

# Rainer Bischoff

## List of Publications by Year in descending order

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275  
papers

10,727  
citations

30068

54  
h-index

48312

88  
g-index

293  
all docs

293  
docs citations

293  
times ranked

13646  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chemical isotope labeling for quantitative proteomics. <i>Mass Spectrometry Reviews</i> , 2023, 42, 546-576.	5.4	20
2	Analytical tools for the characterization of deamidation in monoclonal antibodies. <i>Journal of Chromatography Open</i> , 2022, 2, 100025.	2.2	5
3	Identification of damage associated molecular patterns and extracellular matrix proteins as major constituents of the surface proteome of lung implantable silicone/nitinol devices. <i>Acta Biomaterialia</i> , 2022, 141, 209-218.	8.3	5
4	Analytical and pharmacological consequences of the in vivo deamidation of trastuzumab and pertuzumab. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 1513-1524.	3.7	10
5	Plasma sRAGE levels strongly associate with centrilobular emphysema assessed by HRCT scans. <i>Respiratory Research</i> , 2022, 23, 15.	3.6	7
6	Nanoporous Gold Catalyst for the Oxidative N-Dealkylation of Drug Molecules: A Method for Synthesis of N-Dealkylated Metabolites. <i>ChemMedChem</i> , 2022, , .	3.2	3
7	Large molecule bioanalysis by LC-MS: beyond simply quantifying. <i>Bioanalysis</i> , 2022, 14, 397-400.	1.5	0
8	N-Dealkylation of Amines. <i>Molecules</i> , 2022, 27, 3293.	3.8	16
9	Selective quantification of the 22-kDa isoform of human growth hormone 1 in serum and plasma by immunocapture and LC-MS/MS. <i>Analytical and Bioanalytical Chemistry</i> , 2022, 414, 6187-6200.	3.7	5
10	An antibody-free LC-MS/MS method for the quantification of intact insulin-like growth factors 1 and 2 in human plasma. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 2035-2044.	3.7	7
11	Soluble receptor for advanced glycation end products (sRAGE) as a biomarker of COPD. <i>Respiratory Research</i> , 2021, 22, 127.	3.6	26
12	Data Sharing Under the General Data Protection Regulation. <i>Hypertension</i> , 2021, 77, 1029-1035.	2.7	47
13	Isolation of extracellular vesicles with combined enrichment methods. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2021, 1169, 122604.	2.3	90
14	The Isotopic Ac-IP Tag Enables Multiplexed Proteome Quantification in Data-Independent Acquisition Mode. <i>Analytical Chemistry</i> , 2021, 93, 8196-8202.	6.5	11
15	TEMPO-Mediated Electrochemical N-Dealkylation of Opiate Alkaloids. <i>ChemElectroChem</i> , 2021, 8, 2590-2596.	3.4	13
16	Online-2D NanoLC-MS for Crude Serum Proteome Profiling: Assessing Sample Preparation Impact on Proteome Composition. <i>Analytical Chemistry</i> , 2021, 93, 9663-9668.	6.5	8
17	Pipelines and Systems for Threshold-Avoiding Quantification of LC-MS/MS Data. <i>Analytical Chemistry</i> , 2021, 93, 11215-11224.	6.5	6
18	Enrichment and Liquid Chromatography-Mass Spectrometry Analysis of Trastuzumab and Pertuzumab Using Affimer Reagents. <i>Analytical Chemistry</i> , 2021, 93, 13597-13605.	6.5	8

