David M Lubman

List of Publications by Year
in descending order

197	8,097	34105 52	69250 77
papers	citations	h-index	g-index

199	199	199	7059
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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. Analytical Chemistry, 2000, 72, 1099-1111.	6.5	240
2	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
3	Differentiation of bacteria using protein profiles from matrixâ€assisted laser desorption/ionization timeâ€ofâ€flight mass spectrometry. Rapid Communications in Mass Spectrometry, 1994, 8, 1026-1030.	1.5	187
4	Plasma Glycoprotein Profiling for Colorectal Cancer Biomarker Identification by Lectin Glycoarray and Lectin Blot. Journal of Proteome Research, 2008, 7, 1693-1703.	3.7	174
5	Protein pIShifts due to Posttranslational Modifications in the Separation and Characterization of Proteins. Analytical Chemistry, 2005, 77, 2745-2755.	6.5	155
6	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
7	Protein Digest Analysis by Pressurized Capillary Electrochromatography Using an Ion Trap Storage/Reflectron Time-of-Flight Mass Detector. Analytical Chemistry, 1997, 69, 2908-2913.	6.5	141
8	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
9	Comparison of an Optimized Ultracentrifugation Method versus Size-Exclusion Chromatography for Isolation of Exosomes from Human Serum. Journal of Proteome Research, 2018, 17, 3599-3605.	3.7	136
10	A 2-D Liquid Separations/Mass Mapping Method for Interlysate Comparison of Ovarian Cancers. Analytical Chemistry, 2002, 74, 1779-1791.	6.5	124
11	CD90 is Identified as a Candidate Marker for Cancer Stem Cells in Primary High-Grade Gliomas Using Tissue Microarrays. Molecular and Cellular Proteomics, 2012, 11, M111.010744.	3.8	122
12	Aberrant glycosylation and cancer biomarker discovery: a promising and thorny journey. Clinical Chemistry and Laboratory Medicine, 2019, 57, 407-416.	2.3	111
13	Pancreatic Cancer Serum Detection Using a Lectin/Glyco-Antibody Array Method. Journal of Proteome Research, 2009, 8, 483-492.	3.7	109
14	Two-dimensional liquid separationsâ€“mass mapping of proteins from human cancer cell lysates. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2002, 782, 183-196.	2.3	108
15	Glycoprotein Biomarker Panel for Pancreatic Cancer Discovered by Quantitative Proteomics Analysis. Journal of Proteome Research, 2014, 13, 1873-1884.	3.7	107
16	An ion trap storage/timeâ€ofâ€flight mass spectrometer. Review of Scientific Instruments, 1992, 63, 4277-4284.	1.3	103
17	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
18	Identification and Confirmation of Differentially Expressed Fucosylated Glycoproteins in the Serum of Ovarian Cancer Patients Using a Lectin Array and LCâ€“MS/MS. Journal of Proteome Research, 2012, 11, 4541-4552.	3.7	102

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19	Screening of Glycosylation Patterns in Serum Using Natural Glycoprotein Microarrays and Multi-Lectin Fluorescence Detection. Analytical Chemistry, 2006, 78, 6411-6421.	6.5	99
20	Use of a Mixed-Mode Packing and Voltage Tuning for Peptide Mixture Separation in Pressurized Capillary Electrochromatography with an Ion Trap Storage/Reflectron Time-of-Flight Mass Spectrometer Detector. Analytical Chemistry, 1999, 71, 1786-1791.	6.5	93
21	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. Rapid Communications in Mass Spectrometry, 2001, 15, 291-296.	1.5	92
22	Detection of electrospray ionization using a quadrupole ion trap storage/reflectron time-of-flight mass spectrometer. Analytical Chemistry, 1993, 65, 2614-2620.	6.5	91
