

# Guodong Chen

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

1,413  
citations

331259

21  
h-index

329751

37  
g-index

45  
all docs

45  
docs citations

45  
times ranked

1442  
citing authors

#	ARTICLE	IF	CITATIONS
1	Hydrogen/deuterium exchange mass spectrometry for probing higher order structure of protein therapeutics: methodology and applications. <i>Drug Discovery Today</i> , 2014, 19, 95-102.	3.2	176
2	Application of LC/MS to proteomics studies: current status and future prospects. <i>Drug Discovery Today</i> , 2009, 14, 465-471.	3.2	83
3	Fast Photochemical Oxidation of Proteins (FPOP) Maps the Epitope of EGFR Binding to Adnectin. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 2084-2092.	1.2	79
4	Higher order structure characterization of protein therapeutics by hydrogen/deuterium exchange mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 6541-6558.	1.9	76
5	Mapping the Energetic Epitope of an Antibody/Interleukin-23 Interaction with Hydrogen/Deuterium Exchange, Fast Photochemical Oxidation of Proteins Mass Spectrometry, and Alanine Shave Mutagenesis. <i>Analytical Chemistry</i> , 2017, 89, 2250-2258.	3.2	72
6	Isomerization and Oxidation in the Complementarity-Determining Regions of a Monoclonal Antibody: A Study of the Modification-Structure-Function Correlations by Hydrogen-Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 2041-2050.	3.2	66
7	Applications of LC/MS in structure identifications of small molecules and proteins in drug discovery. <i>Journal of Mass Spectrometry</i> , 2007, 42, 279-287.	0.7	65
8	Characterization of protein therapeutics by mass spectrometry: recent developments and future directions. <i>Drug Discovery Today</i> , 2011, 16, 58-64.	3.2	63
9	Using Hydrogen/Deuterium Exchange Mass Spectrometry to Study Conformational Changes in Granulocyte Colony Stimulating Factor upon PEGylation. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 498-504.	1.2	53
10	LC-MS for protein characterization: current capabilities and future trends. <i>Expert Review of Proteomics</i> , 2008, 5, 435-444.	1.3	50
11	Orthogonal Mass Spectrometry-Based Footprinting for Epitope Mapping and Structural Characterization: The IL-6 Receptor upon Binding of Protein Therapeutics. <i>Analytical Chemistry</i> , 2017, 89, 7742-7749.	3.2	47
12	Interlaboratory Comparison of Hydrogen-Deuterium Exchange Mass Spectrometry Measurements of the Fab Fragment of NISTmAb. <i>Analytical Chemistry</i> , 2019, 91, 7336-7345.	3.2	44
13	Characterization of antibody-drug conjugates by mass spectrometry: advances and future trends. <i>Drug Discovery Today</i> , 2016, 21, 850-855.	3.2	42
14	Hydrogen/deuterium exchange mass spectrometry and computational modeling reveal a discontinuous epitope of an antibody/TL1A Interaction. <i>MAbs</i> , 2018, 10, 95-103.	2.6	39
15	Epitope and Paratope Mapping of PD-1/Nivolumab by Mass Spectrometry-Based Hydrogen-Deuterium Exchange, Cross-linking, and Molecular Docking. <i>Analytical Chemistry</i> , 2020, 92, 9086-9094.	3.2	38
16	An Integrated Approach for Determining a Protein-Protein Binding Interface in Solution and an Evaluation of Hydrogen-Deuterium Exchange Kinetics for Adjudicating Candidate Docking Models. <i>Analytical Chemistry</i> , 2019, 91, 15709-15717.	3.2	32
17	Hydrogen/deuterium exchange mass spectrometry applied to IL-23 interaction characteristics: potential impact for therapeutics. <i>Expert Review of Proteomics</i> , 2015, 12, 159-169.	1.3	28
18	Technical Decision Making With Higher Order Structure Data: Perspectives on Higher Order Structure Characterization From the Biopharmaceutical Industry. <i>Journal of Pharmaceutical Sciences</i> , 2016, 105, 3465-3470.	1.6	26