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19	Combined Metabolic and Chemical (CoMetChem) Labeling Using Stable Isotopes—a Strategy to Reveal Site-Specific Histone Acetylation and Deacetylation Rates by LC–MS. <i>Analytical Chemistry</i> , 2021, 93, 12872-12880.	6.5	2
20	The “un-shrunk” partial correlation in Gaussian graphical models. <i>BMC Bioinformatics</i> , 2021, 22, 424.	2.6	0
21	Molecular markers for cervical cancer screening. <i>Expert Review of Proteomics</i> , 2021, 18, 675-691.	3.0	21
22	Change of charge variant composition of trastuzumab upon stressing at physiological conditions. <i>Journal of Chromatography A</i> , 2021, 1655, 462506.	3.7	15
23	Adsorptive Microtiter Plates As Solid Supports in Affinity Purification Workflows. <i>Journal of Proteome Research</i> , 2021, 20, 5218-5221.	3.7	3
24	Meta-Inflammation and Metabolic Reprogramming of Macrophages in Diabetes and Obesity: The Importance of Metabolites. <i>Frontiers in Immunology</i> , 2021, 12, 746151.	4.8	77
25	Proteomics approach to identify COPD-related changes in pulmonary fibroblasts. , 2021, , .		2
26	Non-Antibody-Based Binders for the Enrichment of Proteins for Analysis by Mass Spectrometry. <i>Biomolecules</i> , 2021, 11, 1791.	4.0	8
27	Effect of Trastuzumab–HER2 Complex Formation on Stress-Induced Modifications in the CDRs of Trastuzumab. <i>Frontiers in Chemistry</i> , 2021, 9, 794247.	3.6	4
28	A Versatile Isobaric Tag Enables Proteome Quantification in Data-Dependent and Data-Independent Acquisition Modes. <i>Analytical Chemistry</i> , 2020, 92, 16149-16157.	6.5	18
29	A Collision-Induced Dissociation Cleavable Isobaric Tag for Peptide Fragment Ion-Based Quantification in Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 3817-3824.	3.7	7
30	Electrochemical N-demethylation of tropane alkaloids. <i>Green Chemistry</i> , 2020, 22, 6455-6463.	9.0	13
31	In Matrix Derivatization Combined with LC-MS/MS Results in Ultrasensitive Quantification of Plasma Free Metanephrines and Catecholamines. <i>Analytical Chemistry</i> , 2020, 92, 9072-9078.	6.5	44
32	Female Specific Association of Low Insulin-Like Growth Factor 1 (IGF1) Levels with Increased Risk of Premature Mortality in Renal Transplant Recipients. <i>Journal of Clinical Medicine</i> , 2020, 9, 293.	2.4	3
33	Integrated proteogenomic approach identifying a protein signature of COPD and a new splice variant of SORBS1. <i>Thorax</i> , 2020, 75, 180-183.	5.6	16
34	Intact protein quantification in biological samples by liquid chromatography – high-resolution mass spectrometry: somatropin in rat plasma. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2020, 1144, 122079.	2.3	7
35	Selective Maleylation-Directed Isobaric Peptide Termini Labeling for Accurate Proteome Quantification. <i>Analytical Chemistry</i> , 2020, 92, 7836-7844.	6.5	11
36	Targeted imaging of integrins in cancer tissues using photocleavable Ru(II) polypyridine complexes as mass-tags. <i>Chemical Communications</i> , 2020, 56, 5941-5944.	4.1	12

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37	Cigarette smoking prior to blood sampling acutely affects serum levels of the chronic obstructive pulmonary disease biomarker surfactant protein D. <i>Clinical Chemistry and Laboratory Medicine</i> , 2020, 58, e138-e141.	2.3	0
38	Exact hypothesis testing for shrinkage-based Gaussian graphical models. <i>Bioinformatics</i> , 2019, 35, 5011-5017.	4.1	8
39	Intact protein bioanalysis by liquid chromatography – High-resolution mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2019, 1110-1111, 155-167.	2.3	27
40	Separation of deamidated peptides with mixed-mode chromatography using phospholipid-functionalized monolithic stationary phases. <i>Journal of Chromatography A</i> , 2019, 1603, 417-421.	3.7	9
41	Quantification of surfactant protein D (SPD) in human serum by liquid chromatography-mass spectrometry (LC-MS). <i>Talanta</i> , 2019, 202, 507-513.	5.5	12
42	Confounding Factors Affecting sRAGE as a Biomarker for Chronic Obstructive Pulmonary Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 200, 114-114.	5.6	4
43	Pre- and Post-analytical Factors in Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2019, 1959, 1-22.	0.9	7
44	Mass spectrometric analysis of PTM dynamics using stable isotope labeled metabolic precursors in cell culture. <i>Analyst</i> , 2019, 144, 6812-6833.	3.5	3
45	Reply to Biswas: Acute and Chronic Effects of Cigarette Smoking on sRAGE. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 806-807.	5.6	5
46	Imaging of protein distribution in tissues using mass spectrometry: An interdisciplinary challenge. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 112, 13-28.	11.4	37
47	Targeted Proteomics to Study Mitochondrial Biology. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1158, 101-117.	1.6	1
48	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. <i>Talanta</i> , 2018, 182, 414-421.	5.5	25
49	Cleavable Crosslinkers as Tissue Fixation Reagents for Proteomic Analysis. <i>ChemBioChem</i> , 2018, 19, 736-743.	2.6	5
50	A quantitative LC-MS/MS method for insulin-like growth factor 1 in human plasma. <i>Clinical Chemistry and Laboratory Medicine</i> , 2018, 56, 1905-1912.	2.3	17
51	Assessment of Sample Preparation Bias in Mass Spectrometry-Based Proteomics. <i>Analytical Chemistry</i> , 2018, 90, 5405-5413.	6.5	51
52	Tutorial: Correction of shifts in single-stage LC-MS(/MS) data. <i>Analytica Chimica Acta</i> , 2018, 999, 37-53.	5.4	12
53	Comparison of Targeted Mass Spectrometry Techniques with an Immunoassay: A Case Study for HSP90. <i>Proteomics - Clinical Applications</i> , 2018, 12, 1700107.	1.6	17
54	Running a wheel activity delays mitochondrial respiratory flux decline in aging mouse muscle via a post-transcriptional mechanism. <i>Aging Cell</i> , 2018, 17, e12700.	6.7	31

