

Zhongqi Zhang

List of Publications by Year in descending order

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55
papers

5,214
citations

159585

30
h-index

161849

54
g-index

57
all docs

57
docs citations

57
times ranked

4697
citing authors

#	ARTICLE	IF	CITATIONS
1	Determination of amide hydrogen exchange by mass spectrometry: A new tool for protein structure elucidation. <i>Protein Science</i> , 1993, 2, 522-531.	7.6	908
2	A universal algorithm for fast and automated charge state deconvolution of electrospray mass-to-charge ratio spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 1998, 9, 225-233.	2.8	478
3	High-mannose glycans on the Fc region of therapeutic IgG antibodies increase serum clearance in humans. <i>Glycobiology</i> , 2011, 21, 949-959.	2.5	411
4	Probing the Non-covalent Structure of Proteins by Amide Hydrogen Exchange and Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1997, 32, 135-146.		381
5	Mass spectrometry for structural characterization of therapeutic antibodies. <i>Mass Spectrometry Reviews</i> , 2009, 28, 147-176.	5.4	287
6	Prediction of Low-Energy Collision-Induced Dissociation Spectra of Peptides. <i>Analytical Chemistry</i> , 2004, 76, 3908-3922.	6.5	259
7	Human IgG2 Antibodies Display Disulfide-mediated Structural Isoforms. <i>Journal of Biological Chemistry</i> , 2008, 283, 16194-16205.	3.4	252
8	Mass measurement and top-down HPLC/MS analysis of intact monoclonal antibodies on a hybrid linear quadrupole ion trap-orbitrap mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1415-1424.	2.8	137
9	Naturally occurring glycan forms of human immunoglobulins G1 and G2. <i>Molecular Immunology</i> , 2010, 47, 2074-2082.	2.2	133
10	Amide Hydrogen Exchange Determined by Mass Spectrometry: Application to Rabbit Muscle Aldolase. <i>Biochemistry</i> , 1996, 35, 779-791.	2.5	130
11	Probing noncovalent structural features of proteins by mass spectrometry. <i>Mass Spectrometry Reviews</i> , 1994, 13, 411-429.	5.4	126
12	Prediction of Low-Energy Collision-Induced Dissociation Spectra of Peptides with Three or More Charges. <i>Analytical Chemistry</i> , 2005, 77, 6364-6373.	6.5	118
13	Improved Protein Hydrogen/Deuterium Exchange Mass Spectrometry Platform with Fully Automated Data Processing. <i>Analytical Chemistry</i> , 2012, 84, 4942-4949.	6.5	104
14	Large-Scale Identification and Quantification of Covalent Modifications in Therapeutic Proteins. <i>Analytical Chemistry</i> , 2009, 81, 8354-8364.	6.5	92
15	Molecular basis for the loss-of-function effects of the Alzheimer's disease-associated R47H variant of the immune receptor TREM2. <i>Journal of Biological Chemistry</i> , 2018, 293, 12634-12646.	3.4	88
16	Discovery and Characterization of a Photo-Oxidative Histidine-Histidine Cross-Link in IgG1 Antibody Utilizing ¹⁸ O-Labeling and Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 4940-4948.	6.5	84
17	G/U and Certain Wobble Position Mismatches as Possible Main Causes of Amino Acid Misincorporations. <i>Biochemistry</i> , 2013, 52, 8165-8176.	2.5	82
18	Comparison of continuous and pulsed labeling amide hydrogen exchange/mass spectrometry for studies of protein dynamics. <i>Journal of the American Society for Mass Spectrometry</i> , 1999, 10, 675-684.	2.8	80

