Rainer Bischoff

List of Publications by Year in descending order

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275 papers 10,727 citations

54 h-index 48315 88 g-index

293 all docs

293 docs citations

times ranked

293

13646 citing authors

#	Article	IF	Citations
1	Physiology and pathophysiology of matrix metalloproteases. Amino Acids, 2011, 41, 271-290.	2.7	630
2	Protein Tyrosine Nitration: Selectivity, Physicochemical and Biological Consequences, Denitration, and Proteomics Methods for the Identification of Tyrosine-Nitrated Proteins. Journal of Proteome Research, 2009, 8, 3222-3238.	3.7	337
3	Identification of a heparin-binding hemagglutinin present in mycobacteria Journal of Experimental Medicine, 1996, 184, 993-1001.	8.5	277
4	An Automated On-Line Multidimensional HPLC System for Protein and Peptide Mapping with Integrated Sample Preparation. Analytical Chemistry, 2002, 74, 809-820.	6.5	274
5	Recommendations for Biomarker Identification and Qualification in Clinical Proteomics. Science Translational Medicine, 2010, 2, 46ps42.	12.4	273
6	Cytoplasmic p21 expression levels determine cisplatin resistance in human testicular cancer. Journal of Clinical Investigation, 2010, 120, 3594-3605.	8.2	193
7	Receptor–ligand binding assays: Technologies and Applications. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2005, 829, 1-25.	2.3	160
8	Active Metalloproteases of the A Disintegrin And Metalloprotease (ADAM) Family: Biological Function and Structure. Journal of Proteome Research, 2011, 10, 17-33.	3.7	159
9	Molecular characterization of the mycobacterial heparin-binding hemagglutinin, a mycobacterial adhesin. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 12625-12630.	7.1	154
10	Protein biogenesis machinery is a driver of replicative aging in yeast. ELife, 2015, 4, e08527.	6.0	151
11	Protein mapping by two-dimensional high performance liquid chromatography. Journal of Chromatography A, 2000, 893, 293-305.	3.7	144
12	Negative electrospray ionization mass spectrometry of synthetic and chemically modified oligonucleotides. Nucleic Acids Research, 1994, 22, 3895-3903.	14.5	142
13	Glycopeptide enrichment and separation for protein glycosylation analysis. Journal of Separation Science, 2012, 35, 2341-2372.	2.5	138
14	Malnutrition-associated liver steatosis and ATP depletion is caused by peroxisomal and mitochondrial dysfunction. Journal of Hepatology, 2016, 65, 1198-1208.	3.7	133
15	Amino acids: Chemistry, functionality and selected non-enzymatic post-translational modifications. Journal of Proteomics, 2012, 75, 2275-2296.	2.4	131
16	Quantitative Proteomics and Metabolomics Analysis of Normal Human Cerebrospinal Fluid Samples*. Molecular and Cellular Proteomics, 2010, 9, 2063-2075.	3.8	127
17	Sample preparation of human serum for the analysis of tumor markers. Journal of Chromatography A, 2003, 1009, 171-178.	3.7	124
18	A Critical Assessment of Feature Selection Methods for Biomarker Discovery in Clinical Proteomics. Molecular and Cellular Proteomics, 2013, 12, 263-276.	3.8	120

