

David M Lubman

List of Publications by Year in descending order

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197
papers

8,097
citations

34105

52
h-index

69250

77
g-index

199
all docs

199
docs citations

199
times ranked

7059
citing authors

#	ARTICLE	IF	CITATIONS
1	David M. Lubman "The University of Michigan" A retrospective in research. <i>Mass Spectrometry Reviews</i> , 2023, 42, 643-651.	5.4	0
2	A guide to mass spectrometric analysis of extracellular vesicle proteins for biomarker discovery. <i>Mass Spectrometry Reviews</i> , 2023, 42, 844-872.	5.4	27
3	A Fucosylated Glycopeptide as a Candidate Biomarker for Early Diagnosis of NASH Hepatocellular Carcinoma Using a Stepped HCD Method and PRM Evaluation. <i>Frontiers in Oncology</i> , 2022, 12, 818001.	2.8	7
4	Glycopeptides with Sialyl Lewis Antigen in Serum Haptoglobin as Candidate Biomarkers for Nonalcoholic Steatohepatitis Hepatocellular Carcinoma Using a Higher-Energy Collision-Induced Dissociation Parallel Reaction Monitoring-Mass Spectrometry Method. <i>ACS Omega</i> , 2022, 7, 22850-22860.	3.5	10
5	A novel method of high-purity extracellular vesicle enrichment from microliter-scale human serum for proteomic analysis. <i>Electrophoresis</i> , 2021, 42, 245-256.	2.4	18
6	Intestinal extracellular vesicles are altered by vertical sleeve gastrectomy. <i>American Journal of Physiology - Renal Physiology</i> , 2021, 320, G153-G165.	3.4	3
7	A Panel of Glycopeptides as Candidate Biomarkers for Early Diagnosis of NASH Hepatocellular Carcinoma Using a Stepped HCD Method and PRM Evaluation. <i>Journal of Proteome Research</i> , 2021, 20, 3278-3289.	3.7	23
8	GlycoHybridSeq: Automated Identification of N-Linked Glycopeptides Using Electron Transfer/High-Energy Collision Dissociation (ETHcD). <i>Journal of Proteome Research</i> , 2021, 20, 3345-3352.	3.7	9
9	Rapid separation of blood plasma exosomes from low-density lipoproteins via a hydrophobic interaction chromatography method on a polyester capillary-channeled polymer fiber phase. <i>Analytica Chimica Acta</i> , 2021, 1167, 338578.	5.4	27
10	PRM-MS Quantitative Analysis of Isomeric N-Glycopeptides Derived from Human Serum Haptoglobin of Patients with Cirrhosis and Hepatocellular Carcinoma. <i>Metabolites</i> , 2021, 11, 563.	2.9	16
11	Label-free quantitative proteomic analysis of serum extracellular vesicles differentiating patients of alcoholic and nonalcoholic fatty liver diseases. <i>Journal of Proteomics</i> , 2021, 245, 104278.	2.4	10
12	Column-based Technology for CD9-HPLC Immunoaffinity Isolation of Serum Extracellular Vesicles. <i>Journal of Proteome Research</i> , 2021, 20, 4901-4911.	3.7	20
13	Glycopeptide Biomarkers in Serum Haptoglobin for Hepatocellular Carcinoma Detection in Patients with Nonalcoholic Steatohepatitis. <i>Journal of Proteome Research</i> , 2020, 19, 3452-3466.	3.7	37
14	Quantitative Analysis of α -1-Antitrypsin Glycosylation Isoforms in HCC Patients Using LC-HCD-PRM-MS. <i>Analytical Chemistry</i> , 2020, 92, 8201-8208.	6.5	21
15	Comprehensive Detection of Single Amino Acid Variants and Evaluation of Their Deleterious Potential in a PANC-1 Cell Line. <i>Journal of Proteome Research</i> , 2020, 19, 1635-1646.	3.7	11
16	Input of serum haptoglobin fucosylation profile in the diagnosis of hepatocellular carcinoma in patients with non-cirrhotic liver disease. <i>Clinics and Research in Hepatology and Gastroenterology</i> , 2020, 44, 681-691.	1.5	8
17	Single Amino Acid Variant Discovery in Small Numbers of Cells. <i>Journal of Proteome Research</i> , 2019, 18, 417-425.	3.7	13
18	Aberrant glycosylation and cancer biomarker discovery: a promising and thorny journey. <i>Clinical Chemistry and Laboratory Medicine</i> , 2019, 57, 407-416.	2.3	111