23	A two-dimensional liquid-phase separation method coupled with mass spectrometry for proteomic studies of breast cancer and biomarker identification. Proteomics, 2004, 4, 562-577.	2.2	91
24	Quantitative Proteomic Analysis of Serum Exosomes from Patients with Locally Advanced Pancreatic Cancer Undergoing Chemoradiotherapy. Journal of Proteome Research, 2017, 16, 1763-1772.	3.7	87
25	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. Analytical Chemistry, 2003, 75, 2299-2308.	6.5	83
26	Characterization of SDSâ˜PAGE-Separated Proteins by Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry. Analytical Chemistry, 1996, 68, 1012-1018.	6.5	80
27	Use of a Polybrene Capillary Coating in Capillary Electrophoresis for Rapid Analysis of Hemoglobin Variants with On-Line Detection via an Ion Trap Storage/Reflectron Time-of-Flight Mass Spectrometer. Analytical Chemistry, 1997, 69, 2451-2456.	6.5	78
28	Rapid screening of genetic polymorphisms using buccal cell DNA with detection by matrix-assisted laser desorption/ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 1995, 9, 735-743.	1.5	75
29	Identification of Glycoprotein Markers for Pancreatic Cancer CD24⁺CD44⁺ Stem-like Cells Using Nano-LCâ€“MS/MS and Tissue Microarray. Journal of Proteome Research, 2012, 11, 2272-2281.	3.7	73
30	Differential Screening and Mass Mapping of Proteins from Premalignant and Cancer Cell Lines Using Nonporous Reversed-Phase HPLC Coupled with Mass Spectrometric Analysis. Analytical Chemistry, 2001, 73, 1219-1227.	6.5	72
31	High-Performance Chemical Isotope Labeling Liquid Chromatography Mass Spectrometry for Exosome Metabolomics. Analytical Chemistry, 2018, 90, 8314-8319.	6.5	72
32	Identification of Cell Surface Glycoprotein Markers for Glioblastoma-Derived Stem-Like Cells Using a Lectin Microarray and LCâ˜MS/MS Approach. Journal of Proteome Research, 2010, 9, 2565-2572.	3.7	71
33	Use of an Ion Trap Storage/Reflectron Time-of-Flight Mass Spectrometer as a Rapid and Sensitive Detector for Capillary Electrophoresis in Protein Digest Analysis. Analytical Chemistry, 1996, 68, 3388-3396.	6.5	69
34	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. Rapid Communications in Mass Spectrometry, 2001, 15, 1649-1661.	1.5	69
35	Identification and Confirmation of Biomarkers Using an Integrated Platform for Quantitative Analysis of Glycoproteins and Their Glycosylations. Journal of Proteome Research, 2010, 9, 798-805.	3.7	68
36	Mass Spectrometric Assay for Analysis of Haptoglobin Fucosylation in Pancreatic Cancer. Journal of Proteome Research, 2011, 10, 2602-2611.	3.7	68

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37	Open-Tubular Capillary Electrochromatography with an On-Line Ion Trap Storage/Reflectron Time-of-Flight Mass Detector for Ultrafast Peptide Mixture Analysis. Analytical Chemistry, 1997, 69, 320-326.	6.5	67
38	Membrane Glycoproteins Associated with Breast Tumor Cell Progression Identified by a Lectin Affinity Approach. Journal of Proteome Research, 2008, 7, 4313-4325.	3.7	67
39	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
40	Pulsed laser desorption method for volatilizing thermally labile molecules for supersonic jet spectroscopy. Review of Scientific Instruments, 1988, 59, 557-561.	1.3	65
41	LCâ€MS/MS isomeric profiling of permethylated Nâ€glycans derived from serum haptoglobin of hepatocellular carcinoma (HCC) and cirrhotic patients. Electrophoresis, 2017, 38, 2160-2167.	2.4	65
42	Glycoproteomic markers of hepatocellular carcinomaâ€mass spectrometry based approaches. Mass Spectrometry Reviews, 2019, 38, 265-290.	5.4	64
43	Determination of Bacterial Protein Profiles by Matrix-assisted Laser Desorption/Ionization Mass Spectrometry with High-performance Liquid Chromatography. , 1996, 10, 1219-1226.		63