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19	Internal standards in the quantitative determination of protein biopharmaceuticals using liquid chromatography coupled to mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2012, 893-894, 1-14.	2.3	115
20	A novel insect defensin mediates the inducible antibacterial activity in larvae of the dragonfly Aeschna cyanea (Paleoptera, Odonata). FEBS Journal, 1992, 209, 977-984.	0.2	112
21	HDAC 3-selective inhibitor RGFP966 demonstrates anti-inflammatory properties in RAW 264.7 macrophages and mouse precision-cut lung slices by attenuating NF-κB p65 transcriptional activity. Biochemical Pharmacology, 2016, 108, 58-74.	4.4	105
22	Methodological advances in the discovery of protein and peptide disease markers. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2004, 803, 27-40.	2.3	102
23	Cigarette smoke irreversibly modifies glutathione in airway epithelial cells. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2007, 293, L1156-L1162.	2.9	102
24	The Effect of Preanalytical Factors on Stability of the Proteome and Selected Metabolites in Cerebrospinal Fluid (CSF). Journal of Proteome Research, 2009, 8, 5511-5522.	3.7	102
25	Quantitative Proteomics and Metabolomics Analysis of Normal Human Cerebrospinal Fluid Samples. Molecular and Cellular Proteomics, 2010, 9, 2063-2075.	3.8	101
26	Photoaffinity Labeling in Activity-Based Protein Profiling. Topics in Current Chemistry, 2011, 324, 85-113.	4.0	100
27	Nucleic acid resolution by mixed-mode chromatography. Journal of Chromatography A, 1984, 296, 329-337.	3.7	93
28	Isolation of extracellular vesicles with combined enrichment methods. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2021, 1169, 122604.	2.3	90
29	Multidimensional chromatography coupled to mass spectrometry in analysing complex proteomics samples. Journal of Separation Science, 2010, 33, 1421-1437.	2.5	86
30	Silica monolithic columns: Synthesis, characterisation and applications to the analysis of biological molecules. Journal of Separation Science, 2005, 28, 1628-1641.	2.5	85
31	Improvement of Recovery and Repeatability in Liquid Chromatographyâ^'Mass Spectrometry Analysis of Peptides. Journal of Proteome Research, 2007, 6, 781-791.	3.7	83
32	Deamidation of asparagine and glutamine residues in proteins and peptides: structural determinants and analytical methodology. Biomedical Applications, 1994, 662, 261-278.	1.7	81
33	LC-MS/MS-Based Monitoring of <i>In Vivo</i> Protein Biotransformation: Quantitative Determination of Trastuzumab and Its Deamidation Products in Human Plasma. Analytical Chemistry, 2016, 88, 1871-1877.	6.5	81
34	Optimized Time Alignment Algorithm for LCâ^'MS Data: Correlation Optimized Warping Using Component Detection Algorithm-Selected Mass Chromatograms. Analytical Chemistry, 2008, 80, 7012-7021.	6.5	79
35	Disruption of the MDM2–p53 interaction strongly potentiates p53-dependent apoptosis in cisplatin-resistant human testicular carcinoma cells via the Fas/FasL pathway. Cell Death and Disease, 2011, 2, e148-e148.	6.3	77
36	Meta-Inflammation and Metabolic Reprogramming of Macrophages in Diabetes and Obesity: The Importance of Metabolites. Frontiers in Immunology, 2021, 12, 746151.	4.8	77

