

# Jimmy K Eng

## List of Publications by Year in descending order

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157  
papers

35,165  
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8755

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161  
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161  
docs citations

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times ranked

30514  
citing authors

#	ARTICLE	IF	CITATIONS
1	In Vivo Cross-Linking MS Reveals Conservation in OmpA Linkage to Different Classes of $\beta$ -Lactamase Enzymes. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 190-195.	2.8	13
2	Systemic Proteome Alterations Linked to Early Stage Pancreatic Cancer in Diabetic Patients. <i>Cancers</i> , 2020, 12, 1534.	3.7	18
3	Full-Featured, Real-Time Database Searching Platform Enables Fast and Accurate Multiplexed Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 2026-2034.	3.7	171
4	Extending Comet for Global Amino Acid Variant and Post-Translational Modification Analysis Using the PSI Extended FASTA Format. <i>Proteomics</i> , 2020, 20, e1900362.	2.2	18
5	Predictive proteomic signatures for response of pancreatic cancer patients receiving chemotherapy. <i>Clinical Proteomics</i> , 2019, 16, 31.	2.1	16
6	In Vivo Proteome of <i>Pseudomonas aeruginosa</i> in Airways of Cystic Fibrosis Patients. <i>Journal of Proteome Research</i> , 2019, 18, 2601-2612.	3.7	23
7	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	3.7	22
8	A Tandem Mass Spectrometry Sequence Database Search Method for Identification of O-Fucosylated Proteins by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2019, 18, 652-663.	3.7	16
9	Tools for 3D Interactome Visualization. <i>Journal of Proteome Research</i> , 2019, 18, 753-758.	3.7	26
10	Mango: A General Tool for Collision Induced Dissociation-Cleavable Cross-Linked Peptide Identification. <i>Analytical Chemistry</i> , 2018, 90, 6028-6034.	6.5	39
11	Sipros Ensemble improves database searching and filtering for complex metaproteomics. <i>Bioinformatics</i> , 2018, 34, 795-802.	4.1	35
12	Bifunctional Immunity Proteins Protect Bacteria against FtsZ-Targeting ADP-Ribosylating Toxins. <i>Cell</i> , 2018, 175, 1380-1392.e14.	28.9	109
13	Quantitative Proteomics Based on Optimized Data-Independent Acquisition in Plasma Analysis. <i>Journal of Proteome Research</i> , 2017, 16, 665-676.	3.7	39
14	Extracellular Matrix Proteins Mediate HIV-1 gp120 Interactions with $\beta$ - $\beta$ . <i>Journal of Virology</i> , 2017, 91, .	3.4	8
15	Large-Scale and Targeted Quantitative Cross-Linking MS Using Isotope-Labeled Protein Interaction Reporter (PIR) Cross-Linkers. <i>Journal of Proteome Research</i> , 2017, 16, 720-727.	3.7	38
16	XLinkDB 2.0: integrated, large-scale structural analysis of protein crosslinking data. <i>Bioinformatics</i> , 2016, 32, 2716-2718.	4.1	54
17	Spectral Library Searching To Identify Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2016, 15, 1725-1731.	3.7	12
18	In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in <i>Acinetobacter baumannii</i> strain AB5075. <i>Nature Communications</i> , 2016, 7, 13414.	12.8	81

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19	InÂVivo Conformational Dynamics of Hsp90 and Its Interactors. Cell Chemical Biology, 2016, 23, 716-726.	5.2	73
20	Visualization of Host-Poliovirus Interaction Topologies Using Protein Interaction Reporter Technology. Journal of Virology, 2016, 90, 1973-1987.	3.4	38
21	A General Method for Targeted Quantitative Cross-Linking Mass Spectrometry. PLoS ONE, 2016, 11, e0167547.	2.5	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.	12.8	77
24	Dynamic Proteome Response of Pseudomonas aeruginosa to Tobramycin Antibiotic Treatment. Molecular and Cellular Proteomics, 2015, 14, 2126-2137.	3.8	37
25	A Deeper Look into Cometâ€™ Implementation and Features. Journal of the American Society for Mass Spectrometry, 2015, 26, 1865-1874.	2.8	175
26	Probing the Protein Interaction Network of Pseudomonas aeruginosa Cells by Chemical Cross-Linking Mass Spectrometry. Structure, 2015, 23, 762-773.	3.3	71
27	CruX: Rapid Open Source Protein Tandem Mass Spectrometry Analysis. Journal of Proteome Research, 2014, 13, 4488-4491.	3.7	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.	3.7	130
29	Comet: An openâ€™source <sc>MS</sc>/<sc>MS</sc> sequence database search tool. Proteomics, 2013, 13, 22-24.	2.2	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.	3.7	50
31	Protein Interactions, Post-translational Modifications and Topologies in Human Cells. Molecular and Cellular Proteomics, 2013, 12, 1451-1467.	3.8	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.	7.1	31
33	Protein Kinase PKN1 Represses Wnt/Î²-Catenin Signaling in Human Melanoma Cells. Journal of Biological Chemistry, 2013, 288, 34658-34670.	3.4	29
34	A Mass Spectrometry Proteomics Data Management Platform. Molecular and Cellular Proteomics, 2012, 11, 824-831.	3.8	31
35	A likelihood-based scoring method for peptide identification using mass spectrometry. Annals of Applied Statistics, 2012, 6, .	1.1	4
36	<b><i>De Novo</i></b> 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.	2.8	10