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19	Evaluation of AGP Fucosylation as a Marker for Hepatocellular Carcinoma of Three Different Etiologies. <i>Scientific Reports</i> , 2019, 9, 11580.	3.3	17
20	Platelet Factor 4 as a Novel Exosome Marker in MALDI-MS Analysis of Exosomes from Human Serum. <i>Analytical Chemistry</i> , 2019, 91, 13297-13305.	6.5	38
21	Serum Protein Biomarkers of Fibrosis Aid in Risk Stratification of Future Stricturing Complications in Pediatric Crohn's Disease. <i>American Journal of Gastroenterology</i> , 2019, 114, 777-785.	0.4	31
22	Glycoproteomic markers of hepatocellular carcinoma—mass spectrometry based approaches. <i>Mass Spectrometry Reviews</i> , 2019, 38, 265-290.	5.4	64
23	A Method for Isolation and Proteomic Analysis of Outer Membrane Vesicles from Fecal Samples by LC-MS/MS. <i>Journal of Proteomics and Bioinformatics</i> , 2019, 12, 38-42.	0.4	7
24	Circulating Microvesicles from Pancreatic Cancer Accelerate the Migration and Proliferation of PANC-1 Cells. <i>Journal of Proteome Research</i> , 2018, 17, 1690-1699.	3.7	13
25	The analysis of alpha α 1 α antitrypsin glycosylation with direct LC-MS/MS. <i>Electrophoresis</i> , 2018, 39, 2351-2361.	2.4	22
26	Differential Quantitative Determination of Site-Specific Intact N-Glycopeptides in Serum Haptoglobin between Hepatocellular Carcinoma and Cirrhosis Using LC-ETHcD-MS/MS. <i>Journal of Proteome Research</i> , 2018, 18, 359-371.	3.7	50
27	Comparison of an Optimized Ultracentrifugation Method versus Size-Exclusion Chromatography for Isolation of Exosomes from Human Serum. <i>Journal of Proteome Research</i> , 2018, 17, 3599-3605.	3.7	136
28	High-Performance Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry for Exosome Metabolomics. <i>Analytical Chemistry</i> , 2018, 90, 8314-8319.	6.5	72
29	Single Amino Acid Variant Profiles of Subpopulations in the MCF-7 Breast Cancer Cell Line. <i>Journal of Proteome Research</i> , 2017, 16, 842-851.	3.7	10
30	Quantitative Proteomic Analysis of Serum Exosomes from Patients with Locally Advanced Pancreatic Cancer Undergoing Chemoradiotherapy. <i>Journal of Proteome Research</i> , 2017, 16, 1763-1772.	3.7	87
31	LC-MS/MS isomeric profiling of permethylated N-glycans derived from serum haptoglobin of hepatocellular carcinoma (HCC) and cirrhotic patients. <i>Electrophoresis</i> , 2017, 38, 2160-2167.	2.4	65
32	Serum Glycoproteome Profiles for Distinguishing Intestinal Fibrosis from Inflammation in Crohn's Disease. <i>PLoS ONE</i> , 2017, 12, e0170506.	2.5	20
33	Annexin A10 is a candidate marker associated with the progression of pancreatic precursor lesions to adenocarcinoma. <i>PLoS ONE</i> , 2017, 12, e0175039.	2.5	20
34	Protein Markers Associated with an ALDH Sub-Population in Colorectal Cancer. <i>Journal of Proteomics and Bioinformatics</i> , 2016, 9, 238-247.	0.4	4
35	A procedure for the analysis of site-specific and structure-specific fucosylation in alpha α 1 α antitrypsin. <i>Electrophoresis</i> , 2016, 37, 2624-2632.	2.4	10
36	Development of an Integrated Pipeline for Profiling Microbial Proteins from Mouse Fecal Samples by LC-MS/MS. <i>Journal of Proteome Research</i> , 2016, 15, 3635-3642.	3.7	17