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37	Chemically Modified, Immobilized Trypsin Reactor with Improved Digestion Efficiency. Journal of Proteome Research, 2005, 4, 1805-1813.	3.7	74
38	High-Sensitivity LC-MS/MS Quantification of Peptides and Proteins in Complex Biological Samples: The Impact of Enzymatic Digestion and Internal Standard Selection on Method Performance. Analytical Chemistry, 2013, 85, 9528-9535.	6. 5	74
39	Application of electrospray mass spectrometry to the characterization of recombinant proteins up to 44 kDa. Biological Mass Spectrometry, 1990, 19, 692-704.	0.5	73
40	Cigarette smoke induces endoplasmic reticulum stress response and proteasomal dysfunction in human alveolar epithelial cells. Experimental Physiology, 2013, 98, 316-325.	2.0	72
41	HDAC1-3 inhibitor MS-275 enhances IL10 expression in RAW264.7 macrophages and reduces cigarette smoke-induced airway inflammation in mice. Scientific Reports, 2017, 7, 45047.	3.3	69
42	Analysis of human serum by liquid chromatography–mass spectrometry: Improved sample preparation and data analysis. Journal of Chromatography A, 2006, 1120, 142-150.	3.7	65
43	Electrochemical Oxidation and Cleavage of Tyrosine- and Tryptophan-Containing Tripeptides. Analytical Chemistry, 2010, 82, 7556-7565.	6.5	65
44	Probes for Non-invasive Matrix Metalloproteinase-targeted Imaging with PET and SPECT. Current Pharmaceutical Design, 2013, 19, 4647-4672.	1.9	65
45	Electrochemistry-Mass Spectrometry in Drug Metabolism and Protein Research. Mini-Reviews in Medicinal Chemistry, 2008, 8, 46-56.	2.4	63
46	Chemically synthesized hydrophobic anion-exchange high-performance liquid chromatography supports used for oligonucleotide resolution by mixed mode chromatography. Journal of Chromatography A, 1983, 270, 117-126.	3.7	62
47	Integrated Quantification and Identification of Aldehydes and Ketones in Biological Samples. Analytical Chemistry, 2014, 86, 5089-5100.	6.5	62
48	Analysis of Recombinant Schistosoma mansoni Antigen rSmp28 by On-Line Liquid Chromatography-Mass Spectrometry Combined with Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis. Analytical Biochemistry, 1994, 216, 127-134.	2.4	61
49	Automated multi-dimensional liquid chromatography: sample preparation and identification of peptides from human blood filtrate. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2004, 803, 121-130.	2.3	60
50	A novel method for the introduction of an aliphatic primary amino group at the $5\hat{a} \in \mathbb{Z}^2$ terminus of synthetic oligonucleotides. Tetrahedron Letters, 1986, 27, 3991-3994.	1.4	59
51	A noise model for mass spectrometry based proteomics. Bioinformatics, 2008, 24, 1070-1077.	4.1	59
52	The Impact of Delayed Storage on the Measured Proteome and Metabolome of Human Cerebrospinal Fluid. Clinical Chemistry, 2011, 57, 1703-1711.	3.2	59
53	tRNA separation by high-performance liquid chromatography using an aggregate of ods-hypersil and trioctyl-methylammonium chloride. Journal of Chromatography A, 1983, 257, 305-315.	3.7	58
54	Selective Acylation of Primary Amines in Peptides and Proteins. Journal of Proteome Research, 2007, 6, 4770-4776.	3.7	57

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55	Lidocaine Oxidation by Electrogenerated Reactive Oxygen Species in the Light of Oxidative Drug Metabolism. Analytical Chemistry, 2010, 82, 7625-7633.	6.5	57
56	Sequence-specific deamidation: isolation and biochemical characterization of succinimide intermediates of recombinant hirudin. Biochemistry, 1993, 32, 725-734.	2.5	54
57	LC–MS analysis of phospholipids and lysophospholipids in human bronchoalveolar lavage fluid. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2005, 814, 21-28.	2.3	54
58	Boron-Doped Diamond Electrodes for the Electrochemical Oxidation and Cleavage of Peptides. Analytical Chemistry, 2013, 85, 6626-6632.	6.5	53
59	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431.	3.7	53
60	Time Alignment Algorithms Based on Selected Mass Traces for Complex LC-MS Data. Journal of Proteome Research, 2010, 9, 1483-1495.	3.7	52
61	Electrochemistry in the Mimicry of Oxidative Drug Metabolism by Cytochrome P450s. Current Drug Metabolism, 2011, 12, 359-371.	1.2	51
62	Profiling and Identification of Cerebrospinal Fluid Proteins in a Rat EAE Model of Multiple Sclerosis. Journal of Proteome Research, 2012, 11, 2048-2060.	3.7	51
63	Stability of energy metabolites—An often overlooked issue in metabolomics studies: A review. Electrophoresis, 2015, 36, 2156-2169.	2.4	51
64	Assessment of Sample Preparation Bias in Mass Spectrometry-Based Proteomics. Analytical Chemistry, 2018, 90, 5405-5413.	6.5	51
65	One- vs two-phase extraction: re-evaluation of sample preparation procedures for untargeted lipidomics in plasma samples. Analytical and Bioanalytical Chemistry, 2018, 410, 5859-5870.	3.7	51
66	Expression of active recombinant human \$alpha;1-antitrypsin in transgenic rabbits. Journal of Biotechnology, 1991, 18, 193-204.	3.8	49
67	Chemical and technical challenges in the analysis of central carbon metabolites by liquid-chromatography mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2014, 966, 21-33.	2.3	49
68	Introduction of 5′-terminal functional groups into synthetic oligonucleotides for selective immobilization. Analytical Biochemistry, 1987, 164, 336-344.	2.4	48
69	Inhibitory activity and conformational transition of alpha1-proteinase inhibitor variants. FEBS Journal, 1991, 202, 1147-1155.	0.2	48
70	Innovations in Serum and Urine Markers in Prostate Cancer. European Urology, 2005, 48, 1031-1041.	1.9	48
71	Comparative Urine Analysis by Liquid Chromatographyâ^'Mass Spectrometry and Multivariate Statistics: Method Development, Evaluation, and Application to Proteinuria. Journal of Proteome Research, 2007, 6, 194-206.	3.7	48
72	Data Sharing Under the General Data Protection Regulation. Hypertension, 2021, 77, 1029-1035.	2.7	47