44	Determination of the Sites of Posttranslational Modifications in the Charge Isomers of Bovine Myelin Basic Protein by Capillary Electrophoresis-Mass Spectroscopyâ€. Biochemistry, 1998, 37, 2441-2449.	2.5	62
45	Glycoprotein analysis using protein microarrays and mass spectrometry. Mass Spectrometry Reviews, 2010, 29, 830-844.	5.4	62
46	A protein molecular weight map of ES2 clear cell ovarian carcinoma cells using a two-dimensional liquid separations/mass mapping technique. Electrophoresis, 2002, 23, 3168-3181.	2.4	60
47	Comprehensive proteome analysis of ovarian cancers using liquid phase separation, mass mapping and tandem mass spectrometry: A strategy for identification of candidate cancer biomarkers. Proteomics, 2004, 4, 2476-2495.	2.2	59
48	Altered Expression of Sialylated Glycoproteins in Ovarian Cancer Sera Using Lectin-based ELISA Assay and Quantitative Glycoproteomics Analysis. Journal of Proteome Research, 2013, 12, 3342-3352.	3.7	59
49	Separation of Tryptic Digests Using a Modified Buffer in Pressurized Capillary Electrochromatography with an Ion Trap Storage/Reflectron Time-of-Flight Mass Spectrometer. Analytical Chemistry, 1998, 70, 3003-3008.	6.5	58
50	Early Detection and Biomarkers in Pancreatic Cancer. Journal of the National Comprehensive Cancer Network: JNCCN, 2007, 5, 1034-1041.	4.9	58
51	Analytical multiphoton ionization mass spectrometry. Part I. Theory and instrumentation. Mass Spectrometry Reviews, 1988, 7, 535-554.	5.4	56
52	Rapid profiling ofE. coli proteins up to 500 kDa from whole cell lysates using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Rapid Communications in Mass Spectrometry, 1997, 11, 1900-1908.	1.5	56
53	Exosome enrichment of human serum using multiple cycles of centrifugation. Electrophoresis, 2015, 36, 2017-2026.	2.4	55
54	Humoral Response Profiling Reveals Pathways to Prostate Cancer Progression. Molecular and Cellular Proteomics, 2008, 7, 600-611.	3.8	54

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55	Identification of metastasis-associated proteins in a human tumor metastasis model using the mass-mapping technique. Proteomics, 2004, 4, 2754-2765.	2.2	53
56	Overexpression of CD90 (Thy-1) in Pancreatic Adenocarcinoma Present in the Tumor Microenvironment. PLoS ONE, 2014, 9, e115507.	2.5	53
57	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. Analytical Chemistry, 2003, 75, 6209-6217.	6.5	51
58	Differential Quantitative Determination of Site-Specific Intact N-Glycopeptides in Serum Haptoglobin between Hepatocellular Carcinoma and Cirrhosis Using LC-EThcD-MS/MS. Journal of Proteome Research, 2018, 18, 359-371.	3.7	50
59	Rapid Profiling of Induced Proteins in Bacteria Using MALDI-TOF Mass Spectrometric Detection of Nonporous RP HPLC-Separated Whole Cell Lysates. Analytical Chemistry, 1999, 71, 3894-3900.	6.5	48
60	Mass-Selected Site-Specific Core-Fucosylation of Ceruloplasmin in Alcohol-Related Hepatocellular Carcinoma. Journal of Proteome Research, 2014, 13, 2887-2896.	3.7	48
61	Analytical multiphoton ionization mass spectrometry. Part II. Applications. Mass Spectrometry Reviews, 1988, 7, 559-592.	5.4	47
62	Protein microarrays using liquid phase fractionation of cell lysates. Proteomics, 2003, 3, 1228-1235.	2.2	47
63	Matrix-assisted laser desorption/ionization mass sectrometry of restriction enzyme-digested plasmid DNA using an active nafion substrate. Rapid Communications in Mass Spectrometry, 1994, 8, 687-691.	1.5	45
64	Proteomic profiling identifies breast tumor metastasis-associated factors in an isogenic model. Proteomics, 2007, 7, 299-312.	2.2	45
