

# Michael L Gross

## List of Publications by Year in descending order

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89  
papers

2,675  
citations

218381

26  
h-index

223531

46  
g-index

90  
all docs

90  
docs citations

90  
times ranked

3629  
citing authors

#	ARTICLE	IF	CITATIONS
1	Benzoyl Transfer for Footprinting Alcohol-Containing Residues in Higher Order Structural Applications of Mass-Spectrometry-Based Proteomics. <i>Analytical Chemistry</i> , 2022, 94, 1520-1524.	3.2	6
2	Nipah Virus V Protein Binding Alters MDA5 Helicase Folding Dynamics. <i>ACS Infectious Diseases</i> , 2022, 8, 118-128.	1.8	3
3	Hydrogen- <sup>2</sup> deuterium exchange mass spectrometry identifies spatially distinct antibody epitopes on domain III of the Zika virus envelope protein. <i>Journal of Mass Spectrometry</i> , 2021, 56, e4685.	0.7	6
4	Post-HDX Deglycosylation of Fc Gamma Receptor IIIa Glycoprotein Enables HDX Characterization of Its Binding Interface with IgG. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1638-1643.	1.2	9
5	Structural basis for IFN antagonism by human respiratory syncytial virus nonstructural protein 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2020587118.	3.3	12
6	Free-Radical Membrane Protein Footprinting by Photolysis of Perfluoroisopropyl Iodide Partitioned to Detergent Micelle by Sonication. <i>Angewandte Chemie</i> , 2021, 133, 8949-8955.	1.6	0
7	Free-Radical Membrane Protein Footprinting by Photolysis of Perfluoroisopropyl Iodide Partitioned to Detergent Micelle by Sonication. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 8867-8873.	7.2	9
8	Pulsed Hydrogen- <sup>2</sup> Deuterium Exchange Reveals Altered Structures and Mechanisms in the Aggregation of Familial Alzheimer's Disease Mutants. <i>ACS Chemical Neuroscience</i> , 2021, 12, 1972-1982.	1.7	7
9	Footprinting Mass Spectrometry of Membrane Proteins: Ferroportin Reconstituted in Saposin A Picodiscs. <i>Analytical Chemistry</i> , 2021, 93, 11370-11378.	3.2	8
10	Non-canonical proline-tyrosine interactions with multiple host proteins regulate Ebola virus infection. <i>EMBO Journal</i> , 2021, 40, e105658.	3.5	8
11	Carbocation Footprinting of Soluble and Transmembrane Proteins. <i>Analytical Chemistry</i> , 2021, 93, 13101-13105.	3.2	8
12	Diethylpyrocarbonate Footprints a Membrane Protein in Micelles. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2636-2643.	1.2	8
13	Domain-specific biochemical and serological characterization of SARS-CoV-2 nucleocapsid protein. <i>STAR Protocols</i> , 2021, 2, 100906.	0.5	1
14	Nanoparticles and photochemistry for native-like transmembrane protein footprinting. <i>Nature Communications</i> , 2021, 12, 7270.	5.8	14
15	Fluorierte Reagenzien in der Strukturproteomik. <i>Angewandte Chemie</i> , 2020, 132, 5932-5942.	1.6	14
16	The Application of Fluorine-Containing Reagents in Structural Proteomics. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 5880-5889.	7.2	50
17	Site-Specific Siderocalin Binding to Ferric and Ferric-Free Enterobactin As Revealed by Mass Spectrometry. <i>ACS Chemical Biology</i> , 2020, 15, 1154-1160.	1.6	20
18	Protein Footprinting and X-ray Crystallography Reveal the Interaction of PD-L1 and a Macrocyclic Peptide. <i>Biochemistry</i> , 2020, 59, 541-551.	1.2	24