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73	Electrochemical Oxidation by Square-Wave Potential Pulses in the Imitation of Oxidative Drug Metabolism. Analytical Chemistry, 2011, 83, 5519-5525.	6.5	46
74	The histone acetyltransferase p300 inhibitor C646 reduces pro-inflammatory gene expression and inhibits histone deacetylases. Biochemical Pharmacology, 2016, 102, 130-140.	4.4	46
75	Applications of Monolithic Silica Capillary Columns in Proteomics. Journal of Proteome Research, 2003, 2, 633-642.	3.7	44
76	Two-Dimensional Method for Time Aligning Liquid Chromatographyâ^'Mass Spectrometry Data. Analytical Chemistry, 2008, 80, 3095-3104.	6.5	44
77	In Matrix Derivatization Combined with LC-MS/MS Results in Ultrasensitive Quantification of Plasma Free Metanephrines and Catecholamines. Analytical Chemistry, 2020, 92, 9072-9078.	6.5	44
78	Chemical labeling and enrichment of nitrotyrosine-containing peptides. Talanta, 2010, 80, 1503-1512.	5.5	43
79	A 17.6 kbp region located upstream of the rabbit WAP gene directs high level expression of a functional human protein variant in transgenic mouse milk. FEBS Letters, 1992, 305, 265-268.	2.8	41
80	Oxidative protein labeling in mass-spectrometry-based proteomics. Analytical and Bioanalytical Chemistry, 2010, 397, 3441-3455.	3.7	41
81	Quantification of free and total desmosine and isodesmosine in human urine by liquid chromatography tandem mass spectrometry: A comparison of the surrogate-analyte and the surrogate-matrix approach for quantitation. Journal of Chromatography A, 2014, 1326, 13-19.	3.7	41
82	Relationship between plasma and salivary melatonin and cortisol investigated by LC-MS/MS. Clinical Chemistry and Laboratory Medicine, 2017, 55, 1340-1348.	2.3	41
83	Bioconjugation of Supramolecular Metallacages to Integrin Ligands for Targeted Delivery of Cisplatin. Bioconjugate Chemistry, 2018, 29, 3856-3865.	3.6	41
84	Translational Targeted Proteomics Profiling of Mitochondrial Energy Metabolic Pathways in Mouse and Human Samples. Journal of Proteome Research, 2016, 15, 3204-3213.	3.7	40
85	msCompare: A Framework for Quantitative Analysis of Label-free LC-MS Data for Comparative Candidate Biomarker Studies. Molecular and Cellular Proteomics, 2012, 11, M111.015974.	3.8	39
86	OPLAH ablation leads to accumulation of 5-oxoproline, oxidative stress, fibrosis, and elevated fillings pressures: a murine model for heart failure with a preserved ejection fraction. Cardiovascular Research, 2018, 114, 1871-1882.	3.8	38
87	Serum Protein Markers for the Early Detection of Lung Cancer: A Focus on Autoantibodies. Journal of Proteome Research, 2017, 16, 3-13.	3.7	37
88	Imaging of protein distribution in tissues using mass spectrometry: An interdisciplinary challenge. TrAC - Trends in Analytical Chemistry, 2019, 112, 13-28.	11.4	37
89	Analysis of regulatory phosphorylation sites in ZAP-70 by capillary high-performance liquid chromatography coupled to electrospray ionization or matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Biomedical Applications, 2001, 752, 323-334.	1.7	36
90	Accumulation of 5-oxoproline in myocardial dysfunction and the protective effects of OPLAH. Science Translational Medicine, 2017, 9, .	12.4	36