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37	CD90 and CD24 Co-Expression Is Associated with Pancreatic Intraepithelial Neoplasias. PLoS ONE, 2016, 11, e0158021.	2.5	14
38	A quantitative proteomics analysis of MCF7 breast cancer stem and progenitor cell populations. Proteomics, 2015, 15, 3772-3783.	2.2	23
39	Validation of LRG1 as a Potential Biomarker for Detection of Epithelial Ovarian Cancer by a Blinded Study. PLoS ONE, 2015, 10, e0121112.	2.5	27
40	Large-Scale Identification of Core-Fucosylated Glycopeptide Sites in Pancreatic Cancer Serum Using Mass Spectrometry. Journal of Proteome Research, 2015, 14, 1968-1978.	3.7	66
41	Mass-Selected Site-Specific Core-Fucosylation of Serum Proteins in Hepatocellular Carcinoma. Journal of Proteome Research, 2015, 14, 4876-4884.	3.7	37
42	Exosome enrichment of human serum using multiple cycles of centrifugation. Electrophoresis, 2015, 36, 2017-2026.	2.4	55
43	ESI-MS/MS Method for Haptoglobin Fucosylation Analysis in Hepatocellular Carcinoma and Liver Cirrhosis. Journal of Proteome Research, 2015, 14, 5388-5395.	3.7	38
44	Mass Spectrometric N-Glycan Analysis of Haptoglobin from Patient Serum Samples Using a 96-Well Plate Format. Journal of Proteome Research, 2015, 14, 4932-4939.	3.7	30
45	Proteomics Characterization of Primary Human Oral Epithelial Cells Using a Novel Culture Technique for Use in Tissue Regeneration. MOJ Proteomics & Bioinformatics, 2015, 2, .	0.1	0
46	Label-free relative quantification of alpha-2-macroglobulin site-specific core-fucosylation in pancreatic cancer by LC-MS/MS. Electrophoresis, 2014, 35, 2108-2115.	2.4	22
47	Overexpression of CD90 (Thy-1) in Pancreatic Adenocarcinoma Present in the Tumor Microenvironment. PLoS ONE, 2014, 9, e115507.	2.5	53
48	Heterogeneity of The CD90+ Population in Different Stages of Hepatocarcinogenesis. Journal of Proteomics and Bioinformatics, 2014, 07, 296-302.	0.4	10
49	Quantitative Analysis of Single Amino Acid Variant Peptides Associated with Pancreatic Cancer in Serum by an Isobaric Labeling Quantitative Method. Journal of Proteome Research, 2014, 13, 6058-6066.	3.7	26
50	Glycoprotein Biomarker Panel for Pancreatic Cancer Discovered by Quantitative Proteomics Analysis. Journal of Proteome Research, 2014, 13, 1873-1884.	3.7	107
51	Mass-Selected Site-Specific Core-Fucosylation of Ceruloplasmin in Alcohol-Related Hepatocellular Carcinoma. Journal of Proteome Research, 2014, 13, 2887-2896.	3.7	48
52	Analysis of Serum Haptoglobin Fucosylation in Hepatocellular Carcinoma and Liver Cirrhosis of Different Etiologies. Journal of Proteome Research, 2014, 13, 2986-2997.	3.7	103
53	Analysis of Glycan Variation on Glycoproteins from Serum by the Reverse Lectin-Based ELISA Assay. Journal of Proteome Research, 2014, 13, 2197-2204.	3.7	41
54	Insight into Preimplantation Factor (PIF*) Mechanism for Embryo Protection and Development: Target Oxidative Stress and Protein Misfolding (PDI and HSP) through Essential RIPK Binding Site. PLoS ONE, 2014, 9, e100263.	2.5	33