65	Matrix-Assisted Laser Desorption/Ionization Using an Active Perfluorosulfonated Ionomer Film Substrate. Analytical Chemistry, 1994, 66, 3423-3430.	6.5	44
66	Comparative proteomic study of two closely related ovarian endometrioid adenocarcinoma cell lines using cIEF fractionation and pathway analysis. Electrophoresis, 2009, 30, 1119-1131.	2.4	42
67	Classifications of ovarian cancer tissues by proteomic patterns. Proteomics, 2006, 6, 5846-5856.	2.2	41
68	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
69	Two-dimensional liquid chromatography protein expression mapping for differential proteomic analysis of normal and O157:H7 Escherichia coli. BioTechniques, 2003, 35, 1202-1212.	1.8	40
70	A proteomic analysis ofPsychrobacter articus 273-4 adaptation to low temperature and salinity using a 2-D liquid mapping approach. Electrophoresis, 2007, 28, 467-488.	2.4	40
71	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
72	The identification of phosphoglycerate kinaseâ€1 and histone H4 autoantibodies in pancreatic cancer patient serum using a natural protein microarray. Electrophoresis, 2009, 30, 2215-2226.	2.4	38

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73	Target Proteomic Profiling of Frozen Pancreatic CD24+ Adenocarcinoma Tissues by Immuno-Laser Capture Microdissection and Nano-LCâ€“MS/MS. Journal of Proteome Research, 2013, 12, 2791-2804.	3.7	38
74	ESIâ€“LCâ€“MS Method for Haptoglobin Fucosylation Analysis in Hepatocellular Carcinoma and Liver Cirrhosis. Journal of Proteome Research, 2015, 14, 5388-5395.	3.7	38
75	Platelet Factor 4 as a Novel Exosome Marker in MALDI-MS Analysis of Exosomes from Human Serum. Analytical Chemistry, 2019, 91, 13297-13305.	6.5	38
76	Mouse liver selenium-binding protein decreased in abundance by peroxisome proliferators. Electrophoresis, 2000, 21, 2162-2169.	2.4	37
77	Mass-Selected Site-Specific Core-Fucosylation of Serum Proteins in Hepatocellular Carcinoma. Journal of Proteome Research, 2015, 14, 4876-4884.	3.7	37
78	Glycopeptide Biomarkers in Serum Haptoglobin for Hepatocellular Carcinoma Detection in Patients with Nonalcoholic Steatohepatitis. Journal of Proteome Research, 2020, 19, 3452-3466.	3.7	37
79	Simulation of External Ion Injection, Cooling and Extraction Processes with SIMION 6.0 for the Ion Trap/Reflectron Time-of-flight Mass Spectrometer. Rapid Communications in Mass Spectrometry, 1997, 11, 1467-1477.	1.5	36
80	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
81	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
82	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
83	Rapid screening of protein profiles of human breast cancer cell lines using non-porous reversed-phase high performance liquid chromatography separation with matrix-assisted laser desorption/ionization time-of-flight mass spectral analysis. , 1999, 13, 1808-1812.		32
84	Electrophoretic mobility for peptides with post-translational modifications in capillary electrophoresis. Electrophoresis, 2003, 24, 782-793.	2.4	32
85	Proteomic analysis of cold adaptation in a Siberian permafrost bacterium - Exiguobacterium sibiricum 255-15 by two-dimensional liquid separation coupled with mass spectrometry. Proteomics, 2006, 6, 5221-5233.	2.2	32
86	Differential Protein Mapping of Ovarian Serous Adenocarcinomas: Identification of Potential Markers for Distinct Tumor Stage. Journal of Proteome Research, 2009, 8, 1452-1463.	3.7	32
87	Protein profiles and identification of high performance liquid chromatography isolated proteins of cancer cell lines using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Rapid Communications in Mass Spectrometry, 1998, 12, 1986-1993.	1.5	31