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91	Poly(ethylene glycol)-Based Stable Isotope Labeling Reagents for the Quantitative Analysis of Low Molecular Weight Metabolites by LCâ°'MS. Analytical Chemistry, 2008, 80, 9171-9180.	6.5	35
92	A Panel of Regulated Proteins in Serum from Patients with Cervical Intraepithelial Neoplasia and Cervical Cancer. Journal of Proteome Research, 2014, 13, 4995-5007.	3.7	34
93	Purification and biochemical characterization of recombinant .alpha.1-antitrypsin variants expressed in Escherichia coli. Biochemistry, 1991, 30, 3464-3472.	2.5	33
94	Acute and chronic inflammatory responses induced by smoking in individuals susceptible and non-susceptible to development of COPD: from specific disease phenotyping towards novel therapy. Protocol of a cross-sectional study. BMJ Open, 2013, 3, e002178.	1.9	33
95	Bioconjugation strategies to couple supramolecular exo-functionalized palladium cages to peptides for biomedical applications. Chemical Communications, 2017, 53, 1405-1408.	4.1	33
96	Mixed-Mode chromatographic matrices for the resolution of transfer ribonucleic acids. Journal of Chromatography A, 1984, 317, 251-261.	3.7	32
97	Molecularly imprinted solid-phase extraction of cocaine metabolites from aqueous samples. Analytica Chimica Acta, 2005, 542, 14-19.	5.4	32
98	Susceptibility to COPD: Differential Proteomic Profiling after Acute Smoking. PLoS ONE, 2014, 9, e102037.	2.5	32
99	Quantification of biopharmaceuticals and biomarkers in complex biological matrices: a comparison of liquid chromatography coupled to tandem mass spectrometry and ligand binding assays. Expert Review of Proteomics, 2015, 12, 355-374.	3.0	32
100	Biomarker discovery by proteomics: challenges not only for the analytical chemist. Analyst, The, 2006, 131, 1193.	3.5	31
101	Fast, high-efficiency peptide separations on a 50-μm reversed-phase silica monolith in a nanoLC–MS set-up. Journal of Chromatography A, 2006, 1120, 165-172.	3.7	31
102	Chipâ€LCâ€MS for labelâ€free profiling of human serum. Electrophoresis, 2007, 28, 4493-4505.	2.4	31
103	Depletion of high-abundance proteins from serum by immunoaffinity chromatography: A MALDI-FT-MS study. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 847, 65-69.	2.3	31
104	Electrosynthesis methods and approaches for the preparative production of metabolites from parent drugs. TrAC - Trends in Analytical Chemistry, 2015, 70, 58-66.	11.4	31
105	Physicochemical Parameters Affecting the Electrospray Ionization Efficiency of Amino Acids after Acylation. Analytical Chemistry, 2017, 89, 9159-9166.	6.5	31
106	Runningâ€wheel activity delays mitochondrial respiratory flux decline in aging mouse muscle via a postâ€transcriptional mechanism. Aging Cell, 2018, 17, e12700.	6.7	31
107	Isolation of specific tRNAs using an ionic-hydrophobic mixed-mode chromatographic matrix. Analytical Biochemistry, 1985, 151, 526-533.	2.4	30
108	Analysis of proteoglycans derived sulphated disaccharides by liquid chromatography/mass spectrometry. Journal of Chromatography A, 2005, 1080, 43-48.	3.7	30