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55	Characterization of Membrane-Associated Glycoproteins Using Lectin Affinity Chromatography and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 951, 69-77.	0.9	6
56	Altered Expression of Sialylated Glycoproteins in Ovarian Cancer Sera Using Lectin-based ELISA Assay and Quantitative Glycoproteomics Analysis. <i>Journal of Proteome Research</i> , 2013, 12, 3342-3352.	3.7	59
57	Isobaric Protein-Level Labeling Strategy for Serum Glycoprotein Quantification Analysis by Liquid Chromatography-Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 5353-5357.	6.5	27
58	Target Proteomic Profiling of Frozen Pancreatic CD24+ Adenocarcinoma Tissues by Immuno-Laser Capture Microdissection and Nano-LC-MS/MS. <i>Journal of Proteome Research</i> , 2013, 12, 2791-2804.	3.7	38
59	Immunohistochemical staining, laser capture microdissection, and filter-aided sample preparation-assisted proteomic analysis of target cell populations within tissue samples. <i>Electrophoresis</i> , 2013, 34, 1627-1636.	2.4	12
60	CD90 is Identified as a Candidate Marker for Cancer Stem Cells in Primary High-Grade Gliomas Using Tissue Microarrays. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.010744.	3.8	122
61	Identification of Glycoprotein Markers for Pancreatic Cancer CD24 ⁺ CD44 ⁺ Stem-like Cells Using Nano-LC-MS/MS and Tissue Microarray. <i>Journal of Proteome Research</i> , 2012, 11, 2272-2281.	3.7	73
62	Identification and Confirmation of Differentially Expressed Fucosylated Glycoproteins in the Serum of Ovarian Cancer Patients Using a Lectin Array and LC-MS/MS. <i>Journal of Proteome Research</i> , 2012, 11, 4541-4552.	3.7	102
63	An N-glycosylation Analysis of Human Alpha-2-Macroglobulin Using an Integrated Approach. <i>Journal of Proteomics and Bioinformatics</i> , 2012, 05, 127-134.	0.4	31
64	Glycoproteomic Analysis of Glioblastoma Stem Cell Differentiation. <i>Journal of Proteome Research</i> , 2011, 10, 330-338.	3.7	31
65	Mass Spectrometric Assay for Analysis of Haptoglobin Fucosylation in Pancreatic Cancer. <i>Journal of Proteome Research</i> , 2011, 10, 2602-2611.	3.7	68
66	Dose-dependent proteomic analysis of glioblastoma cancer stem cells upon treatment with β -secretase inhibitor. <i>Proteomics</i> , 2011, 11, 4529-4540.	2.2	15
67	Differential profiling studies of N-linked glycoproteins in glioblastoma cancer stem cells upon treatment with β -secretase inhibitor. <i>Proteomics</i> , 2011, 11, 4021-4028.	2.2	25
68	A multiplexed bead assay for profiling glycosylation patterns on serum protein biomarkers of pancreatic cancer. <i>Electrophoresis</i> , 2011, 32, 2028-2035.	2.4	27
69	Development of Micro-scale Sample Preparation and Prefractionation Methods in LC-MS-Based Proteomic Studies. , 2011, , 913-924.		0
70	A comparative phosphoproteomic analysis of a human tumor metastasis model using a label-free quantitative approach. <i>Electrophoresis</i> , 2010, 31, 1842-1852.	2.4	21
71	Glycoprotein analysis using protein microarrays and mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2010, 29, 830-844.	5.4	62
72	Plasma Proteomic Analysis May Identify New Markers for Radiation-Induced Lung Toxicity in Patients With Non-Small-Cell Lung Cancer. <i>International Journal of Radiation Oncology Biology Physics</i> , 2010, 77, 867-876.	0.8	31

