

# Alain Beck

## List of Publications by Year in descending order

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178  
papers

12,595  
citations

22132

59  
h-index

29127

104  
g-index

201  
all docs

201  
docs citations

201  
times ranked

9291  
citing authors

#	ARTICLE	IF	CITATIONS
1	Use of PASEF for Accelerated Protein Sequence Confirmation and De Novo Sequencing with High Data Quality. <i>Methods in Molecular Biology</i> , 2022, 2313, 207-217.	0.4	4
2	Bispecific antibody characterization by a combination of intact and site-specific/chain-specific LC/MS techniques. <i>Talanta</i> , 2022, 236, 122836.	2.9	15
3	Optimized Sample Preparation and Data Processing of Data-Independent Acquisition Methods for the Robust Quantification of Trace-Level Host Cell Protein Impurities in Antibody Drug Products. <i>Journal of Proteome Research</i> , 2021, 20, 923-931.	1.8	17
4	Use of Ultra-short Columns for Therapeutic Protein Separations, Part 2: Designing the Optimal Column Dimension for Reversed-Phase Liquid Chromatography. <i>Analytical Chemistry</i> , 2021, 93, 1285-1293.	3.2	13
5	Use of Ultrashort Columns for Therapeutic Protein Separations. Part 1: Theoretical Considerations and Proof of Concept. <i>Analytical Chemistry</i> , 2021, 93, 1277-1284.	3.2	26
6	Therapeutic Fc $\epsilon$ fusion proteins: Current analytical strategies. <i>Journal of Separation Science</i> , 2021, 44, 35-62.	1.3	78
7	Analysis of Monoclonal Antibody Glycopeptides by Capillary Electrophoresis $\epsilon$ Mass Spectrometry Coupling (CE-MS). <i>Methods in Molecular Biology</i> , 2021, 2271, 97-106.	0.4	4
8	Fast Afucosylation Profiling of Glycoengineered Antibody Subunits by Middle-Up Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021, 2271, 73-83.	0.4	2
9	New wide-pore superficially porous stationary phases with low hydrophobicity applied for the analysis of monoclonal antibodies. <i>Journal of Chromatography A</i> , 2021, 1642, 462050.	1.8	8
10	Alternative mobile phase additives for the characterization of protein biopharmaceuticals in liquid chromatography $\epsilon$ Mass spectrometry. <i>Analytica Chimica Acta</i> , 2021, 1156, 338347.	2.6	14
11	State-of-the-Art Native Mass Spectrometry and Ion Mobility Methods to Monitor Homogeneous Site-Specific Antibody-Drug Conjugates Synthesis. <i>Pharmaceutics</i> , 2021, 14, 498.	1.7	16
12	High-Resolution IMS $\epsilon$ MS to Assign Additional Disulfide Bridge Pairing in Complementarity-Determining Regions of an IgG4 Monoclonal Antibody. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2505-2512.	1.2	13
13	Towards a simple on-line coupling of ion exchange chromatography and native mass spectrometry for the detailed characterization of monoclonal antibodies. <i>Journal of Chromatography A</i> , 2021, 1655, 462499.	1.8	28
14	Ultra-short ion-exchange columns for fast charge variants analysis of therapeutic proteins. <i>Journal of Chromatography A</i> , 2021, 1657, 462568.	1.8	13
15	Quantitative N-Glycan Profiling of Therapeutic Monoclonal Antibodies Performed by Middle-Up Level HILIC-HRMS Analysis. <i>Pharmaceutics</i> , 2021, 13, 1744.	2.0	12
16	NIST Interlaboratory Study on Glycosylation Analysis of Monoclonal Antibodies: Comparison of Results from Diverse Analytical Methods. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 11-30.	2.5	87
17	Efficacy of the Antibody $\epsilon$ Drug Conjugate W0101 in Preclinical Models of IGF-1 Receptor Overexpressing Solid Tumors. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 168-177.	1.9	19
18	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1783-1802.	1.2	67