88	Plasma Proteomic Analysis May Identify New Markers for Radiation-Induced Lung Toxicity in Patients With Nonâ€“Small-Cell Lung Cancer. International Journal of Radiation Oncology Biology Physics, 2010, 77, 867-876.	0.8	31
89	Quantitative Proteomic Profiling Studies of Pancreatic Cancer Stem Cells. Journal of Proteome Research, 2010, 9, 3394-3402.	3.7	31
90	Glycoproteomic Analysis of Glioblastoma Stem Cell Differentiation. Journal of Proteome Research, 2011, 10, 330-338.	3.7	31

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91	Serum Protein Biomarkers of Fibrosis Aid in Risk Stratification of Future Stricturing Complications in Pediatric Crohn's Disease. American Journal of Gastroenterology, 2019, 114, 777-785.	0.4	31
92	An N-glycosylation Analysis of Human Alpha-2-Macroglobulin Using an Integrated Approach. Journal of Proteomics and Bioinformatics, 2012, 05, 127-134.	0.4	31
93	Enhancement of resolution in matrix-assisted laser desorption using an ion-trap storage/reflectron time-of-flight mass spectrometer. Rapid Communications in Mass Spectrometry, 1993, 7, 837-843.	1.5	30
94	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
95	Differential Phosphoprotein Mapping in Cancer Cells Using Protein Microarrays Produced from 2-D Liquid Fractionation. Analytical Chemistry, 2006, 78, 702-710.	6.5	29
96	Ion fragmentation activated by matrix-assisted laser desorption/ionization in an ion-trap/reflectron time-of-flight device. Rapid Communications in Mass Spectrometry, 1994, 8, 407-416.	1.5	27
97	Identification of low molecular weight proteins isolated by 2-D liquid separations. Journal of Mass Spectrometry, 2004, 39, 770-780.	1.6	27
98	A multiplexed bead assay for profiling glycosylation patterns on serum protein biomarkers of pancreatic cancer. Electrophoresis, 2011, 32, 2028-2035.	2.4	27
99	Isobaric Protein-Level Labeling Strategy for Serum Glycoprotein Quantification Analysis by Liquid Chromatographyâ€“Tandem Mass Spectrometry. Analytical Chemistry, 2013, 85, 5353-5357.	6.5	27
100	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
101	Rapid separation of blood plasma exosomes from low-density lipoproteins via a hydrophobic interaction chromatography method on a polyester capillary-channeled polymer fiber phase. Analytica Chimica Acta, 2021, 1167, 338578.	5.4	27
102	A guide to mass spectrometric analysis of extracellular vesicle proteins for biomarker discovery. Mass Spectrometry Reviews, 2023, 42, 844-872.	5.4	27
103	The Use of On-line Capillary Electrophoresis/Electrospray Ionization with Detection via an Ion Trap Storage/Reflectron Time-of-flight Mass Spectrometer for Rapid Mutation-site Analysis of Hemoglobin Variants. , 1997, 11, 99-108.		26
104	Profiling the progression of cancer: Separation of microsomal proteins in MCF10 breast epithelial cell lines using nonporous chromatophoresis. Proteomics, 2003, 3, 1256-1269.	2.2	26
105	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
106	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. Biomedical Applications, 2000, 748, 167-177.	1.7	25
107	Differential profiling studies of Nâ€linked glycoproteins in glioblastoma cancer stem cells upon treatment with Î³â€secretase inhibitor. Proteomics, 2011, 11, 4021-4028.	2.2	25
108	Protein biomarkers in cancer: natural glycoprotein microarray approaches. Current Opinion in Molecular Therapeutics, 2008, 10, 602-10.	2.8	24

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109	A highâ€temperature pulsed solenoid valve for supersonic jet introduction up to 550â€‰Â°C. Review of Scientific Instruments, 1989, 60, 499-501.	1.3	23