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73	The identification of auto-antibodies in pancreatic cancer patient sera using a naturally fractionated Panc-1 cell line. <i>Cancer Biomarkers</i> , 2010, 7, 25-37.	1.7	23
74	Identification of Cell Surface Glycoprotein Markers for Glioblastoma-Derived Stem-Like Cells Using a Lectin Microarray and LC-MS/MS Approach. <i>Journal of Proteome Research</i> , 2010, 9, 2565-2572.	3.7	71
75	Quantitative Proteomic Profiling Studies of Pancreatic Cancer Stem Cells. <i>Journal of Proteome Research</i> , 2010, 9, 3394-3402.	3.7	31
76	Serum Autoantibody Profiling Using a Natural Glycoprotein Microarray for the Prognosis of Early Melanoma. <i>Journal of Proteome Research</i> , 2010, 9, 6044-6051.	3.7	23
77	Identification and Confirmation of Biomarkers Using an Integrated Platform for Quantitative Analysis of Glycoproteins and Their Glycosylations. <i>Journal of Proteome Research</i> , 2010, 9, 798-805.	3.7	68
78	Comparative proteomic study of two closely related ovarian endometrioid adenocarcinoma cell lines using cIEF fractionation and pathway analysis. <i>Electrophoresis</i> , 2009, 30, 1119-1131.	2.4	42
79	The identification of phosphoglycerate kinase-1 and histone H4 autoantibodies in pancreatic cancer patient serum using a natural protein microarray. <i>Electrophoresis</i> , 2009, 30, 2215-2226.	2.4	38
80	A novel phosphoprotein analysis scheme for assessing changes in premalignant and malignant breast cell lines using 2D liquid separations, protein microarrays, and tandem mass spectrometry. <i>Proteomics - Clinical Applications</i> , 2009, 3, 51-66.	1.6	10
81	Pancreatic Cancer Serum Detection Using a Lectin/Glyco-Antibody Array Method. <i>Journal of Proteome Research</i> , 2009, 8, 483-492.	3.7	109
82	Differential Protein Mapping of Ovarian Serous Adenocarcinomas: Identification of Potential Markers for Distinct Tumor Stage. <i>Journal of Proteome Research</i> , 2009, 8, 1452-1463.	3.7	32
83	Proteomic Insights: Cryoadaptation of Permafrost Bacteria. <i>Soil Biology</i> , 2009, , 169-181.	0.8	4
84	Analysis of Protein Glycosylation and Phosphorylation Using Liquid Phase Separation, Protein Microarray Technology, and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2009, 492, 321-351.	0.9	11
85	Comparative proteomic analysis of low stage and high stage endometrioid ovarian adenocarcinomas. <i>Proteomics - Clinical Applications</i> , 2008, 2, 571-584.	1.6	14
86	Micro-proteome analysis using micro-chromatofocusing in intact protein separations. <i>Journal of Chromatography A</i> , 2008, 1194, 3-10.	3.7	8
87	Plasma Glycoprotein Profiling for Colorectal Cancer Biomarker Identification by Lectin Glycoarray and Lectin Blot. <i>Journal of Proteome Research</i> , 2008, 7, 1693-1703.	3.7	174
88	Enhanced Detection of Autoantibodies on Protein Microarrays Using a Modified Protein Digestion Technique. <i>Journal of Proteome Research</i> , 2008, 7, 2553-2561.	3.7	11
89	Membrane Glycoproteins Associated with Breast Tumor Cell Progression Identified by a Lectin Affinity Approach. <i>Journal of Proteome Research</i> , 2008, 7, 4313-4325.	3.7	67
90	Humoral Response Profiling Reveals Pathways to Prostate Cancer Progression. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 600-611.	3.8	54