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19	Trifluoroethanol Partially Unfolds G93A SOD1 Leading to Protein Aggregation: A Study by Native Mass Spectrometry and FPOP Protein Footprinting. <i>Biochemistry</i> , 2020, 59, 3650-3659.	1.2	7
20	Protein higher-order-structure determination by fast photochemical oxidation of proteins and mass spectrometry analysis. <i>Nature Protocols</i> , 2020, 15, 3942-3970.	5.5	32
21	Organic Solvents for Enhanced Proteolysis of Stable Proteins for Hydrogen-Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 11553-11557.	3.2	15
22	Uncovering a membrane-distal conformation of KRAS available to recruit RAF to the plasma membrane. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24258-24268.	3.3	34
23	Calcium Binding to the Innate Immune Protein Human Calprotectin Revealed by Integrated Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2020, 142, 13372-13383.	6.6	13
24	Fast Protein Footprinting by X-ray Mediated Radical Trifluoromethylation. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1019-1024.	1.2	18
25	Revisiting high-resolution crystal structure of Phormidium rubidum phycocyanin. <i>Photosynthesis Research</i> , 2020, 144, 349-360.	1.6	5
26	Mass Spectrometry-Based Protein Footprinting for Higher-Order Structure Analysis: Fundamentals and Applications. <i>Chemical Reviews</i> , 2020, 120, 4355-4454.	23.0	149
27	Substrate Recognition by the Class II Lanthipeptide Synthetase HalM2. <i>ACS Chemical Biology</i> , 2020, 15, 1473-1486.	1.6	24
28	A Multifunctional Chemical Agent as an Attenuator of Amyloid Burden and Neuroinflammation in Alzheimer's Disease. <i>ACS Chemical Neuroscience</i> , 2020, 11, 1471-1481.	1.7	25
29	Top-Down Analysis of In-Source HDX of Native Protein Ions. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1151-1154.	1.2	9
30	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
31	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	9.0	452
32	A novel chlorophyll protein complex in the repair cycle of photosystem II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21907-21913.	3.3	34
33	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
34	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
35	Composite Conformational Changes of Signaling Proteins upon Ligand Binding Revealed by a Single Approach: Calcium-Calmodulin Study. <i>Analytical Chemistry</i> , 2019, 91, 12560-12567.	3.2	16
36	Recognition of Human IgG1 by Fcγ3 Receptors: Structural Insights from Hydrogen-Deuterium Exchange and Fast Photochemical Oxidation of Proteins Coupled with Mass Spectrometry. <i>Biochemistry</i> , 2019, 58, 1074-1080.	1.2	28