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109	Data processing pipelines for comprehensive profiling of proteomics samples by label-free LC–MS for biomarker discovery. Talanta, 2011, 83, 1209-1224.	5.5	30
110	Activity-based enrichment of matrix metalloproteinases using reversible inhibitors as affinity ligands. Journal of Chromatography A, 2003, 1009, 155-169.	3.7	29
111	Solid-Phase Synthesis of Succinylhydroxamate Peptides:  Functionalized Matrix Metalloproteinase Inhibitors. Organic Letters, 2006, 8, 1705-1708.	4.6	28
112	Electrochemical oxidation by square-wave potential pulses in the imitation of phenacetin to acetaminophen biotransformation. Analyst, The, 2011, 136, 5064.	3.5	28
113	Analysis of biopharmaceutical proteins in biological matrices by LC-MS/MS I. Sample preparation. TrAC - Trends in Analytical Chemistry, 2013, 48, 41-51.	11.4	28
114	Recombinant Cholera Toxin B-Subunit in Escherichia coli: High-Level Secretion, Purification, and Characterization. Protein Expression and Purification, 1994, 5, 518-526.	1.3	27
115	In Situ Surface-Enhanced Raman Spectroelectrochemical Analysis System with a Hemin Modified Nanostructured Gold Surface. Analytical Chemistry, 2015, 87, 2588-2592.	6.5	27
116	Intact protein bioanalysis by liquid chromatography – High-resolution mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2019, 1110-1111, 155-167.	2.3	27
117	An integrated high-performance liquid chromatography–mass spectrometry system for the activity-dependent analysis of matrix metalloproteases. Journal of Chromatography A, 2008, 1189, 417-425.	3.7	26
118	Controlling detrimental effects of metal cations in the quantification of energy metabolites via ultrahigh pressure-liquid chromatography–electrospray-tandem mass spectrometry by employing acetylacetone as a volatile eluent modifier. Journal of Chromatography A, 2013, 1294, 87-97.	3.7	26
119	Multidimensional separation of tryptic peptides from human serum proteins using reversed-phase, strong cation exchange, weak anion exchange, and fused-core fluorinated stationary phases. Journal of Separation Science, 2013, 36, 3463-3470.	2.5	26
120	Soluble receptor for advanced glycation end products (sRAGE) as a biomarker of COPD. Respiratory Research, 2021, 22, 127.	3.6	26
121	Antibody-free workflows for protein quantification by LC–MS/MS. Bioanalysis, 2015, 7, 763-779.	1.5	25
122	A fully validated liquid chromatography-mass spectrometry method for the quantification of the soluble receptor of advanced glycation end-products (sRAGE) in serum using immunopurification in a 96-well plate format. Talanta, 2018, 182, 414-421.	5.5	25
123	Purification and characterization of the recombinant human dopamine D2S receptor from Pichia pastoris. Protein Expression and Purification, 2004, 33, 176-184.	1.3	24
124	Proteomic analysis of human epithelial lining fluid by microfluidicsâ€based nano <scp>LC</scp> â€ <scp>MS</scp> / <scp>MS</scp> : A feasibility study. Electrophoresis, 2013, 34, 2683-2694.	2.4	24
125	Targeting transcription factor lysine acetylation in inflammatory airway diseases. Epigenomics, 2017, 9, 1013-1028.	2.1	24
126	Targeted LC-MS/MS for the evaluation of proteomics biomarkers in the blood of neonates with necrotizing enterocolitis and late-onset sepsis. Analytical and Bioanalytical Chemistry, 2018, 410, 7163-7175.	3.7	24