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19	Toward Automation of Collision-Induced Unfolding Experiments through Online Size Exclusion Chromatography Coupled to Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 12900-12908.	3.2	18
20	Antibody-Drug Conjugates: The Last Decade. <i>Pharmaceuticals</i> , 2020, 13, 245.	1.7	207
21	Middle Level IM-MS and CIU Experiments for Improved Therapeutic Immunoglobulin Subclass Fingerprinting. <i>Analytical Chemistry</i> , 2020, 92, 8827-8835.	3.2	14
22	Glycan-Mediated Technology for Obtaining Homogeneous Site-Specific Conjugated Antibody-Drug Conjugates: Synthesis and Analytical Characterization by Using Complementary Middle-up LC/HRMS Analysis. <i>Analytical Chemistry</i> , 2020, 92, 8170-8177.	3.2	17
23	Impact of the column on effluent pH in cation exchange pH gradient chromatography, a practical study. <i>Journal of Chromatography A</i> , 2020, 1626, 461350.	1.8	11
24	Coupling non-denaturing chromatography to mass spectrometry for the characterization of monoclonal antibodies and related products. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2020, 185, 113207.	1.4	38
25	Determination of size variants by CE-SDS for approved therapeutic antibodies: Key implications of subclasses and light chain specificities. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2020, 184, 113166.	1.4	30
26	Combination of intact, middle-up and bottom-up levels to characterize 7 therapeutic monoclonal antibodies by capillary electrophoresis - Mass spectrometry. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2020, 182, 113107.	1.4	39
27	Drug Loading and Distribution of ADCs After Reduction or IdeS Digestion and Reduction. <i>Methods in Molecular Biology</i> , 2020, 2078, 187-195.	0.4	2
28	Analysis of ADCs by Native Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2020, 2078, 197-211.	0.4	2
29	Characterization of the Primary Structure of Cysteine-Linked Antibody-Drug Conjugates Using Capillary Electrophoresis with Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2020, 2078, 263-272.	0.4	3
30	A Case Study to Identify the Drug Conjugation Site of a Site-Specific Antibody-Drug-Conjugate Using Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2419-2429.	1.2	23
31	Glycosylation of biosimilars: Recent advances in analytical characterization and clinical implications. <i>Analytica Chimica Acta</i> , 2019, 1089, 1-18.	2.6	62
32	Proof of Concept To Achieve Infinite Selectivity for the Chromatographic Separation of Therapeutic Proteins. <i>Analytical Chemistry</i> , 2019, 91, 12954-12961.	3.2	30
33	Cutting-edge multi-level analytical and structural characterization of antibody-drug conjugates: present and future. <i>Expert Review of Proteomics</i> , 2019, 16, 337-362.	1.3	47
34	Tuning selectivity in cation-exchange chromatography applied for monoclonal antibody separations, part 2: Evaluation of recent stationary phases. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2019, 172, 320-328.	1.4	17
35	Insights from capillary electrophoresis approaches for characterization of monoclonal antibodies and antibody drug conjugates in the period 2016-2018. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2019, 1122-1123, 1-17.	1.2	50
36	Tuning selectivity in cation-exchange chromatography applied for monoclonal antibody separations, part 1: Alternative mobile phases and fine tuning of the separation. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2019, 168, 138-147.	1.4	28