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55	Omics Technology: Lipidomics and Its Pitfalls During the Preanalytical Stage. , 2018, , .		0
56	Quantification of the soluble Receptor of Advanced Glycation End-Products (sRAGE) by LC-MS after enrichment by strong cation exchange (SCX) solid-phase extraction (SPE) at the protein level. Analytica Chimica Acta, 2018, 1043, 45-51.	5.4	8
57	Bioconjugation of Supramolecular Metallacages to Integrin Ligands for Targeted Delivery of Cisplatin. Bioconjugate Chemistry, 2018, 29, 3856-3865.	3.6	41
58	Improving selectivity and sensitivity of protein quantitation by LC-MS/MS: determination of somatropin in rat plasma. Bioanalysis, 2018, 10, 1009-1021.	1.5	11
59	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
60	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
61	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
62	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
63	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
64	LC-MS analysis of key components of the glutathione cycle in tissues and body fluids from mice with myocardial infarction. Journal of Pharmaceutical and Biomedical Analysis, 2018, 160, 289-296.	2.8	15
65	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
66	Proteomic alterations in early stage cervical cancer. Oncotarget, 2018, 9, 18128-18147.	1.8	20
67	Cigarette smoking acutely decreases the serum levels of the COPD biomarker sRAGE. , 2018, , .		0
68	Bioconjugation strategies to couple supramolecular exo-functionalized palladium cages to peptides for biomedical applications. Chemical Communications, 2017, 53, 1405-1408.	4.1	33
69	Assuring Consistent Performance of an Insulin-Like Growth Factor 1 MALDIimmunoassay by Monitoring Measurement Quality Indicators. Analytical Chemistry, 2017, 89, 6188-6195.	6.5	12
70	The relevance of K <sub>i</sub> calculation for bi-substrate enzymes illustrated by kinetic evaluation of a novel lysine (K) acetyltransferase 8 inhibitor. European Journal of Medicinal Chemistry, 2017, 136, 480-486.	5.5	7
71	Targeting transcription factor lysine acetylation in inflammatory airway diseases. Epigenomics, 2017, 9, 1013-1028.	2.1	24
72	Specific Affinity Enrichment of Electrochemically Cleaved Peptides Based on Cu(II)-Mediated Spirolactone Tagging. Analytical Chemistry, 2017, 89, 7123-7129.	6.5	7