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37	Near-atomic structure of a giant virus. <i>Nature Communications</i> , 2019, 10, 388.	5.8	61
38	Structural basis for neutralization of <i>Plasmodium vivax</i> by naturally acquired human antibodies that target DBP. <i>Nature Microbiology</i> , 2019, 4, 1486-1496.	5.9	52
39	Inhibition of Marburg Virus RNA Synthesis by a Synthetic Anti-VP35 Antibody. <i>ACS Infectious Diseases</i> , 2019, 5, 1385-1396.	1.8	14
40	Hydroxyl-Radical Reaction Pathways for the Fast Photochemical Oxidation of Proteins Platform As Revealed by <sup>18</sup> O Isotopic Labeling. <i>Analytical Chemistry</i> , 2019, 91, 9238-9245.	3.2	22
41	Mechanistic Studies of the Kinase Domains of Class IV Lanthipeptide Synthetases. <i>ACS Chemical Biology</i> , 2019, 14, 1583-1592.	1.6	20
42	Native Mass Spectrometry, Ion Mobility, Electron-Capture Dissociation, and Modeling Provide Structural Information for Gas-Phase Apolipoprotein E Oligomers. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 876-885.	1.2	25
43	A Single Approach Reveals the Composite Conformational Changes, Order of Binding, and Affinities for Calcium Binding to Calmodulin. <i>Analytical Chemistry</i> , 2019, 91, 5508-5512.	3.2	26
44	The Ebola Viral Protein 35 N-Terminus Is a Parallel Tetramer. <i>Biochemistry</i> , 2019, 58, 657-664.	1.2	13
45	Protonation of curcumin triggers sequential double cyclization in the gas-phase: An electrospray mass spectrometry and DFT study. <i>International Journal of Mass Spectrometry</i> , 2019, 438, 107-114.	0.7	2
46	Protein-Metal-Ion Interactions Studied by Mass Spectrometry-Based Footprinting with Isotope-Encoded Benzhydrazide. <i>Analytical Chemistry</i> , 2019, 91, 1416-1423.	3.2	22
47	A Fast Photochemical Oxidation of Proteins (FPOP) platform for free-radical reactions: the carbonate radical anion with peptides and proteins. <i>Free Radical Biology and Medicine</i> , 2019, 131, 126-132.	1.3	24
48	Primary and Higher Order Structure of the Reaction Center from the Purple Phototrophic Bacterium <i>Blastochloris viridis</i> : A Test for Native Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018, 17, 1615-1623.	1.8	4
49	Mass Spectrometry-Based Fast Photochemical Oxidation of Proteins (FPOP) for Higher Order Structure Characterization. <i>Accounts of Chemical Research</i> , 2018, 51, 736-744.	7.6	85
50	Pulsed Hydrogen-Deuterium Exchange Illuminates the Aggregation Kinetics of $\alpha$ -Synuclein, the Causative Agent for Parkinson's Disease. <i>ACS Chemical Neuroscience</i> , 2018, 9, 1469-1476.	1.7	23
51	Membrane Protein Structure in Live Cells: Methodology for Studying Drug Interaction by Mass Spectrometry-Based Footprinting. <i>Biochemistry</i> , 2018, 57, 286-294.	1.2	14
52	Understanding curli amyloid-protein aggregation by hydrogen-deuterium exchange and mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2017, 420, 16-23.	0.7	12
53	Mapping the Energetic Epitope of an Antibody/Interleukin-23 Interaction with Hydrogen/Deuterium Exchange, Fast Photochemical Oxidation of Proteins Mass Spectrometry, and Alanine Scavenger Mutagenesis. <i>Analytical Chemistry</i> , 2017, 89, 2250-2258.	3.2	72
54	Mapping the Binding Interface of VEGF and a Monoclonal Antibody Fab-1 Fragment with Fast Photochemical Oxidation of Proteins (FPOP) and Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 850-858.	1.2	51

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55	Evolutionary fine-tuning of conformational ensembles in FimH during host-pathogen interactions. <i>Science Advances</i> , 2017, 3, e1601944.	4.7	50
56	Mass spectrometry-based cross-linking study shows that the Psb28 protein binds to cytochrome <i>c</i> <sub>559</sub> in Photosystem II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2224-2229.	3.3	42
57	Deamidation Slows Curli Amyloid-Protein Aggregation. <i>Biochemistry</i> , 2017, 56, 2865-2872.	1.2	15
58	A Molecular Mechanism for Nonphotochemical Quenching in Cyanobacteria. <i>Biochemistry</i> , 2017, 56, 2812-2823.	1.2	24
59	A Focus Honoring R. Graham Cooks's™ Election to the National Academy of Sciences. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 986-990.	1.2	0
60	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
61	Hydrogen-Deuterium Exchange Mass Spectrometry Reveals Calcium Binding Properties and Allosteric Regulation of Downstream Regulatory Element Antagonist Modulator (DREAM). <i>Biochemistry</i> , 2017, 56, 3523-3530.	1.2	9
62	Native Mass Spectrometry Analysis of Oligomerization States of Fluorescence Recovery Protein and Orange Carotenoid Protein: Two Proteins Involved in the Cyanobacterial Photoprotection Cycle. <i>Biochemistry</i> , 2017, 56, 160-166.	1.2	26
63	Laser-Initiated Radical Trifluoromethylation of Peptides and Proteins: Application to Mass Spectrometry-Based Protein Footprinting. <i>Angewandte Chemie</i> , 2017, 129, 14195-14198.	1.6	9
64	Native Mass Spectrometry, Ion mobility, and Collision-Induced Unfolding Categorize Malaria Antigen/Antibody Binding. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2515-2518.	1.2	17
65	Laser-Initiated Radical Trifluoromethylation of Peptides and Proteins: Application to Mass Spectrometry-Based Protein Footprinting. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 14007-14010.	7.2	74
66	Peptide-Level Interactions between Proteins and Small-Molecule Drug Candidates by Two Hydrogen-Deuterium Exchange MS-Based Methods: The Example of Apolipoprotein E3. <i>Analytical Chemistry</i> , 2017, 89, 10687-10695.	3.2	14
67	Reactive oxygen species leave a damage trail that reveals water channels in Photosystem II. <i>Science Advances</i> , 2017, 3, eaao3013.	4.7	31
68	Protonated N -alkyl-2-nitroanilines undergo intramolecular oxidation of the alkyl chain upon collisional activation. <i>International Journal of Mass Spectrometry</i> , 2017, 413, 75-80.	0.7	1
69	Native MS and ECD Characterization of a Fab-Antigen Complex May Facilitate Crystallization for X-ray Diffraction. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1139-1142.	1.2	22
70	Dimerization Controls Marburg Virus VP24-dependent Modulation of Host Antioxidative Stress Responses. <i>Journal of Molecular Biology</i> , 2016, 428, 3483-3494.	2.0	26
71	Protein Footprinting by Carbenes on a Fast Photochemical Oxidation of Proteins (FPOP) Platform. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 552-555.	1.2	44
72	Electron-capture dissociation and ion mobility mass spectrometry for characterization of the hemoglobin protein assembly. <i>Protein Science</i> , 2015, 24, 1325-1332.	3.1	26