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37	Macro- and Micro-Heterogeneity of Natural and Recombinant IgG Antibodies. <i>Antibodies</i> , 2019, 8, 18.	1.2	71
38	Structural Analysis of Monoclonal Antibodies by Ultrahigh Resolution MALDI In-Source Decay FT-ICR Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 2079-2085.	3.2	48
39	Intact monoclonal antibodies separation and analysis by sheathless capillary electrophoresis-mass spectrometry. <i>European Journal of Mass Spectrometry</i> , 2019, 25, 324-332.	0.5	20
40	Structure, heterogeneity and developability assessment of therapeutic antibodies. <i>MAbs</i> , 2019, 11, 239-264.	2.6	186
41	Orthogonal Middle-up Approaches for Characterization of the Glycan Heterogeneity of Etanercept by Hydrophilic Interaction Chromatography Coupled to High-Resolution Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 873-880.	3.2	29
42	Characterization of an antibody-drug conjugate by hydrophilic interaction chromatography coupled to mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1080, 37-41.	1.2	39
43	Analytical comparability study of recombinant monoclonal antibody therapeutics. <i>MAbs</i> , 2018, 10, 513-538.	2.6	63
44	Development of Comprehensive Online Two-Dimensional Liquid Chromatography/Mass Spectrometry Using Hydrophilic Interaction and Reversed-Phase Separations for Rapid and Deep Profiling of Therapeutic Antibodies. <i>Analytical Chemistry</i> , 2018, 90, 5923-5929.	3.2	78
45	Hyphenation of size exclusion chromatography to native ion mobility mass spectrometry for the analytical characterization of therapeutic antibodies and related products. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1086, 176-183.	1.2	69
46	An Online Four-Dimensional HIC-SEC-IM-MS Methodology for Proof-of-Concept Characterization of Antibody Drug Conjugates. <i>Analytical Chemistry</i> , 2018, 90, 1578-1586.	3.2	75
47	Utility of a high coverage phenyl-bonding and wide-pore superficially porous particle for the analysis of monoclonal antibodies and related products. <i>Journal of Chromatography A</i> , 2018, 1549, 63-76.	1.8	36
48	Current possibilities of liquid chromatography for the characterization of antibody-drug conjugates. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 147, 493-505.	1.4	54
49	Monoclonal antibody N-glycosylation profiling using capillary electrophoresis-MS Mass spectrometry: Assessment and method validation. <i>Talanta</i> , 2018, 178, 530-537.	2.9	50
50	Multiplexed Middle-Down Mass Spectrometry as a Method for Revealing Light and Heavy Chain Connectivity in a Monoclonal Antibody. <i>Analytical Chemistry</i> , 2018, 90, 12527-12535.	3.2	38
51	A Novel Online Four-Dimensional SEC-SEC-IM-MS Methodology for Characterization of Monoclonal Antibody Size Variants. <i>Analytical Chemistry</i> , 2018, 90, 13929-13937.	3.2	49
52	High-resolution separation of monoclonal antibodies mixtures and their charge variants by an alternative and generic CZE method. <i>Electrophoresis</i> , 2018, 39, 2083-2090.	1.3	24
53	Native Mass Spectrometry, Ion Mobility, and Collision-Induced Unfolding for Conformational Characterization of IgG4 Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2018, 90, 8865-8872.	3.2	51
54	Unraveling the mysteries of modern size exclusion chromatography - the way to achieve confident characterization of therapeutic proteins. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1092, 368-378.	1.2	48