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73	HDAC1-3 inhibitor MS-275 enhances IL10 expression in RAW264.7 macrophages and reduces cigarette smoke-induced airway inflammation in mice. <i>Scientific Reports</i> , 2017, 7, 45047.	3.3	69
74	A 6-alkylsalicylate histone acetyltransferase inhibitor inhibits histone acetylation and pro-inflammatory gene expression in murine precision-cut lung slices. <i>Pulmonary Pharmacology and Therapeutics</i> , 2017, 44, 88-95.	2.6	15
75	Mechanism of aromatic hydroxylation of lidocaine at a Pt electrode under acidic conditions. <i>Electrochimica Acta</i> , 2017, 224, 636-641.	5.2	6
76	Relationship between plasma and salivary melatonin and cortisol investigated by LC-MS/MS. <i>Clinical Chemistry and Laboratory Medicine</i> , 2017, 55, 1340-1348.	2.3	41
77	Physicochemical Parameters Affecting the Electrospray Ionization Efficiency of Amino Acids after Acylation. <i>Analytical Chemistry</i> , 2017, 89, 9159-9166.	6.5	31
78	Accumulation of 5-oxoproline in myocardial dysfunction and the protective effects of OPLAH. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	36
79	The degradation of nucleotide triphosphates extracted under boiling ethanol conditions is prevented by the yeast cellular matrix. <i>Metabolomics</i> , 2017, 13, 1.	3.0	11
80	Serum Protein Markers for the Early Detection of Lung Cancer: A Focus on Autoantibodies. <i>Journal of Proteome Research</i> , 2017, 16, 3-13.	3.7	37
81	Activity-Dependent Photoaffinity Labeling of Metalloproteases. <i>Methods in Molecular Biology</i> , 2017, 1491, 103-111.	0.9	2
82	Malnutrition-associated liver steatosis and ATP depletion is caused by peroxisomal and mitochondrial dysfunction. <i>Journal of Hepatology</i> , 2016, 65, 1198-1208.	3.7	133
83	Microbial Flavoprotein Monooxygenases as Mimics of Mammalian Flavin-Containing Monooxygenases for the Enantioselective Preparation of Drug Metabolites. <i>Drug Metabolism and Disposition</i> , 2016, 44, 1270-1276.	3.3	14
84	Quantitative antibody-free LC-MS/MS analysis of sTRAIL in sputum and saliva at the sub-ng/mL level. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1032, 205-210.	2.3	11
85	Radiation chemical studies of Gly-Met-Gly in aqueous solution. <i>Free Radical Research</i> , 2016, 50, S24-S39.	3.3	13
86	Proteogenomics: Key Driver for Clinical Discovery and Personalized Medicine. <i>Advances in Experimental Medicine and Biology</i> , 2016, 926, 21-47.	1.6	17
87	Suppression of Surface-Enhanced Raman Scattering on Gold Nanostructures by Metal Adhesion Layers. <i>Journal of Physical Chemistry C</i> , 2016, 120, 18756-18762.	3.1	7
88	Highly sensitive antibody-free LC-MS/MS quantification of rhTRAIL in serum. <i>Bioanalysis</i> , 2016, 8, 881-890.	1.5	10
89	Translational Targeted Proteomics Profiling of Mitochondrial Energy Metabolic Pathways in Mouse and Human Samples. <i>Journal of Proteome Research</i> , 2016, 15, 3204-3213.	3.7	40
90	Electrochemical Protein Cleavage in a Microfluidic Cell with Integrated Boron Doped Diamond Electrodes. <i>Analytical Chemistry</i> , 2016, 88, 9190-9198.	6.5	16