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37	In Vivo Application of Photocleavable Protein Interaction Reporter Technology. <i>Journal of Proteome Research</i> , 2012, 11, 1027-1041.	3.7	29
38	Accurate Peptide Fragment Mass Analysis: Multiplexed Peptide Identification and Quantification. <i>Journal of Proteome Research</i> , 2012, 11, 1621-1632.	3.7	86
39	Cross-linking Measurements of the <i>Potato leafroll virus</i> Reveal Protein Interaction Topologies Required for Virion Stability, Aphid Transmission, and Virusâ€“Plant Interactions. <i>Journal of Proteome Research</i> , 2012, 11, 2968-2981.	3.7	62
40	Sites of ubiquitin attachment in <i>Saccharomyces cerevisiae</i>. <i>Proteomics</i> , 2012, 12, 236-240.	2.2	43
41	iProphet: Multi-level Integrative Analysis of Shotgun Proteomic Data Improves Peptide and Protein Identification Rates and Error Estimates. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.007690.	3.8	490
42	Fast Parallel Tandem Mass Spectral Library Searching Using GPU Hardware Acceleration. <i>Journal of Proteome Research</i> , 2011, 10, 2882-2888.	3.7	47
43	The Fasted/Fed Mouse Metabolic Acetylome: N6-Acetylation Differences Suggest Acetylation Coordinates Organ-Specific Fuel Switching. <i>Journal of Proteome Research</i> , 2011, 10, 4134-4149.	3.7	68
44	A Face in the Crowd: Recognizing Peptides Through Database Search. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R111.009522.	3.8	147
45	Microdialysis Combined with Proteomics for Protein Identification in Breast Tumor Microenvironment In Vivo. <i>Cancer Microenvironment</i> , 2011, 4, 61-71.	3.1	13
46	Cross-linking Measurements of In Vivo Protein Complex Topologies. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006841.	3.8	81
47	Installation and Use of LabKey Server for Proteomics. <i>Current Protocols in Bioinformatics</i> , 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. <i>Genes and Cancer</i> , 2011, 2, 956-978.	1.9	12
49	Index-ion Triggered MS2 Ion Quantification: A Novel Proteomics Approach for Reproducible Detection and Quantification of Targeted Proteins in Complex Mixtures. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005611.	3.8	26
50	A guided tour of the Transâ€“Proteomic Pipeline. <i>Proteomics</i> , 2010, 10, 1150-1159.	2.2	710
51	Transâ€“Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. <i>Proteomics</i> , 2010, 10, 1190-1195.	2.2	39
52	Quantitative analysis of the secretome of TGFâ€“ $\beta$ 2 signalingâ€“deficient mammary fibroblasts. <i>Proteomics</i> , 2010, 10, 2458-2470.	2.2	37
53	Differential Protein Expression Profiles in Estrogen Receptor-Positive and -Negative Breast Cancer Tissues Using Label-Free Quantitative Proteomics. <i>Genes and Cancer</i> , 2010, 1, 251-271.	1.9	38
54	ChromEval: A Software Application for the Rapid Evaluation of HPLC System Performance in Proteomic Applications. <i>Analytical Chemistry</i> , 2010, 82, 5060-5068.	6.5	1

