery. Molecular and Cellular Proteomics, 2003, 2, 1164-1176.	2.5	12
125	The Application of New Software Tools to Quantitative Protein Profiling Via Isotope-coded Affinity Tag (ICAT) and Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2003, 2, 426-427.	2.5	52
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128	Code Developments to Improve the Efficiency of Automated MS/MS Spectra Interpretation. Journal of Proteome Research, 2002, 1, 211-215.	1.8	198
129	Proteome Analysis of Low-Abundance Proteins Using Multidimensional Chromatography and Isotope-Coded Affinity Tags. Journal of Proteome Research, 2002, 1, 47-54.	1.8	329
130	Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network. Science, 2001, 292, 929-934.	6.0	1,921
131	Differential stable isotope labeling of peptides for quantitation andde novo sequence derivation. Rapid Communications in Mass Spectrometry, 2001, 15, 1214-1221.	0.7	277
132	In vivo MHC class II presentation of cytosolic proteins revealed by rapid automated tandem mass spectrometry and functional analyses. European Journal of Immunology, 2001, 31, 1485-1494.	1.6	136
133	Quantitative profiling of differentiation-induced microsomal proteins using isotope-coded affinity tags and mass spectrometry. Nature Biotechnology, 2001, 19, 946-951.	9.4	913
134	The innate immune response to bacterial flagellin is mediated by Toll-like receptor 5. Nature, 2001, 410, 1099-1103.	13.7	3,186
135	In vivo MHC class II presentation of cytosolic proteins revealed by rapid automated tandem mass spectrometry and functional analyses. , 2001, 31, 1485.		1
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137	Proteomics of rat liver Golgi complex: Minor proteins are identified through sequential fractionation. Electrophoresis, 2000, 21, 3441-3459.	1.3	98
138	MASS SPECTRAL INVESTIGATIONS ON MICROORGANISMS. Toxin Reviews, 2000, 19, 95-117.	1.5	32
139	Automated Identification of Amino Acid Sequence Variations in Proteins by HPLC/Microspray Tandem Mass Spectrometry. Analytical Chemistry, 2000, 72, 757-763.	3.2	224
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144	Method To Compare Collision-Induced Dissociation Spectra of Peptides: Potential for Library Searching and Subtractive Analysis. Analytical Chemistry, 1998, 70, 3557-3565.	3.2	182

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145	High Throughput Analysis of Tandem Mass Spectrometry Data for Peptides. Laboratory Automation News, 1997, 2, 28-31.	0.2	0
146	Emerging tandem-mass-spectrometry techniques for the rapid identification of proteins. Trends in Biotechnology, 1997, 15, 418-425.	4.9	120
147	Tutorial review. Future prospects for the analysis of complex biological systems using micro-column liquid chromatographyâ€"electrospray tandem mass spectrometry. Analyst, The, 1996, 121, 65R-76R.	1.7	84
148	Peer Reviewed: Mining Genomes with MS. Analytical Chemistry, 1996, 68, 534A-540A.	3.2	88
149	Microcolumn Liquid Chromatographyâ€"Electrospray Ionization Tandem Mass Spectrometry. ACS Symposium Series, 1996, , 207-225.	0.5	2
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151	Search of sequence databases with uninterpreted high-energy collision-induced dissociation spectra of peptides. Journal of the American Society for Mass Spectrometry, 1996, 7, 1089-1098.	1.2	78
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154	Method to Correlate Tandem Mass Spectra of Modified Peptides to Amino Acid Sequences in the Protein Database. Analytical Chemistry, 1995, 67, 1426-1436.	3.2	1,219
155	An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database. Journal of the American Society for Mass Spectrometry, 1994, 5, 976-989.	1.2	5,912
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