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91	Efficient and Selective Chemical Labeling of Electrochemically Generated Peptides Based on Spirolactone Chemistry. <i>Analytical Chemistry</i> , 2016, 88, 6465-6471.	6.5	4
92	HDAC 3-selective inhibitor RGFP966 demonstrates anti-inflammatory properties in RAW 264.7 macrophages and mouse precision-cut lung slices by attenuating NF- $\kappa$ B p65 transcriptional activity. <i>Biochemical Pharmacology</i> , 2016, 108, 58-74.	4.4	105
93	Site-specific quantification of lysine acetylation in the N-terminal tail of histone H4 using a double-labelling, targeted UHPLC MS/MS approach. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 3547-3553.	3.7	6
94	Identification of Analytical Factors Affecting Complex Proteomics Profiles Acquired in a Factorial Design Study with Analysis of Variance: Simultaneous Component Analysis. <i>Analytical Chemistry</i> , 2016, 88, 4229-4238.	6.5	10
95	The histone acetyltransferase p300 inhibitor C646 reduces pro-inflammatory gene expression and inhibits histone deacetylases. <i>Biochemical Pharmacology</i> , 2016, 102, 130-140.	4.4	46
96	LC-MS/MS-Based Monitoring of <i>In Vivo</i> Protein Biotransformation: Quantitative Determination of Trastuzumab and Its Deamidation Products in Human Plasma. <i>Analytical Chemistry</i> , 2016, 88, 1871-1877.	6.5	81
97	Genomic variability and protein species "Improving sequence coverage for proteogenomics. <i>Journal of Proteomics</i> , 2016, 134, 25-36.	2.4	10
98	Covalent immobilization of a flavoprotein monooxygenase via its flavin cofactor. <i>Enzyme and Microbial Technology</i> , 2016, 82, 138-143.	3.2	20
99	Free Urinary Desmosine and Isodesmosine as COPD Biomarkers: The Relevance of Confounding Factors. <i>Chronic Obstructive Pulmonary Diseases (Miami, Fla )</i> , 2016, 3, 560-569.	0.7	7
100	Prioritization of COPD protein biomarkers, based on a systematic study of the literature. <i>Advances in Precision Medicine</i> , 2016, 1, 4.	0.3	4
101	ADAM10 mediates the house dust mite-induced release of chemokine ligand CCL20 by airway epithelium. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2015, 70, 1545-1552.	5.7	16
102	Stability of energy metabolites "An often overlooked issue in metabolomics studies: A review. <i>Electrophoresis</i> , 2015, 36, 2156-2169.	2.4	51
103	Metalloproteinase Profiling in Lung Transplant Recipients With Good Outcome and Bronchiolitis Obliterans Syndrome. <i>Transplantation</i> , 2015, 99, 1946-1952.	1.0	15
104	Quantification of biopharmaceuticals and biomarkers in complex biological matrices: a comparison of liquid chromatography coupled to tandem mass spectrometry and ligand binding assays. <i>Expert Review of Proteomics</i> , 2015, 12, 355-374.	3.0	32
105	Optimization of reaction parameters for the electrochemical oxidation of lidocaine with a Design of Experiments approach. <i>Electrochimica Acta</i> , 2015, 171, 23-28.	5.2	13
106	In Situ Surface-Enhanced Raman Spectroelectrochemical Analysis System with a Hemin Modified Nanostructured Gold Surface. <i>Analytical Chemistry</i> , 2015, 87, 2588-2592.	6.5	27
107	Surface-modified electrodes in the mimicry of oxidative drug metabolism. <i>TrAC - Trends in Analytical Chemistry</i> , 2015, 70, 50-57.	11.4	14
108	Antibody-free workflows for protein quantification by LC-MS/MS. <i>Bioanalysis</i> , 2015, 7, 763-779.	1.5	25



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109	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3415-3431.	3.7	53
110	MicroPET Evaluation of a Hydroxamate-Based MMP Inhibitor, [18F]FB-ML5, in a Mouse Model of Cigarette Smoke-Induced Acute Airway Inflammation. <i>Molecular Imaging and Biology</i> , 2015, 17, 680-687.	2.6	5
111	Absolute Quantification of the Total and Antidrug Antibody-Bound Concentrations of Recombinant Human $\beta$ -Glucosidase in Human Plasma Using Protein G Extraction and LC-MS/MS. <i>Analytical Chemistry</i> , 2015, 87, 4394-4401.	6.5	20
112	Electrosynthesis methods and approaches for the preparative production of metabolites from parent drugs. <i>TrAC - Trends in Analytical Chemistry</i> , 2015, 70, 58-66.	11.4	31
113	High-sensitivity quantitation of a Nanobody <sup>®</sup> in plasma by single-cartridge multidimensional SPE and ultra-performance LC-MS/MS. <i>Bioanalysis</i> , 2015, 7, 53-64.	1.5	10
114	In Vitro Transcription/Translation System: A Versatile Tool in the Search for Missing Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3441-3451.	3.7	11
115	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. <i>Bioorganic and Medicinal Chemistry</i> , 2015, 23, 192-202.	3.0	17
116	Protein biogenesis machinery is a driver of replicative aging in yeast. <i>ELife</i> , 2015, 4, e08527.	6.0	151
117	Susceptibility to COPD: Differential Proteomic Profiling after Acute Smoking. <i>PLoS ONE</i> , 2014, 9, e102037.	2.5	32
118	Inversion of peak elution order prevents uniform time alignment of complex liquid-chromatography coupled to mass spectrometry datasets. <i>Journal of Chromatography A</i> , 2014, 1373, 61-72.	3.7	4
119	Chemical and technical challenges in the analysis of central carbon metabolites by liquid-chromatography mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2014, 966, 21-33.	2.3	49
120	Integrated Quantification and Identification of Aldehydes and Ketones in Biological Samples. <i>Analytical Chemistry</i> , 2014, 86, 5089-5100.	6.5	62
121	A Panel of Regulated Proteins in Serum from Patients with Cervical Intraepithelial Neoplasia and Cervical Cancer. <i>Journal of Proteome Research</i> , 2014, 13, 4995-5007.	3.7	34
122	Proteomic Studies Related to Genetic Determinants of Variability in Protein Concentrations. <i>Journal of Proteome Research</i> , 2014, 13, 5-14.	3.7	15
123	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. <i>Journal of Chromatography A</i> , 2014, 1326, 13-19.	3.7	41
124	Simultaneous serum desalting and total protein determination by macroporous reversed-phase chromatography. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 3195-3203.	3.7	9
125	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. <i>Analytical Chemistry</i> , 2013, 85, 9528-9535.	6.5	74
126	Antibody-Free LC-MS/MS Quantification of rhTRAIL in Human and Mouse Serum. <i>Analytical Chemistry</i> , 2013, 85, 10754-10760.	6.5	22