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91	Incorporation of Genomics and Proteomics in Drug and Biomarker Development. , 2008, , 713-721.		0
92	Protein biomarkers in cancer: natural glycoprotein microarray approaches. Current Opinion in Molecular Therapeutics, 2008, 10, 602-10.	2.8	24
93	Comparative Proteomics Analysis of Barrett Metaplasia and Esophageal Adenocarcinoma Using Two-dimensional Liquid Mass Mapping. Molecular and Cellular Proteomics, 2007, 6, 987-999.	3.8	33
94	Differential expression of acidic proteins with progression in the MCF10 model of human breast disease. International Journal of Oncology, 2007, 31, 941.	3.3	2
95	Early Detection and Biomarkers in Pancreatic Cancer. Journal of the National Comprehensive Cancer Network: JNCCN, 2007, 5, 1034-1041.	4.9	58
96	N-linked Glycosylation Profiling of Pancreatic Cancer Serum Using Capillary Liquid Phase Separation Coupled with Mass Spectrometric Analysis. Journal of Proteome Research, 2007, 6, 1126-1138.	3.7	150
97	Glycoprotein Microarrays with Multi-Lectin Detection:Â Unique Lectin Binding Patterns as a Tool for Classifying Normal, Chronic Pancreatitis and Pancreatic Cancer Sera. Journal of Proteome Research, 2007, 6, 1864-1874.	3.7	138
98	A proteomic analysis of Psychrobacter articus 273-4 adaptation to low temperature and salinity using a 2-D liquid mapping approach. Electrophoresis, 2007, 28, 467-488.	2.4	40
99	Comprehensive analysis of proteins of pH fractionated samples using monolithic LC/MS/MS, intact MW measurement and MALDI-QIT-TOF MS. Journal of Mass Spectrometry, 2007, 42, 312-334.	1.6	9
100	Characterization of apolipoprotein and apolipoprotein precursors in pancreatic cancer serum samples via two-dimensional liquid chromatography and mass spectrometry. Journal of Chromatography A, 2007, 1162, 117-125.	3.7	39
101	Comparative proteomic analysis of B. cenocepacia using two-dimensional liquid separations coupled with mass spectrometry. Analytica Chimica Acta, 2007, 592, 91-100.	5.4	14
102	Proteomic profiling identifies breast tumor metastasis-associated factors in an isogenic model. Proteomics, 2007, 7, 299-312.	2.2	45
103	Differential expression of ribosomal proteins in a human metastasis model identified by coupling 2-D liquid chromatography and mass spectrometry. Cancer Genomics and Proteomics, 2007, 4, 329-39.	2.0	12
104	Differential Phosphoprotein Mapping in Cancer Cells Using Protein Microarrays Produced from 2-D Liquid Fractionation. Analytical Chemistry, 2006, 78, 702-710.	6.5	29
105	Screening of Glycosylation Patterns in Serum Using Natural Glycoprotein Microarrays and Multi-Lectin Fluorescence Detection. Analytical Chemistry, 2006, 78, 6411-6421.	6.5	99
106	Monolithic Column HPLC Separation of Intact Proteins Analyzed by LC-MALDI Using On-Plate Digestion:Â An Approach To Integrate Protein Separation and Identification. Analytical Chemistry, 2006, 78, 5198-5204.	6.5	34
107	Comparative Serum Glycoproteomics Using Lectin Selected Sialic Acid Glycoproteins with Mass Spectrometric Analysis:Â Application to Pancreatic Cancer Serum. Journal of Proteome Research, 2006, 5, 1792-1802.	3.7	209
108	Proteomic analysis of estrogen response of premalignant human breast cells using a 2-D liquid separation/mass mapping technique. Proteomics, 2006, 6, 3847-3861.	2.2	21