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55	Characterizing various monoclonal antibodies with milder reversed phase chromatography conditions. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1096, 1-10.	1.2	25
56	Protocols for the analytical characterization of therapeutic monoclonal antibodies. III – Denaturing chromatographic techniques hyphenated to mass spectrometry. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2018, 1096, 95-106.	1.2	28
57	Biopharmaceutical Applications of Capillary Electromigration Methods. , 2018, , 453-480.		6
58	Hydrophilic Interaction Chromatography Hyphenated with Mass Spectrometry: A Powerful Analytical Tool for the Comparison of Originator and Biosimilar Therapeutic Monoclonal Antibodies at the Middle-up Level of Analysis. <i>Analytical Chemistry</i> , 2017, 89, 2086-2092.	3.2	77
59	Top-down analysis of immunoglobulin G isotypes 1 and 2 with electron transfer dissociation on a high-field Orbitrap mass spectrometer. <i>Journal of Proteomics</i> , 2017, 159, 67-76.	1.2	47
60	Development of a fast workflow to screen the charge variants of therapeutic antibodies. <i>Journal of Chromatography A</i> , 2017, 1498, 147-154.	1.8	31
61	Top-down and middle-down approach by fraction collection enrichment using off-line capillary electrophoresis – mass spectrometry coupling: Application to monoclonal antibody F c/2 charge variants. <i>Journal of Chromatography A</i> , 2017, 1498, 120-127.	1.8	31
62	Insights from native mass spectrometry approaches for top- and middle- level characterization of site-specific antibody-drug conjugates. <i>MAbs</i> , 2017, 9, 801-811.	2.6	55
63	Protocols for the analytical characterization of therapeutic monoclonal antibodies. I – Non-denaturing chromatographic techniques. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1058, 73-84.	1.2	42
64	Analysis of recombinant monoclonal antibodies in hydrophilic interaction chromatography: A generic method development approach. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2017, 145, 24-32.	1.4	32
65	Protocols for the analytical characterization of therapeutic monoclonal antibodies. II – Enzymatic and chemical sample preparation. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1060, 325-335.	1.2	59
66	Orthogonal liquid chromatography–mass spectrometry methods for the comprehensive characterization of therapeutic glycoproteins, from released glycans to intact protein level. <i>Journal of Chromatography A</i> , 2017, 1498, 128-146.	1.8	70
67	Strategies and challenges for the next generation of antibody–drug conjugates. <i>Nature Reviews Drug Discovery</i> , 2017, 16, 315-337.	21.5	1,527
68	Determination of isoelectric points and relative charge variants of 23 therapeutic monoclonal antibodies. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1065-1066, 119-128.	1.2	135
69	Forced degradation of recombinant monoclonal antibodies: A practical guide. <i>MAbs</i> , 2017, 9, 1217-1230.	2.6	163
70	Characterization of 30 therapeutic antibodies and related products by size exclusion chromatography: Feasibility assessment for future mass spectrometry hyphenation. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1065-1066, 35-43.	1.2	73
71	Epitope characterization of anti-JAM-A antibodies using orthogonal mass spectrometry and surface plasmon resonance approaches. <i>MAbs</i> , 2017, 9, 1317-1326.	2.6	11
72	Comprehensive study on the effects of sodium and potassium additives in size exclusion chromatographic separations of protein biopharmaceuticals. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2017, 144, 242-251.	1.4	25