110	Procedures for detection of DNA by matrix-assisted laser desorption/ionization mass spectrometry using a modified nafion film substrate. Rapid Communications in Mass Spectrometry, 1995, 9, 1172-1176.	1.5	23
111	Three-dimensional protein map according to pI, hydrophobicity and molecular mass. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2002, 774, 53-58.	2.3	23
112	The identification of auto-antibodies in pancreatic cancer patient sera using a naturally fractionated Panc-1 cell line. Cancer Biomarkers, 2010, 7, 25-37.	1.7	23
113	Serum Autoantibody Profiling Using a Natural Glycoprotein Microarray for the Prognosis of Early Melanoma. Journal of Proteome Research, 2010, 9, 6044-6051.	3.7	23
114	A quantitative proteomics analysis of MCF7 breast cancer stem and progenitor cell populations. Proteomics, 2015, 15, 3772-3783.	2.2	23
115	A Panel of Glycopeptides as Candidate Biomarkers for Early Diagnosis of NASH Hepatocellular Carcinoma Using a Stepped HCD Method and PRM Evaluation. Journal of Proteome Research, 2021, 20, 3278-3289.	3.7	23
116	Genotyping of Apolipoprotein E by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. , 1998, 12, 1045-1050.		22
117	On-Line Capillary Electrophoresis/Microelectrospray Ionization-Tandem Mass Spectrometry Using an Ion Trap Storage/Time-of-Flight Mass Spectrometer with SWIFT Technology. Analytical Chemistry, 1999, 71, 3591-3597.	6.5	22
118	Labelâ€free relative quantification of alphaâ€2â€macroglobulin siteâ€specific coreâ€fucosylation in pancreatic cancer by LCâ€MS/MS. Electrophoresis, 2014, 35, 2108-2115.	2.4	22
119	The analysis of alphaâ€1â€antitrypsin glycosylation with direct LCâ€MS/MS. Electrophoresis, 2018, 39, 2351-2361.	2.4	22
120	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
121	Automated integration of monolith-based protein separation with on-plate digestion for mass spectrometric analysis of esophageal adenocarcinoma human epithelial samples. Electrophoresis, 2006, 27, 3643-3651.	2.4	21
122	Classification of Cancer Cell Lines Using an Automated Two-dimensional Liquid Mapping Method with Hierarchical Clustering Techniques. Molecular and Cellular Proteomics, 2006, 5, 43-52.	3.8	21
123	A comparative phosphoproteomic analysis of a human tumor metastasis model using a labelâ€free quantitative approach. Electrophoresis, 2010, 31, 1842-1852.	2.4	21
124	Quantitative Analysis of Î±-1-Antitrypsin Glycosylation Isoforms in HCC Patients Using LC-HCD-PRM-MS. Analytical Chemistry, 2020, 92, 8201-8208.	6.5	21
125	Column-based Technology for CD9-HPLC Immunoaffinity Isolation of Serum Extracellular Vesicles. Journal of Proteome Research, 2021, 20, 4901-4911.	3.7	20
126	Serum Glycoproteome Profiles for Distinguishing Intestinal Fibrosis from Inflammation in Crohn's Disease. PLoS ONE, 2017, 12, e0170506.	2.5	20

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127	Annexin A10 is a candidate marker associated with the progression of pancreatic precursor lesions to adenocarcinoma. PLoS ONE, 2017, 12, e0175039.	2.5	20
128	Resonant two-photon ionization for the identification of thermal decomposition products in the laser desorption of small peptides. Rapid Communications in Mass Spectrometry, 1989, 3, 12-16.	1.5	19
129	Matrix-assisted Laser Desorption/Ionization Time-of-flight Mass Spectrometry as a Rapid Screening Method to Detect Mutations Causing Tay-Sachs Disease. Rapid Communications in Mass Spectrometry, 1997, 11, 1144-1150.	1.5	19
130	Design of a pulsed valve for highâ€pressure NH3 injection into supersonic beam/mass spectrometry. Review of Scientific Instruments, 1988, 59, 2460-2463.	1.3	18