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109	Proteomic analysis of cold adaptation in a Siberian permafrost bacterium - <i>Exiguobacterium sibiricum</i> 255-15 by two-dimensional liquid separation coupled with mass spectrometry. <i>Proteomics</i> , 2006, 6, 5221-5233.	2.2	32
110	Classifications of ovarian cancer tissues by proteomic patterns. <i>Proteomics</i> , 2006, 6, 5846-5856.	2.2	41
111	Toward high sequence coverage of proteins in human breast cancer cells using on-line monolith-based HPLC-ESI-TOF MS compared to CE MS. <i>Electrophoresis</i> , 2006, 27, 2126-2138.	2.4	14
112	Automated integration of monolith-based protein separation with on-plate digestion for mass spectrometric analysis of esophageal adenocarcinoma human epithelial samples. <i>Electrophoresis</i> , 2006, 27, 3643-3651.	2.4	21
113	Classification of Cancer Cell Lines Using an Automated Two-dimensional Liquid Mapping Method with Hierarchical Clustering Techniques. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 43-52.	3.8	21
114	Mass mapping of cancer cell lysates using two-dimensional liquid separations, electrospray-time of flight-mass spectrometry, and automated data processing. <i>Electrophoresis</i> , 2005, 26, 248-256.	2.4	16
115	Protein pI Shifts due to Posttranslational Modifications in the Separation and Characterization of Proteins. <i>Analytical Chemistry</i> , 2005, 77, 2745-2755.	6.5	155
116	A two-dimensional liquid-phase separation method coupled with mass spectrometry for proteomic studies of breast cancer and biomarker identification. <i>Proteomics</i> , 2004, 4, 562-577.	2.2	91
117	Comprehensive proteome analysis of ovarian cancers using liquid phase separation, mass mapping and tandem mass spectrometry: A strategy for identification of candidate cancer biomarkers. <i>Proteomics</i> , 2004, 4, 2476-2495.	2.2	59
118	Identification of metastasis-associated proteins in a human tumor metastasis model using the mass-mapping technique. <i>Proteomics</i> , 2004, 4, 2754-2765.	2.2	53
119	Narrow-band fractionation of proteins from whole cell lysates using isoelectric membrane focusing and nonporous reversed-phase separations. <i>Electrophoresis</i> , 2004, 25, 949-958.	2.4	18
120	Identification of low molecular weight proteins isolated by 2-D liquid separations. <i>Journal of Mass Spectrometry</i> , 2004, 39, 770-780.	1.6	27
121	Use of two-dimensional liquid fractionation for separation of proteins from cell lysates without the presence of methionine oxidation. <i>Journal of Chromatography A</i> , 2004, 1053, 133-142.	3.7	12
122	Electrophoretic mobility for peptides with post-translational modifications in capillary electrophoresis. <i>Electrophoresis</i> , 2003, 24, 782-793.	2.4	32
123	Protein microarrays using liquid phase fractionation of cell lysates. <i>Proteomics</i> , 2003, 3, 1228-1235.	2.2	47
124	Profiling the progression of cancer: Separation of microsomal proteins in MCF10 breast epithelial cell lines using nonporous chromatophoresis. <i>Proteomics</i> , 2003, 3, 1256-1269.	2.2	26
125	Proteomic Analysis Using 2-D Liquid Separations of Intact Proteins From Whole Cell Lysates. <i>Current Protocols in Protein Science</i> , 2003, 34, Unit 23.3.	2.8	4
126	A Comparison of Drug-Treated and Untreated HCT-116 Human Colon Adenocarcinoma Cells Using a 2-D Liquid Separation Mapping Method Based upon Chromatofocusing PI Fractionation. <i>Analytical Chemistry</i> , 2003, 75, 2299-2308.	6.5	83