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73	Evaluation of size exclusion chromatography columns packed with sub-3 $\mu$ m particles for the analysis of biopharmaceutical proteins. <i>Journal of Chromatography A</i> , 2017, 1498, 80-89.	1.8	64
74	Analysis of antibody-drug conjugates by comprehensive on-line two-dimensional hydrophobic interaction chromatography x reversed phase liquid chromatography hyphenated to high resolution mass spectrometry. I - Optimization of separation conditions. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1032, 103-111.	1.2	51
75	Comparison of originator and biosimilar therapeutic monoclonal antibodies using comprehensive two-dimensional liquid chromatography coupled with time-of-flight mass spectrometry. <i>MAbs</i> , 2016, 8, 1224-1234.	2.6	76
76	A novel antagonist anti- $\epsilon$ Met antibody with antitumor activities targeting both ligand-dependent and ligand-independent $\epsilon$ Met receptors. <i>International Journal of Cancer</i> , 2016, 139, 1851-1863.	2.3	18
77	Cutting-edge capillary electrophoresis characterization of monoclonal antibodies and related products. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1032, 61-78.	1.2	76
78	Characterization of therapeutic antibodies and related products by two-dimensional liquid chromatography coupled with UV absorbance and mass spectrometric detection. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1032, 51-60.	1.2	69
79	Potential of hydrophilic interaction chromatography for the analytical characterization of protein biopharmaceuticals. <i>Journal of Chromatography A</i> , 2016, 1448, 81-92.	1.8	80
80	Insights from native mass spectrometry and ion mobility-mass spectrometry for antibody and antibody-based product characterization. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1032, 79-90.	1.2	48
81	Hydrophobic interaction chromatography for the characterization of monoclonal antibodies and related products. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2016, 130, 3-18.	1.4	104
82	Rapid and improved characterization of therapeutic antibodies and antibody related products using IdeS digestion and subunit analysis. <i>Analyst</i> , The, 2016, 141, 3114-3125.	1.7	85
83	Impact of organic modifier and temperature on protein denaturation in hydrophobic interaction chromatography. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2016, 131, 124-132.	1.4	28
84	Analysis of antibody-drug conjugates by comprehensive on-line two-dimensional hydrophobic interaction chromatography x reversed phase liquid chromatography hyphenated to high resolution mass spectrometry. II- Identification of sub-units for the characterization of even and odd load drug species. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1032, 91-102.	1.2	30
85	A new anti-human Fc method to capture and analyze ADCs for characterization of drug distribution and the drug-to-antibody ratio in serum from pre-clinical species. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2016, 1032, 149-154.	1.2	13
86	Advanced assessment of the physicochemical characteristics of Remicade <sup>®</sup> and Inflectra <sup>®</sup> by sensitive LC/MS techniques. <i>MAbs</i> , 2016, 8, 1021-1034.	2.6	36
87	A New Anti-CXCR4 Antibody That Blocks the CXCR4/SDF-1 Axis and Mobilizes Effector Cells. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1890-1899.	1.9	28
88	Independent highly sensitive characterization of asparagine deamidation and aspartic acid isomerization by sheathless CZE-ESI-MS/MS. <i>Journal of Mass Spectrometry</i> , 2016, 51, 150-158.	0.7	31
89	Practical method development for the separation of monoclonal antibodies and antibody-drug-conjugate species in hydrophobic interaction chromatography, part 2: Optimization of the phase system. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2016, 121, 161-173.	1.4	46
90	Full validation of therapeutic antibody sequences by middle-up mass measurements and middle-down protein sequencing. <i>MAbs</i> , 2016, 8, 318-330.	2.6	55