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127	Resolution of RNA using high-performance liquid chromatography. Biomedical Applications, 1987, 418, 51-72.	1.7	23
128	Functional Proteomics on Zincâ€Dependent Metalloproteinases using Inhibitor Probes. ChemMedChem, 2009, 4, 164-170.	3.2	23
129	Capillary gel electrophoresis of oligonucleotides: prediction of migration times using base-specific migration coefficients. Journal of Chromatography A, 1994, 680, 479-489.	3.7	22
130	Activity-Based Matrix Metallo-Protease Enrichment Using Automated, Inhibitor Affinity Extractions. Journal of Proteome Research, 2006, 5, 1186-1194.	3.7	22
131	Antibody-Free LC-MS/MS Quantification of rhTRAIL in Human and Mouse Serum. Analytical Chemistry, 2013, 85, 10754-10760.	6.5	22
132	Analysis of the Lipidated Recombinant Outer Surface Protein A fromBorrelia burgdorferiby Mass Spectrometry. Analytical Biochemistry, 1997, 246, 52-61.	2.4	21
133	Lipopolycationic Telomers for Gene Transfer: Synthesis and Evaluation of Their in Vitro Transfection Efficiency. Journal of Medicinal Chemistry, 2000, 43, 1367-1379.	6.4	21
134	Influence of clotting time on the protein composition of serum samples based on LC–MS dataâ⁻†. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 1281-1291.	2.3	21
135	Antibodyâ€Free Detection of Protein Tyrosine Nitration in Tissue Sections. ChemBioChem, 2011, 12, 2016-2020.	2.6	21
136	Molecular markers for cervical cancer screening. Expert Review of Proteomics, 2021, 18, 675-691.	3.0	21
137	Current Technological Challenges in Biomarker Discovery and Validation. European Journal of Mass Spectrometry, 2010, 16, 101-121.	1.0	20
138	Absolute Quantification of the Total and Antidrug Antibody-Bound Concentrations of Recombinant Human α-Glucosidase in Human Plasma Using Protein G Extraction and LC-MS/MS. Analytical Chemistry, 2015, 87, 4394-4401.	6.5	20
139	Covalent immobilization of a flavoprotein monooxygenase via its flavin cofactor. Enzyme and Microbial Technology, 2016, 82, 138-143.	3.2	20
140	Affimers as an Alternative to Antibodies in an Affinity LC–MS Assay for Quantification of the Soluble Receptor of Advanced Glycation End-Products (sRAGE) in Human Serum. Journal of Proteome Research, 2018, 17, 2892-2899.	3.7	20
141	Chemical isotope labeling for quantitative proteomics. Mass Spectrometry Reviews, 2023, 42, 546-576.	5.4	20
142	Proteomic alterations in early stage cervical cancer. Oncotarget, 2018, 9, 18128-18147.	1.8	20
143	Minocycline Effects on the Cerebrospinal Fluid Proteome of Experimental Autoimmune Encephalomyelitis Rats. Journal of Proteome Research, 2012, 11, 4315-4325.	3.7	19
144	Electrocatalytic oxidation of hydrogen peroxide on a platinum electrode in the imitation of oxidative drug metabolism of lidocaine. Analyst, The, 2012, 137, 4698.	3.5	19