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55	A Photocleavable and Mass Spectrometry Identifiable Cross-Linker for Protein Interaction Studies. <i>Analytical Chemistry</i> , 2010, 82, 3556-3566.	6.5	49
56	Precursor Charge State Prediction for Electron Transfer Dissociation Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2010, 9, 5438-5444.	3.7	9
57	Characterizing the connectivity of poly-ubiquitin chains by selected reaction monitoring mass spectrometry. <i>Molecular BioSystems</i> , 2010, 6, 2004.	2.9	35
58	Proteomics data repositories. <i>Proteomics</i> , 2009, 9, 4653-4663.	2.2	39
59	Quantitative Phosphoproteomic Analysis of T Cell Receptor Signaling Reveals System-Wide Modulation of Protein-Protein Interactions. <i>Science Signaling</i> , 2009, 2, ra46.	3.6	330
60	Proteomic Analyses Using <i>Grifola frondosa</i> Metalloendoprotease Lys-N. <i>Journal of Proteome Research</i> , 2009, 8, 1415-1422.	3.7	29
61	Analysis of RP-HPLC Loading Conditions for Maximizing Peptide Identifications in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2009, 8, 4161-4168.	3.7	12
62	MaRiMba: A Software Application for Spectral Library-Based MRM Transition List Assembly. <i>Journal of Proteome Research</i> , 2009, 8, 4396-4405.	3.7	80
63	Building consensus spectral libraries for peptide identification in proteomics. <i>Nature Methods</i> , 2008, 5, 873-875.	19.0	255
64	A Fast SEQUEST Cross Correlation Algorithm. <i>Journal of Proteome Research</i> , 2008, 7, 4598-4602.	3.7	214
65	The Standard Protein Mix Database: A Diverse Data Set To Assist in the Production of Improved Peptide and Protein Identification Software Tools. <i>Journal of Proteome Research</i> , 2008, 7, 96-103.	3.7	156
66	Quantification of the Compositional Information Provided by Immonium Ions on a Quadrupole-Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2008, 80, 5596-5606.	6.5	40
67	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1389-1396.	3.8	472
68	MRMer, an Interactive Open Source and Cross-platform System for Data Extraction and Visualization of Multiple Reaction Monitoring Experiments. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2270-2278.	3.8	80
69	Global Survey of Human T Leukemic Cells by Integrating Proteomics and Transcriptomics Profiling. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1343-1353.	3.8	31
70	Identification of Putative Androgen Receptor Interaction Protein Modules. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 252-271.	3.8	51
71	Proteomics Analysis of Human Coronary Atherosclerotic Plaque. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1088-1102.	3.8	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. <i>Journal of Proteome Research</i> , 2007, 6, 3962-3975.	3.7	171
74	An integrated chemical, mass spectrometric and computational strategy for (quantitative) phosphoproteomics: application to <i>Drosophila melanogaster</i> Kc167 cells. <i>Molecular BioSystems</i> , 2007, 3, 275.	2.9	76
75	Contribution of Protein Fractionation to Depth of Analysis of the Serum and Plasma Proteomes. <i>Journal of Proteome Research</i> , 2007, 6, 3558-3565.	3.7	153
76	A Platform for Accurate Mass and Time Analyses of Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2007, 6, 2685-2694.	3.7	76
77	Development and validation of a spectral library searching method for peptide identification from MS/MS. <i>Proteomics</i> , 2007, 7, 655-667.	2.2	487
78	A combined dataset of human cerebrospinal fluid proteins identified by multi-dimensional chromatography and tandem mass spectrometry. <i>Proteomics</i> , 2007, 7, 469-473.	2.2	111
79	Direct cancer tissue proteomics: a method to identify candidate cancer biomarkers from formalin-fixed paraffin-embedded archival tissues. <i>Oncogene</i> , 2007, 26, 65-76.	5.9	129
80	Head-to-Head Comparison of Serum Fractionation Techniques. <i>Journal of Proteome Research</i> , 2007, 6, 828-836.	3.7	152
81	Analysis of the <i>Saccharomyces cerevisiae</i> proteome with PeptideAtlas. <i>Genome Biology</i> , 2006, 7, R106.	9.6	60
82	UniPep—a database for human N-linked glycosites: a resource for biomarker discovery. <i>Genome Biology</i> , 2006, 7, R73.	9.6	101
83	Characterization of Proteome of Human Cerebrospinal Fluid. <i>International Review of Neurobiology</i> , 2006, 73, 29-98.	2.0	28
84	Computational Proteomics Analysis System (CPAS): An Extensible, Open-Source Analytic System for Evaluating and Publishing Proteomic Data and High Throughput Biological Experiments. <i>Journal of Proteome Research</i> , 2006, 5, 1024-1024.	3.7	4
85	Computational Proteomics Analysis System (CPAS): An Extensible, Open-Source Analytic System for Evaluating and Publishing Proteomic Data and High Throughput Biological Experiments. <i>Journal of Proteome Research</i> , 2006, 5, 112-121.	3.7	204
86	Quality Control Metrics for LC-MS Feature Detection Tools Demonstrated on <i>Saccharomyces cerevisiae</i> Proteomic Profiles. <i>Journal of Proteome Research</i> , 2006, 5, 1527-1534.	3.7	31
87	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. , 2006, , 289-315.		0
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. <i>Nature Biotechnology</i> , 2006, 24, 333-338.	17.5	309
90	General framework for developing and evaluating database scoring algorithms using the TANDEM search engine. <i>Bioinformatics</i> , 2006, 22, 2830-2832.	4.1	209