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19	Structural mass spectrometry in biologics discovery: advances and future trends. <i>Drug Discovery Today</i> , 2012, 17, 1323-1330.	3.2	25
20	Utility of Ion Mobility Mass Spectrometry for Drug-to-Antibody Ratio Measurements in Antibody-Drug Conjugates. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1791-1794.	1.2	24
21	Slow Off-Rate Modified Aptamer (SOMAmer) as a Novel Reagent in Immunoassay Development for Accurate Soluble Glypican-3 Quantification in Clinical Samples. <i>Analytical Chemistry</i> , 2018, 90, 5162-5170.	3.2	24
22	Probing Conformational Dynamics of Tau Protein by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 174-182.	1.2	23
23	Molecular perspective of antibody aggregates and their adsorption on Protein A resin. <i>Journal of Chromatography A</i> , 2016, 1457, 66-75.	1.8	22
24	Quantification of <i>in vivo</i> site-specific Asp isomerization and Asn deamidation of mAbs in animal serum using IP-LC-MS. <i>Bioanalysis</i> , 2016, 8, 1611-1622.	0.6	20
25	Characterization of Aggregation Propensity of a Human Fc-Fusion Protein Therapeutic by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 795-802.	1.2	20
26	High-resolution MS for structural characterization of protein therapeutics: advances and future directions. <i>Bioanalysis</i> , 2013, 5, 1299-1313.	0.6	19
27	The Influence of Adnectin Binding on the Extracellular Domain of Epidermal Growth Factor Receptor. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 2093-2102.	1.2	17
28	The use of fast photochemical oxidation of proteins coupled with mass spectrometry in protein therapeutics discovery and development. <i>Drug Discovery Today</i> , 2019, 24, 829-834.	3.2	16
29	Conformational Assessment of Adnectin and Adnectin-Drug Conjugate by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1524-1531.	1.2	15
30	Integrated Approach for Characterizing Bispecific Antibody/Antigens Complexes and Mapping Binding Epitopes with SEC/MALS, Native Mass Spectrometry, and Protein Footprinting. <i>Analytical Chemistry</i> , 2020, 92, 10709-10716.	3.2	14
31	Mapping binding epitopes of monoclonal antibodies targeting major histocompatibility complex class I chain-related A (MICA) with hydrogen/deuterium exchange and electron-transfer dissociation mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 1693-1700.	1.9	14
32	Hydrogen-Deuterium Exchange and Hydroxyl Radical Footprinting for Mapping Hydrophobic Interactions of Human Bromodomain with a Small Molecule Inhibitor. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2795-2804.	1.2	13
33	Mapping the Binding Interface in a Noncovalent Size Variant of a Monoclonal Antibody Using Native Mass Spectrometry, Hydrogen-Deuterium Exchange Mass Spectrometry, and Computational Analysis. <i>Journal of Pharmaceutical Sciences</i> , 2017, 106, 3222-3229.	1.6	10
34	Characterization of disulfide linkages in recombinant human granulocyte colony stimulating factor. <i>Rapid Communications in Mass Spectrometry</i> , 2013, 27, 940-946.	0.7	9
35	Recent advancements in mass spectrometry for higher order structure characterization of protein therapeutics. <i>Drug Discovery Today</i> , 2022, 27, 196-206.	3.2	9
36	Higher-Order Structure Characterization of NKG2A/CD94 Protein Complex and Anti-NKG2A Antibody Binding Epitopes by Mass Spectrometry-Based Protein Footprinting Strategies. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1567-1574.	1.2	8

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37	Advances in mass spectrometry-based epitope mapping of protein therapeutics. Journal of Pharmaceutical and Biomedical Analysis, 2022, 215, 114754.	1.4	8
38	Humanization of a strategic CD3 epitope enables evaluation of clinical T-cell engagers in a fully immunocompetent in vivo model. Scientific Reports, 2022, 12, 3530.	1.6	5
39	Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS) Centroid Data Measured between 3.6 Å°C and 25.4 Å°C for the Fab Fragment of NISTmAb. Journal of Research of the National Institute of Standards and Technology, 2019, 124, 1-7.	0.4	3
40	Mass Spectrometric Characterization in Protein Therapeutics Discovery. , 2013, , 163-205.		2