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127	PREFACE. Introduction to Biomarker Discovery and Validation. RSC Drug Discovery Series, 2013, , P005-P008.	0.3	0
128	Innovations in studying in vivo cell behavior and pharmacology in complex tissues â€“ microvascular endothelial cells in the spotlight. Cell and Tissue Research, 2013, 354, 647-669.	2.9	16
129	Electron Transfer and Collision Induced Dissociation of Non-Derivatized and Derivatized Desmosine and Isodesmosine. Journal of the American Society for Mass Spectrometry, 2013, 24, 83-91.	2.8	6
130	A Critical Assessment of Feature Selection Methods for Biomarker Discovery in Clinical Proteomics. Molecular and Cellular Proteomics, 2013, 12, 263-276.	3.8	120
131	Cigarette smoke induces endoplasmic reticulum stress response and proteasomal dysfunction in human alveolar epithelial cells. Experimental Physiology, 2013, 98, 316-325.	2.0	72
132	Chemical labeling of electrochemically cleaved peptides. Rapid Communications in Mass Spectrometry, 2013, 27, 546-552.	1.5	8
133	Controlling detrimental effects of metal cations in the quantification of energy metabolites via ultrahigh pressure-liquid chromatographyâ€“electrospray-tandem mass spectrometry by employing acetylacetone as a volatile eluent modifier. Journal of Chromatography A, 2013, 1294, 87-97.	3.7	26
134	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
135	Proteomic analysis of human epithelial lining fluid by microfluidicsâ€“based nano<sc>LC</sc>â€“<sc>MS</sc>/<sc>MS</sc>: A feasibility study. Electrophoresis, 2013, 34, 2683-2694.	2.4	24
136	Boron-Doped Diamond Electrodes for the Electrochemical Oxidation and Cleavage of Peptides. Analytical Chemistry, 2013, 85, 6626-6632.	6.5	53
137	Analysis of biopharmaceuticals. TrAC - Trends in Analytical Chemistry, 2013, 48, 40.	11.4	1
138	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
139	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
140	Probes for Non-invasive Matrix Metalloproteinase-targeted Imaging with PET and SPECT. Current Pharmaceutical Design, 2013, 19, 4647-4672.	1.9	65
141	Bioinformatics and Statistics: LCâ€“MS(/MS) Data Preprocessing for Biomarker Discovery. RSC Drug Discovery Series, 2013, , 199-225.	0.3	0
142	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
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	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

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145	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
146	Electrochemical oxidation of quaternary ammonium electrolytes: Unexpected side reactions in organic electrochemistry. Electrochemistry Communications, 2012, 21, 54-57.	4.7	6
147	Glycopeptide enrichment and separation for protein glycosylation analysis. Journal of Separation Science, 2012, 35, 2341-2372.	2.5	138
148	Enrichment and Detection of Tyrosine–Nitrated Proteins. Current Protocols in Protein Science, 2012, 69, Unit 14.13.	2.8	13
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