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91	A suite of algorithms for the comprehensive analysis of complex protein mixtures using high-resolution LC-MS. <i>Bioinformatics</i> , 2006, 22, 1902-1909.	4.1	250
92	The PeptideAtlas project. <i>Nucleic Acids Research</i> , 2006, 34, D655-D658.	14.5	733
93	Systematic Characterization of Nuclear Proteome during Apoptosis. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1131-1145.	3.8	62
94	Quantitative proteomics of cerebrospinal fluid from patients with Alzheimer disease. <i>Journal of Alzheimer's Disease</i> , 2005, 7, 125-133.	2.6	160
95	Protein Identification Using TurboSEQUEST. <i>Current Protocols in Bioinformatics</i> , 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. <i>Nature Methods</i> , 2005, 2, 591-598.	19.0	302
98	Proteomic analysis of synaptosomes using isotope-coded affinity tags and mass spectrometry. <i>Proteomics</i> , 2005, 5, 2531-2541.	2.2	117
99	An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis. <i>Proteomics</i> , 2005, 5, 3475-3490.	2.2	332
100	Human Plasma PeptideAtlas. <i>Proteomics</i> , 2005, 5, 3497-3500.	2.2	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. <i>Proteomics</i> , 2005, 5, 3226-3245.	2.2	766
102	An alternative sampling algorithm for use in liquid chromatography/tandem mass spectrometry experiments. <i>Rapid Communications in Mass Spectrometry</i> , 2005, 19, 589-596.	1.5	13
103	Tandem mass spectrometry database searching. , 2005, , .		0
104	The <i>Pseudomonas aeruginosa</i> Proteome during Anaerobic Growth. <i>Journal of Bacteriology</i> , 2005, 187, 8185-8190.	2.2	75
105	High Throughput Proteome Screening for Biomarker Detection. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 182-190.	3.8	124
106	A uniform proteomics MS/MS analysis platform utilizing open XML file formats. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0017.	7.2	620
107	Quantitative proteomic analysis of age-related changes in human cerebrospinal fluid. <i>Neurobiology of Aging</i> , 2005, 26, 207-227.	3.1	162
108	Pancreatic Cancer Proteome: The Proteins That Underlie Invasion, Metastasis, and Immunologic Escape. <i>Gastroenterology</i> , 2005, 129, 1187-1197.	1.3	185