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91	Structural characterization of antibody drug conjugate by a combination of intact, middle-up and bottom-up techniques using sheathless capillary electrophoresis and Tandem mass spectrometry as nanoESI infusion platform and separation method. <i>Analytica Chimica Acta</i> , 2016, 918, 50-59.	2.6	70
92	Characterization of cetuximab Fc/2 dimers by off-line CZE-MS. <i>Analytica Chimica Acta</i> , 2016, 908, 168-176.	2.6	44
93	A sensitive multidimensional method for the detection, characterization, and quantification of trace free drug species in antibody-drug conjugate samples using mass spectral detection. <i>MAbs</i> , 2016, 8, 306-317.	2.6	38
94	Cutting-edge mass spectrometry methods for the multi-level structural characterization of antibody-drug conjugates. <i>Expert Review of Proteomics</i> , 2016, 13, 157-183.	1.3	91
95	On-Chip Mesoporous Functionalized Magnetic Microspheres for Protein Sequencing by Extended Bottom-up Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 1775-1784.	3.2	15
96	Practical method development for the separation of monoclonal antibodies and antibody-drug-conjugate species in hydrophobic interaction chromatography, part 1: optimization of the mobile phase. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2016, 118, 393-403.	1.4	61
97	Glycoform Separation and Characterization of Cetuximab Variants by Middle-up Off-Line Capillary Zone Electrophoresis-UV/Electrospray Ionization-MS. <i>Analytical Chemistry</i> , 2015, 87, 6240-6250.	3.2	72
98	Intact Antibody Characterization Using Orbitrap Mass Spectrometry. <i>ACS Symposium Series</i> , 2015, , 289-315.	0.5	2
99	Characterization of antibody drug conjugate positional isomers at cysteine residues by peptide mapping LC-MS analysis. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2015, 981-982, 9-13.	1.2	56
100	Cutting-edge mass spectrometry characterization of originator, biosimilar and biobetter antibodies. <i>Journal of Mass Spectrometry</i> , 2015, 50, 285-297.	0.7	109
101	Systematic evaluation of mobile phase additives for the LC-MS characterization of therapeutic proteins. <i>Talanta</i> , 2015, 136, 60-67.	2.9	34
102	Native mass spectrometry and ion mobility characterization of trastuzumab emtansine, a lysine-linked antibody drug conjugate. <i>Protein Science</i> , 2015, 24, 1210-1223.	3.1	113
103	Direct Identification of Rituximab Main Isoforms and Subunit Analysis by Online Selective Comprehensive Two-Dimensional Liquid Chromatography-Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 8307-8315.	3.2	90
104	Absolute and multiplex quantification of antibodies in serum using PSAQ standards and LC-MS/MS. <i>Bioanalysis</i> , 2015, 7, 1237-1251.	0.6	18
105	Characterization of cation exchanger stationary phases applied for the separations of therapeutic monoclonal antibodies. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2015, 111, 169-176.	1.4	34
106	Characterization of the N-Terminal Heterogeneities of Monoclonal Antibodies Using In-Gel Charge Derivatization of $\epsilon$ -Amines and LC-MS/MS. <i>Analytical Chemistry</i> , 2015, 87, 3784-3790.	3.2	28
107	Ion-exchange chromatography for the characterization of biopharmaceuticals. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2015, 113, 43-55.	1.4	186
108	Adsorption and recovery issues of recombinant monoclonal antibodies in reversed-phase liquid chromatography. <i>Journal of Separation Science</i> , 2015, 38, 1-8.	1.3	42

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109	Method development for the separation of monoclonal antibody charge variants in cation exchange chromatography, Part I: Salt gradient approach. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2015, 102, 33-44.	1.4	133
110	Method development for the separation of monoclonal antibody charge variants in cation exchange chromatography, Part II: pH gradient approach. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2015, 102, 282-289.	1.4	113
111	Monitoring therapeutic monoclonal antibodies in brain tumor. <i>MABs</i> , 2014, 6, 1385-1393.	2.6	18
112	Antibody-drug conjugates. <i>MABs</i> , 2014, 6, 15-17.	2.6	131
113	Antibody-drug conjugate model fast characterization by LC-MS following IdeS proteolytic digestion. <i>MABs</i> , 2014, 6, 173-184.	2.6	104
114	World Antibody-Drug Conjugate Summit, October 15-16, 2013, San Francisco, CA. <i>MABs</i> , 2014, 6, 18-29.	2.6	15
115	Analysis of monoclonal antibody by a novel CE-UV/MALDI-MS interface. <i>Electrophoresis</i> , 2014, 35, 2986-2995.	1.3	40
116	Monoclonal antibodies biosimilarity assessment using transient isotachopheresis capillary zone electrophoresis-tandem mass spectrometry. <i>MABs</i> , 2014, 6, 1464-1473.	2.6	58
117	Theory and practice of size exclusion chromatography for the analysis of protein aggregates. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2014, 101, 161-173.	1.4	226
118	Innovative Native MS Methodologies for Antibody Drug Conjugate Characterization: High Resolution Native MS and IM-MS for Average DAR and DAR Distribution Assessment. <i>Analytical Chemistry</i> , 2014, 86, 10674-10683.	3.2	147
119	Full Antibody Primary Structure and Microvariant Characterization in a Single Injection Using Transient Isotachopheresis and Sheathless Capillary Electrophoresis-Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 9074-9081.	3.2	80
120	Advantages of Extended Bottom-Up Proteomics Using Sap9 for Analysis of Monoclonal Antibodies. <i>Analytical Chemistry</i> , 2014, 86, 9945-9953.	3.2	50
121	Middle-Down Analysis of Monoclonal Antibodies with Electron Transfer Dissociation Orbitrap Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 3005-3012.	3.2	147
122	Characterization of Therapeutic Antibodies and Related Products. <i>Analytical Chemistry</i> , 2013, 85, 715-736.	3.2	509
123	Noncovalent Mass Spectrometry for the Characterization of Antibody/Antigen Complexes. <i>Methods in Molecular Biology</i> , 2013, 988, 243-268.	0.4	8
124	NanoLC Chips MS/MS for the Characterization of N-Glycopeptides Generated from Trypsin Digestion of a Monoclonal Antibody. <i>Methods in Molecular Biology</i> , 2013, 988, 81-91.	0.4	4
125	Cetuximab Fab and Fc N-Glycan Fast Characterization Using IdeS Digestion and Liquid Chromatography Coupled to Electrospray Ionization Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 988, 93-113.	0.4	47
126	Analytical characterization of biosimilar antibodies and Fc-fusion proteins. <i>TrAC - Trends in Analytical Chemistry</i> , 2013, 48, 81-95.	5.8	104