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127	High Sequence Coverage of Proteins Isolated from Liquid Separations of Breast Cancer Cells Using Capillary Electrophoresis-Time-of-Flight MS and MALDI-TOF MS Mapping. <i>Analytical Chemistry</i> , 2003, 75, 6209-6217.	6.5	51
128	Two-dimensional liquid chromatography protein expression mapping for differential proteomic analysis of normal and O157:H7 <i>Escherichia coli</i> . <i>BioTechniques</i> , 2003, 35, 1202-1212.	1.8	40
129	A 2-D Liquid Separations/Mass Mapping Method for Interlysate Comparison of Ovarian Cancers. <i>Analytical Chemistry</i> , 2002, 74, 1779-1791.	6.5	124
130	A protein molecular weight map of ES2 clear cell ovarian carcinoma cells using a two-dimensional liquid separations/mass mapping technique. <i>Electrophoresis</i> , 2002, 23, 3168-3181.	2.4	60
131	Three-dimensional protein map according to pI, hydrophobicity and molecular mass. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002, 774, 53-58.	2.3	23
132	Two-dimensional liquid separationsâ€“mass mapping of proteins from human cancer cell lysates. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002, 782, 183-196.	2.3	108
133	Differential Screening and Mass Mapping of Proteins from Premalignant and Cancer Cell Lines Using Nonporous Reversed-Phase HPLC Coupled with Mass Spectrometric Analysis. <i>Analytical Chemistry</i> , 2001, 73, 1219-1227.	6.5	72
134	Comparison of the capabilities of liquid isoelectric focusingâ€“one-dimensional nonporous silica reversed-phase liquid chromatographyâ€“electrospray ionization time-of-flight mass spectrometry and liquid isoelectric focusingâ€“one-dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis mass mapping for the analysis of intact protein molecular masses. <i>Biomedical Applications</i> , 2001, 763, 139-148.	1.7	12
135	Chromatofocusing nonporous reversed-phase high-performance liquid chromatography/electrospray ionization time-of-flight mass spectrometry of proteins from human breast cancer whole cell lysates: a novel two-dimensional liquid chromatography/mass spectrometry method. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 291-296.	1.5	92
136	Isoelectric focusing nonporous silica reversed-phase high-performance liquid chromatography/electrospray ionization time-of-flight mass spectrometry: a three-dimensional liquid-phase protein separation method as applied to the human erythroleukemia cell-line. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 1649-1661.	1.5	69
137	Studies of posttranslational modifications in spiny dogfish myelin basic protein. <i>Neurochemical Research</i> , 2001, 26, 539-547.	3.3	16
138	Elucidation of peptide metabolism by on-line immunoaffinity liquid chromatography mass spectrometry. , 2000, 14, 261-269.		9
139	Mouse liver selenium-binding protein decreased in abundance by peroxisome proliferators. <i>Electrophoresis</i> , 2000, 21, 2162-2169.	2.4	37
140	On-line capillary liquid chromatography tandem mass spectrometry on an ion trap/ reflectron time-of-flight mass spectrometer using the sequence tag database search approach for peptide sequencing and protein identification. <i>Journal of the American Society for Mass Spectrometry</i> , 2000, 11, 127-135.	2.8	15
141	Use of non-porous reversed-phase high-performance liquid chromatography for protein profiling and isolation of proteins induced by temperature variations for Siberian permafrost bacteria with identification by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and capillary electrophoresisâ€“electrospray ionization mass spectrometry. <i>Biomedical Applications</i> , 2000, 748, 167-177.	1.7	25
142	Isoelectric Focusing Nonporous RP HPLC:Â A Two-Dimensional Liquid-Phase Separation Method for Mapping of Cellular Proteins with Identification Using MALDI-TOF Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 1099-1111.	6.5	240
143	Elucidation of peptide metabolism by onâ€“line immunoaffinity liquid chromatography mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 261-269.	1.5	1
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