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73	R. Graham Cooks Elected to the National Academy of Sciences. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1057-1058.	1.2	0
74	Nico Nibbering (1938–2014). <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 1829-1831.	1.2	0
75	Mass spectrometry for the biophysical characterization of therapeutic monoclonal antibodies. <i>FEBS Letters</i> , 2014, 588, 308-317.	1.3	123
76	Focus in Honor of Yinsheng Wang, Recipient of the 2013 Biemann Medal. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 1096-1097.	1.2	0
77	David Russell as New Editor for <i>Critical Insights</i> to Replace Carol Robinson. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1821-1822.	1.2	0
78	Mass spectrometry-based carboxyl footprinting of proteins: Method evaluation. <i>International Journal of Mass Spectrometry</i> , 2012, 312, 78-86.	0.7	48
79	Deprotonated N-(2,4-dinitrophenyl)amino acids undergo cyclization in solution and the gas phase. <i>International Journal of Mass Spectrometry</i> , 2011, 306, 232-240.	0.7	8
80	Ion behavior in an electrically compensated ion cyclotron resonance trap. <i>International Journal of Mass Spectrometry</i> , 2011, 300, 143-148.	0.7	6
81	Hydrophobic peptides affect binding of calmodulin and Ca <sup>2+</sup> as explored by H/D amide exchange and mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 85-92.	0.7	17
82	Radical cation/radical reactions: A Fourier transform ion cyclotron resonance study of allyl radical reacting with aromatic radical cations. <i>International Journal of Mass Spectrometry</i> , 2009, 287, 8-15.	0.7	11
83	Estrogen Carcinogenesis: Specific Identification of Estrogen-Modified Nucleobase in Breast Tissue from Women. <i>Chemical Research in Toxicology</i> , 2008, 21, 1509-1513.	1.7	20
84	A Triterpene Glycoside from Black Cohosh that Inhibits Osteoclastogenesis by Modulating RANKL and TNF $\alpha$ Signaling Pathways. <i>Chemistry and Biology</i> , 2007, 14, 860-869.	6.2	53
85	Ion-exchange chromatography followed by ESI-MS for quantitative analysis of sugar monophosphates from glucose catabolism. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 104-107.	1.2	10
86	Application of SIMSTEX to oligomerization of insulin analogs and mutants. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 1526-1534.	1.2	32
87	PLIMSTEX: a novel mass spectrometric method for the quantification of protein–ligand interactions in solution. <i>International Journal of Mass Spectrometry</i> , 2005, 240, 213-220.	0.7	38
88	Accurate mass measurements by Fourier transform mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2005, 24, 286-309.	2.8	120
89	Information for proteomics: ESI-MS titration by sodium ions gives the number of carboxylate groups in peptides. <i>International Journal of Mass Spectrometry</i> , 2004, 231, 113-117.	0.7	14