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127	Rapid and multi-level characterization of trastuzumab using sheathless capillary electrophoresis-tandem mass spectrometry. <i>MAbs</i> , 2013, 5, 479-490.	2.6	80
128	Time Resolved Native Ion-Mobility Mass Spectrometry to Monitor Dynamics of IgG4 Fab Arm Exchange and Bispecific Monoclonal Antibody Formation. <i>Analytical Chemistry</i> , 2013, 85, 9785-9792.	3.2	62
129	Correct primary structure assessment and extensive glyco-profiling of cetuximab by a combination of intact, middle-up, middle-down and bottom-up ESI and MALDI mass spectrometry techniques. <i>MAbs</i> , 2013, 5, 699-710.	2.6	159
130	Approval of the first biosimilar antibodies in Europe. <i>MAbs</i> , 2013, 5, 621-623.	2.6	114
131	Insulin-like growth factor receptor type I as a target for cancer therapy. <i>Frontiers in Bioscience - Scholar</i> , 2013, S5, 439-450.	0.8	9
132	7th Annual European Antibody Congress 2011. <i>MAbs</i> , 2012, 4, 134-152.	2.6	7
133	Marketing approval of mogamulizumab. <i>MAbs</i> , 2012, 4, 419-425.	2.6	193
134	Biosimilar, Biobetter, and Next Generation Antibody Characterization by Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 4637-4646.	3.2	225
135	Biosimilar, biobetter and next generation therapeutic antibodies. <i>MAbs</i> , 2011, 3, 107-110.	2.6	84
136	Therapeutic Fc-fusion proteins and peptides as successful alternatives to antibodies. <i>MAbs</i> , 2011, 3, 415-416.	2.6	156
137	The amazing, multipurpose antibody. <i>MAbs</i> , 2011, 3, 221-222.	2.6	10
138	UV and X-ray structural studies of a 101-residue long Tat protein from a HIV-1 primary isolate and of its mutated, detoxified, vaccine candidate. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1441-1456.	1.5	30
139	Strategies and challenges for the next generation of therapeutic antibodies. <i>Nature Reviews Immunology</i> , 2010, 10, 345-352.	10.6	742
140	GlycoFi's technology to control the glycosylation of recombinant therapeutic proteins. <i>Expert Opinion on Drug Discovery</i> , 2010, 5, 95-111.	2.5	61
141	Structural Characterization of Antibodies by Mass Spectrometry. , 2010, , 613-634.		4
142	Antibody Glycans Characterization. , 2010, , 635-656.		3
143	The next generation of antibody-drug conjugates comes of age. <i>Discovery Medicine</i> , 2010, 10, 329-39.	0.5	78
144	Le mot des coordinateurs. <i>Medecine/Sciences</i> , 2009, 25, 995-996.	0.0	3

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