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109	Investigation of Neutral Loss during Collision-Induced Dissociation of Peptide Ions. <i>Analytical Chemistry</i> , 2005, 77, 4870-4882.	6.5	51
110	Proteomic Analysis of the Intestinal Epithelial Cell Response to Enteropathogenic <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 20127-20136.	3.4	76
111	Integrated Genomic and Proteomic Analyses of Gene Expression in Mammalian Cells. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 960-969.	3.8	689
112	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004, 22, 1459-1466.	17.5	724
113	Identification of TFB5, a new component of general transcription and DNA repair factor IIH. <i>Nature Genetics</i> , 2004, 36, 707-713.	21.4	147
114	A Tool To Visualize and Evaluate Data Obtained by Liquid Chromatography-Electrospray Ionization-Mass Spectrometry. <i>Analytical Chemistry</i> , 2004, 76, 3856-3860.	6.5	88
115	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. <i>Genome Biology</i> , 2004, 6, R9.	9.6	252
116	System-based proteomic analysis of the interferon response in human liver cells. <i>Genome Biology</i> , 2004, 5, R54.	9.6	63
117	Lipid Raft Proteins and Their Identification in T Lymphocytes. <i>Sub-Cellular Biochemistry</i> , 2004, 37, 121-152.	2.4	19
118	Initial Proteome Analysis of Model Microorganism <i>Haemophilus influenzae</i> Strain Rd KW20. <i>Journal of Bacteriology</i> , 2003, 185, 4593-4602.	2.2	66
119	Proteomic analysis of <i>Pseudomonas aeruginosa</i> grown under magnesium limitation. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 742-751.	2.8	79
120	Identification of 2D-gel proteins: A comparison of MALDI/TOF peptide mass mapping to $1\frac{1}{4}$ LC-ESI tandem mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 957-970.	2.8	117
121	The study of macromolecular complexes by quantitative proteomics. <i>Nature Genetics</i> , 2003, 33, 349-355.	21.4	350
122	Identification of androgen-coregulated protein networks from the microsomes of human prostate cancer cells. <i>Genome Biology</i> , 2003, 5, R4.	9.6	40
123	The Application of New Software Tools to Quantitative Protein Profiling Via Isotope-coded Affinity Tag (ICAT) and Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 428-442.	3.8	89
124	PROTEOME-3D: An Interactive Bioinformatics Tool for Large-Scale Data Exploration and Knowledge Discovery. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 1164-1176.	3.8	12
125	The Application of New Software Tools to Quantitative Protein Profiling Via Isotope-coded Affinity Tag (ICAT) and Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 426-427.	3.8	52
126	Quantitative proteomic analysis indicates increased synthesis of a quinolone by <i>Pseudomonas aeruginosa</i> isolates from cystic fibrosis airways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2771-2776.	7.1	137



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127	Complementary Profiling of Gene Expression at the Transcriptome and Proteome Levels in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , 2002, 1, 323-333.	3.8	591
128	Code Developments to Improve the Efficiency of Automated MS/MS Spectra Interpretation. <i>Journal of Proteome Research</i> , 2002, 1, 211-215.	3.7	198
129	Proteome Analysis of Low-Abundance Proteins Using Multidimensional Chromatography and Isotope-Coded Affinity Tags. <i>Journal of Proteome Research</i> , 2002, 1, 47-54.	3.7	329
130	Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network. <i>Science</i> , 2001, 292, 929-934.	12.6	1,921
131	Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1214-1221.	1.5	277
132	In vivo MHC class II presentation of cytosolic proteins revealed by rapid automated tandem mass spectrometry and functional analyses. <i>European Journal of Immunology</i> , 2001, 31, 1485-1494.	2.9	136
133	Quantitative profiling of differentiation-induced microsomal proteins using isotope-coded affinity tags and mass spectrometry. <i>Nature Biotechnology</i> , 2001, 19, 946-951.	17.5	913
134	The innate immune response to bacterial flagellin is mediated by Toll-like receptor 5. <i>Nature</i> , 2001, 410, 1099-1103.	27.8	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
136	Protein Identification by SEQUEST. <i>Principles and Practice</i> , 2001, , 125-142.	0.3	38
137	Proteomics of rat liver Golgi complex: Minor proteins are identified through sequential fractionation. <i>Electrophoresis</i> , 2000, 21, 3441-3459.	2.4	98
138	MASS SPECTRAL INVESTIGATIONS ON MICROORGANISMS. <i>Toxin Reviews</i> , 2000, 19, 95-117.	1.5	32
139	Automated Identification of Amino Acid Sequence Variations in Proteins by HPLC/Microspray Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 757-763.	6.5	224
140	Automated Protein Identification Using Microcolumn Liquid Chromatography-Tandem Mass Spectrometry. , 1999, 112, 553-570.		71
141	Direct analysis of protein complexes using mass spectrometry. <i>Nature Biotechnology</i> , 1999, 17, 676-682.	17.5	2,201
142	Identification of Proteins in Complexes by Solid-Phase Microextraction/Multistep Elution/Capillary Electrophoresis/Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 1999, 71, 2270-2278.	6.5	139
143	High throughput protein characterization by automated reverse-phase chromatography/electrospray tandem mass spectrometry. <i>Protein Science</i> , 1998, 7, 706-719.	7.6	297
144	Method To Compare Collision-Induced Dissociation Spectra of Peptides:Â Potential for Library Searching and Subtractive Analysis. <i>Analytical Chemistry</i> , 1998, 70, 3557-3565.	6.5	182