131	Improved resolution in the detection of oligonucleotides up to 60-mers in matrix-assisted laser desorption/ionization time-of-flight mass spectrometry using pulsed-delayed extraction with a simple high voltage transistor switch. , 1997, 11, 987-992.		18
132	Rapid identification and screening of proteins from whole cell lysates of human erythroleukemia cells in the liquid phase, using non-porous reversed phase high-performance liquid chromatography separations of proteins followed by multi-assisted laser desorption/ionization mass spectrometry analysis and sequence database searching. , 1998, 12, 1994-2003.		18
133	Narrow-band fractionation of proteins from whole cell lysates using isoelectric membrane focusing and nonporous reversed-phase separations. Electrophoresis, 2004, 25, 949-958.	2.4	18
134	A novel method of highâ€purity extracellular vesicle enrichment from microliterâ€scale human serum for proteomic analysis. Electrophoresis, 2021, 42, 245-256.	2.4	18
135	On-line capillary separations/tandem mass spectrometry for protein digest analysis by using an ion trap storage/reflectron time-of flight mass detector. Journal of the American Society for Mass Spectrometry, 1997, 8, 1237-1246.	2.8	17
136	Identification of proteins from two-dimensional gel electrophoresis of human erythroleukemia cells using capillary high performance liquid chromatography/electrospray-ion trap-reflectron time-of-flight mass spectrometry with two-dimensional topographic map analysis of in-gel tryptic digest products. , 1999, 13, 1907-1916.		17
137	Capillary electrophoresis/tandem mass spectrometry for analysis of proteins from two-dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis. , 1999, 13, 2327-2334.		17
138	Development of an Integrated Pipeline for Profiling Microbial Proteins from Mouse Fecal Samples by LCâ€“MS/MS. Journal of Proteome Research, 2016, 15, 3635-3642.	3.7	17
139	Evaluation of AGP Fucosylation as a Marker for Hepatocellular Carcinoma of Three Different Etiologies. Scientific Reports, 2019, 9, 11580.	3.3	17
140	Procedures for Tandem Mass Spectrometry on an Ion Trap Storage/Reflectron Time-of-flight Mass Spectrometer. , 1996, 10, 1911-1920.		16
141	Studies of posttranslational modifications in spiny dogfish myelin basic protein. Neurochemical Research, 2001, 26, 539-547.	3.3	16
142	Mass mapping of cancer cell lysates using two-dimensional liquid separations, electrospray-time of flight-mass spectrometry, and automated data processing. Electrophoresis, 2005, 26, 248-256.	2.4	16
143	PRM-MS Quantitative Analysis of Isomeric N-Glycopeptides Derived from Human Serum Haptoglobin of Patients with Cirrhosis and Hepatocellular Carcinoma. Metabolites, 2021, 11, 563.	2.9	16
144	A continuous flow probe method for onâ€line introduction of liquid samples for detection by laser desorption with resonant twoâ€photon ionization in supersonic beam mass spectrometry. Review of Scientific Instruments, 1991, 62, 957-962.	1.3	15

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145	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. Journal of the American Society for Mass Spectrometry, 2000, 11, 127-135.	2.8	15
146	Doseâ€dependent proteomic analysis of glioblastoma cancer stem cells upon treatment with Î³â€secretase inhibitor. Proteomics, 2011, 11, 4529-4540.	2.2	15
147	Toward high sequence coverage of proteins in human breast cancer cells using on-line monolith-based HPLC-ESI-TOF MS compared to CE MS. Electrophoresis, 2006, 27, 2126-2138.	2.4	14
148	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
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