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145	Cigarette Smoking Acutely Decreases Serum Levels of the Chronic Obstructive Pulmonary Disease Biomarker sRAGE. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 1456-1458.	5.6	19
146	Threshold-Avoiding Proteomics Pipeline. Analytical Chemistry, 2011, 83, 7786-7794.	6.5	18
147	A Versatile Isobaric Tag Enables Proteome Quantification in Data-Dependent and Data-Independent Acquisition Modes. Analytical Chemistry, 2020, 92, 16149-16157.	6.5	18
148	Restricted-access material-based high-molecular-weight protein depletion coupled on-line with nano-liquid chromatography–mass spectrometry for proteomics applications. Journal of Chromatography A, 2007, 1149, 169-177.	3.7	17
149	A dual inhibitor of matrix metalloproteinases and a disintegrin and metalloproteinases, [18F]FB-ML5, as a molecular probe for non-invasive MMP/ADAM-targeted imaging. Bioorganic and Medicinal Chemistry, 2015, 23, 192-202.	3.0	17
150	Proteogenomics: Key Driver for Clinical Discovery and Personalized Medicine. Advances in Experimental Medicine and Biology, 2016, 926, 21-47.	1.6	17
151	A quantitative LC-MS/MS method for insulin-like growth factor 1 in human plasma. Clinical Chemistry and Laboratory Medicine, 2018, 56, 1905-1912.	2.3	17
152	Comparison of Targeted Mass Spectrometry Techniques with an Immunoassay: A Case Study for HSP90α. Proteomics - Clinical Applications, 2018, 12, 1700107.	1.6	17
153	Application of Displacement Chromatography to Online Two-Dimensional Liquid Chromatography Coupled to Tandem Mass Spectrometry Improves Peptide Separation Efficiency and Detectability for the Analysis of Complex Proteomes. Analytical Chemistry, 2018, 90, 9951-9958.	6.5	17
154	Effect of liposome-encapsulated clodronate pretreatment on synthetic vector-mediated gene expression in mice. Gene Therapy, 1999, 6, 448-453.	4. 5	16
155	Determination of regulatory phosphorylation sites in nanogram amounts of a synthetic fragment of ZAP-70 using microprobe NMR and on-line coupled capillary HPLC-NMR. Magnetic Resonance in Chemistry, 2005, 43, 747-754.	1.9	16
156	Study of human lung elastin degradation by different elastases using high-performance liquid chromatography/mass spectrometry. Analytical Biochemistry, 2006, 358, 216-224.	2.4	16
157	A peptide hydroxamate library for enrichment of metalloproteinases: towards an affinity-based metalloproteinase profiling protocol. Organic and Biomolecular Chemistry, 2008, 6, 1244.	2.8	16
158	Differential expression of protease activity in serum samples of prostate carcinoma patients with metastases. Proteomics, 2010, 10, 2348-2358.	2.2	16
159	Quantification of matrix metalloprotease-9 in bronchoalveolar lavage fluid by selected reaction monitoring with microfluidics nano-liquid-chromatography–mass spectrometry. Journal of Chromatography A, 2012, 1246, 103-110.	3.7	16
160	Innovations in studying in vivo cell behavior and pharmacology in complex tissues – microvascular endothelial cells in the spotlight. Cell and Tissue Research, 2013, 354, 647-669.	2.9	16
161	ADAM10 mediates the house dust miteâ€induced release of chemokine ligand CCL20 by airway epithelium. Allergy: European Journal of Allergy and Clinical Immunology, 2015, 70, 1545-1552.	5.7	16
162	Electrochemical Protein Cleavage in a Microfluidic Cell with Integrated Boron Doped Diamond Electrodes. Analytical Chemistry, 2016, 88, 9190-9198.	6. 5	16

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163	Integrated proteogenomic approach identifying a protein signature of COPD and a new splice variant of SORBS1. Thorax, 2020, 75, 180-183.	5.6	16
164	Proteomics of Epithelial Lining Fluid Obtained by Bronchoscopic Microprobe Sampling. Methods in Molecular Biology, 2011, 790, 17-28.	0.9	16
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