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19	Human recombinant [C22A] FK506 binding protein amide hydrogen exchange rates from mass spectrometry match and extend those from NMR. <i>Protein Science</i> , 1997, 6, 2203-2217.	7.6	77
20	De Novo Peptide Sequencing Based on a Divide-and-Conquer Algorithm and Peptide Tandem Spectrum Simulation. <i>Analytical Chemistry</i> , 2004, 76, 6374-6383.	6.5	73
21	De Novo Peptide Sequencing by Two-Dimensional Fragment Correlation Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 2337-2350.	6.5	66
22	Characterization of Variable Regions of Monoclonal Antibodies by Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2007, 79, 5723-5729.	6.5	66
23	LC-MS/MS Peptide Mapping with Automated Data Processing for Routine Profiling of N-Glycans in Immunoglobulins. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 999-1011.	2.8	53
24	Effect of Fc-Glycan Structure on the Conformational Stability of IgG Revealed by Hydrogen/Deuterium Exchange and Limited Proteolysis. <i>Biochemistry</i> , 2016, 55, 860-868.	2.5	46
25	Prediction of Collision-Induced Dissociation Spectra of Common N-Glycopeptides for Glycoform Identification. <i>Analytical Chemistry</i> , 2010, 82, 10194-10202.	6.5	42
26	Retention Time Alignment of LC/MS Data by a Divide-and-Conquer Algorithm. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 764-772.	2.8	40
27	Discovery of Undefined Protein Cross-Linking Chemistry: A Comprehensive Methodology Utilizing ¹⁸ O-Labeling and Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 5900-5908.	6.5	38
28	Rapid LC-MS screening for IgG Fc modifications and allelic variants in blood. <i>Molecular Immunology</i> , 2011, 49, 338-352.	2.2	37
29	Rearrangement of terminal amino acid residues in peptides by protease-catalyzed intramolecular transpeptidation. <i>Analytical Biochemistry</i> , 2006, 356, 282-290.	2.4	36
30	Prediction of Collision-Induced-Dissociation Spectra of Peptides with Post-translational or Process-Induced Modifications. <i>Analytical Chemistry</i> , 2011, 83, 8642-8651.	6.5	36
31	Conformational Difference in Human IgG2 Disulfide Isoforms Revealed by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Biochemistry</i> , 2015, 54, 1956-1962.	2.5	36
32	Impact of Fc N-glycan sialylation on IgG structure. <i>MAbs</i> , 2019, 11, 1381-1390.	5.2	32
33	Prediction of Electron-Transfer/Capture Dissociation Spectra of Peptides. <i>Analytical Chemistry</i> , 2010, 82, 1990-2005.	6.5	30
34	Metabolomics analysis of soy hydrolysates for the identification of productivity markers of mammalian cells for manufacturing therapeutic proteins. <i>Biotechnology Progress</i> , 2015, 31, 522-531.	2.6	28
35	Amino acid misincorporation in recombinant proteins. <i>Biotechnology Advances</i> , 2018, 36, 168-181.	11.7	24
36	MS-based conformation analysis of recombinant proteins in design, optimization and development of biopharmaceuticals. <i>Methods</i> , 2018, 144, 134-151.	3.8	23

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37	An evaluation of instrument types for mass spectrometry-based multi-attribute analysis of biotherapeutics. <i>MABs</i> , 2020, 12, 1783062.	5.2	23
38	Chemical Modifications of Therapeutic Proteins Induced by Residual Ethylene Oxide. <i>Journal of Pharmaceutical Sciences</i> , 2015, 104, 731-739.	3.3	22
39	Automated in-solution protein digestion using a commonly available high-performance liquid chromatography autosampler. <i>Analytical Biochemistry</i> , 2011, 411, 284-291.	2.4	21
40	Automated Precursor Ion Exclusion During LC-MS/MS Data Acquisition for Optimal Ion Identification. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1400-1407.	2.8	21
41	Peptide conformation in gas phase probed by collision-induced dissociation and its correlation to conformation in condensed phases. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 786-794.	2.8	20
42	Optimizing Spectroscopic Signal-to-Noise Ratio in Analysis of Data Collected by a Chromatographic/Spectroscopic System. <i>Analytical Chemistry</i> , 1999, 71, 39-45.	6.5	17
43	Targeted codon optimization improves translational fidelity for an Fc fusion protein. <i>Biotechnology and Bioengineering</i> , 2012, 109, 2770-2777.	3.3	17
44	Metabolic markers associated with high mannose glycan levels of therapeutic recombinant monoclonal antibodies. <i>Journal of Biotechnology</i> , 2015, 203, 22-31.	3.8	17
45	A systematic dissection of sequence elements determining \hat{I}^2 -Klotho and FGF interaction and signaling. <i>Scientific Reports</i> , 2018, 8, 11045.	3.3	17
46	Reliable LC-MS Multiattribute Method for Biotherapeutics by Run-Time Response Calibration. <i>Analytical Chemistry</i> , 2019, 91, 5252-5260.	6.5	16
47	Complete Extraction of Protein Dynamics Information in Hydrogen/Deuterium Exchange Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2020, 92, 6486-6494.	6.5	15
48	Amino Acid Misincorporation Propensities Revealed through Systematic Amino Acid Starvation. <i>Biochemistry</i> , 2018, 57, 6767-6779.	2.5	14
49	Disulfide structure of alfineprase: A recombinant analog of fibrolase. <i>Protein Science</i> , 2001, 10, 1264-1267.	7.6	12
50	Proteomics analysis of altered cellular metabolism induced by insufficient copper level. <i>Journal of Biotechnology</i> , 2014, 189, 15-26.	3.8	11
51	Enabling development, manufacturing, and regulatory approval of biotherapeutics through advances in mass spectrometry. <i>Current Opinion in Biotechnology</i> , 2021, 71, 206-215.	6.6	11
52	A Mass Spectrometric Characterization of Light-Induced Modifications in Therapeutic Proteins. <i>Journal of Pharmaceutical Sciences</i> , 2022, 111, 1556-1564.	3.3	10
53	Genetic Code Expansion in the Engineered Organism Vmax X2: High Yield and Exceptional Fidelity. <i>ACS Central Science</i> , 2021, 7, 1500-1507.	11.3	9
54	Limited Proteolysis Coupled with Mass Spectrometry for Simultaneous Evaluation of a Large Number of Protein Variants for Their Impact on Conformational Stability. <i>Analytical Chemistry</i> , 2021, 93, 14263-14271.	6.5	2

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55	Observation of Heavy-Chain C-Terminal Amidation in Human Endogenous IgG. Journal of Pharmaceutical Sciences, 2022, , .	3.3	2