

Zhongqi Zhang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6380012/publications.pdf>

Version: 2024-02-01

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 | A Mass Spectrometric Characterization of Light-Induced Modifications in Therapeutic Proteins. <i>Journal of Pharmaceutical Sciences</i> , 2022, 111, 1556-1564. | 3.3 | 10 |
| 2 | Observation of Heavy-Chain C-Terminal Amidation in Human Endogenous IgG. <i>Journal of Pharmaceutical Sciences</i> , 2022, , . | 3.3 | 2 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | An evaluation of instrument types for mass spectrometry-based multi-attribute analysis of biotherapeutics. <i>MAbs</i> , 2020, 12, 1783062. | 5.2 | 23 |
| 7 | Complete Extraction of Protein Dynamics Information in Hydrogen/Deuterium Exchange Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2020, 92, 6486-6494. | 6.5 | 15 |
| 8 | Impact of Fc N-glycan sialylation on IgG structure. <i>MAbs</i> , 2019, 11, 1381-1390. | 5.2 | 32 |
| 9 | Reliable LC-MS Multiattribute Method for Biotherapeutics by Run-Time Response Calibration. <i>Analytical Chemistry</i> , 2019, 91, 5252-5260. | 6.5 | 16 |
| 10 | MS-based conformation analysis of recombinant proteins in design, optimization and development of biopharmaceuticals. <i>Methods</i> , 2018, 144, 134-151. | 3.8 | 23 |
| 11 | Amino acid misincorporation in recombinant proteins. <i>Biotechnology Advances</i> , 2018, 36, 168-181. | 11.7 | 24 |
| 12 | Amino Acid Misincorporation Propensities Revealed through Systematic Amino Acid Starvation. <i>Biochemistry</i> , 2018, 57, 6767-6779. | 2.5 | 14 |
| 13 | 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 |
| 14 | A systematic dissection of sequence elements determining Î²-Klotho and FGF interaction and signaling. <i>Scientific Reports</i> , 2018, 8, 11045. | 3.3 | 17 |
| 15 | 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 |
| 16 | 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 |
| 17 | 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 |
| 18 | Conformational Difference in Human IgG2 Disulfide Isoforms Revealed by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Biochemistry</i> , 2015, 54, 1956-1962. | 2.5 | 36 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Chemical Modifications of Therapeutic Proteins Induced by Residual Ethylene Oxide. <i>Journal of Pharmaceutical Sciences</i> , 2015, 104, 731-739. | 3.3 | 22 |
| 20 | Proteomics analysis of altered cellular metabolism induced by insufficient copper level. <i>Journal of Biotechnology</i> , 2014, 189, 15-26. | 3.8 | 11 |
| 21 | 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 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | Improved Protein Hydrogen/Deuterium Exchange Mass Spectrometry Platform with Fully Automated Data Processing. <i>Analytical Chemistry</i> , 2012, 84, 4942-4949. | 6.5 | 104 |
| 26 | Targeted codon optimization improves translational fidelity for an Fc fusion protein. <i>Biotechnology and Bioengineering</i> , 2012, 109, 2770-2777. | 3.3 | 17 |
| 27 | 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 |
| 28 | 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 |
| 29 | 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 |
| 30 | 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 |
| 31 | Rapid LC-MS screening for IgG Fc modifications and allelic variants in blood. <i>Molecular Immunology</i> , 2011, 49, 338-352. | 2.2 | 37 |
| 32 | 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 |
| 33 | Prediction of Collision-Induced Dissociation Spectra of Common <i>N</i> -Glycopeptides for Glycoform Identification. <i>Analytical Chemistry</i> , 2010, 82, 10194-10202. | 6.5 | 42 |
| 34 | Naturally occurring glycan forms of human immunoglobulins G1 and G2. <i>Molecular Immunology</i> , 2010, 47, 2074-2082. | 2.2 | 133 |
| 35 | Prediction of Electron-Transfer/Capture Dissociation Spectra of Peptides. <i>Analytical Chemistry</i> , 2010, 82, 1990-2005. | 6.5 | 30 |
| 36 | Mass spectrometry for structural characterization of therapeutic antibodies. <i>Mass Spectrometry Reviews</i> , 2009, 28, 147-176. | 5.4 | 287 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | 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 |
| 38 | Large-Scale Identification and Quantification of Covalent Modifications in Therapeutic Proteins. <i>Analytical Chemistry</i> , 2009, 81, 8354-8364. | 6.5 | 92 |
| 39 | Human IgG2 Antibodies Display Disulfide-mediated Structural Isoforms. <i>Journal of Biological Chemistry</i> , 2008, 283, 16194-16205. | 3.4 | 252 |
| 40 | Characterization of Variable Regions of Monoclonal Antibodies by Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2007, 79, 5723-5729. | 6.5 | 66 |
| 41 | Rearrangement of terminal amino acid residues in peptides by protease-catalyzed intramolecular transpeptidation. <i>Analytical Biochemistry</i> , 2006, 356, 282-290. | 2.4 | 36 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | Prediction of Low-Energy Collision-Induced Dissociation Spectra of Peptides. <i>Analytical Chemistry</i> , 2004, 76, 3908-3922. | 6.5 | 259 |
| 46 | Disulfide structure of alfineprase: A recombinant analog of fibrolase. <i>Protein Science</i> , 2001, 10, 1264-1267. | 7.6 | 12 |
| 47 | De Novo Peptide Sequencing by Two-Dimensional Fragment Correlation Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 2337-2350. | 6.5 | 66 |
| 48 | 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 |
| 49 | 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 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | Amide Hydrogen Exchange Determined by Mass Spectrometry: Application to Rabbit Muscle Aldolase. <i>Biochemistry</i> , 1996, 35, 779-791. | 2.5 | 130 |
| 54 | Probing noncovalent structural features of proteins by mass spectrometry. <i>Mass Spectrometry Reviews</i> , 1994, 13, 411-429. | 5.4 | 126 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 55 | 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 |