

Thomas J D JÃ,rgensen

List of Publications by Year in descending order

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147566

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3632
citing authors

#	ARTICLE	IF	CITATIONS
1	The changing face of SDS denaturation: Complexes of <i>Thermomyces lanuginosus</i> lipase with SDS at pH 4.0, 6.0 and 8.0. <i>Journal of Colloid and Interface Science</i> , 2022, 614, 214-232.	5.0	15
2	Structural Basis for Dityrosine-Mediated Inhibition of $\hat{\iota}$ -Synuclein Fibrillization. <i>Journal of the American Chemical Society</i> , 2022, 144, 11949-11954.	6.6	6
3	Ultraviolet Photodissociation of Protonated Peptides and Proteins Can Proceed with H/D Scrambling. <i>Analytical Chemistry</i> , 2021, 93, 691-696.	3.2	8
4	The intrinsic instability of the hydrolase domain of lipoprotein lipase facilitates its inactivation by ANGPTL4-catalyzed unfolding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	29
5	Probing the Conformational Dynamics of Affinity-Enhanced T Cell Receptor Variants upon Binding the Peptide-Bound Major Histocompatibility Complex by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Biochemistry</i> , 2021, 60, 859-872.	1.2	3
6	Lipid Peroxidation Products HNE and ONE Promote and Stabilize Alpha-Synuclein Oligomers by Chemical Modifications. <i>Biochemistry</i> , 2021, 60, 3644-3658.	1.2	13
7	Molecular Architecture of the Antiophidic Protein DM64 and its Binding Specificity to Myotoxin II From <i>Bothrops asper</i> Venom. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 787368.	1.6	2
8	Deglycosylation by the Acidic Glycosidase PNGase H ⁺ Enables Analysis of N-Linked Glycoproteins by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 2305-2312.	1.2	16
9	Avoiding H/D Scrambling with Minimal Ion Transmission Loss for HDX-MS/MS-ETD Analysis on a High-Resolution Q-TOF Mass Spectrometer. <i>Analytical Chemistry</i> , 2020, 92, 7453-7461.	3.2	22
10	Unfolding of monomeric lipoprotein lipase by ANGPTL4: Insight into the regulation of plasma triglyceride metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4337-4346.	3.3	56
11	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
12	Did evolution create a flexible ligand-binding cavity in the urokinase receptor through deletion of a plesiotypic disulfide bond?. <i>Journal of Biological Chemistry</i> , 2019, 294, 7403-7418.	1.6	11
13	A disordered acidic domain in GPIHBP1 harboring a sulfated tyrosine regulates lipoprotein lipase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6020-E6029.	3.3	51
14	Dissecting the interaction between transglutaminase 2 and fibronectin. <i>Amino Acids</i> , 2017, 49, 489-500.	1.2	23
15	Uranyl Photocleavage of Phosphopeptides Yields Truncated C-terminally Amidated Peptide Products. <i>ChemBioChem</i> , 2017, 18, 1117-1122.	1.3	9
16	Conformational preludes to the latency transition in PAI-1 as determined by atomistic computer simulations and hydrogen/deuterium-exchange mass spectrometry. <i>Scientific Reports</i> , 2017, 7, 6636.	1.6	11
17	The T-Cell Receptor Can Bind to the Peptide-Bound Major Histocompatibility Complex and Uncomplexed $\hat{\iota}$ ₂ -Microglobulin through Distinct Binding Sites. <i>Biochemistry</i> , 2017, 56, 3945-3961.	1.2	8
18	An Asymmetric Runaway Domain Swap Antithrombin Dimer as a Key Intermediate for Polymerization Revealed by Hydrogen/Deuterium-Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 616-624.	3.2	7

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19	Epitope-dependent Functional Effects of Celiac Disease Autoantibodies on Transglutaminase 2. <i>Journal of Biological Chemistry</i> , 2016, 291, 25542-25552.	1.6	20
20	Copper(II) Ions Increase Plasminogen Activator Inhibitor Type 1 Dynamics in Key Structural Regions That Govern Stability. <i>Biochemistry</i> , 2016, 55, 4386-4398.	1.2	11
21	Removal of N-Linked Glycosylations at Acidic pH by PNGase A Facilitates Hydrogen/Deuterium Exchange Mass Spectrometry Analysis of N-Linked Glycoproteins. <i>Analytical Chemistry</i> , 2016, 88, 12479-12488.	3.2	38
22	An RNA Aptamer Inhibits a Mutation-Induced Inactivating Misfolding of a Serpin. <i>Cell Chemical Biology</i> , 2016, 23, 700-708.	2.5	7
23	The acidic domain of the endothelial membrane protein GPIHBP1 stabilizes lipoprotein lipase activity by preventing unfolding of its catalytic domain. <i>ELife</i> , 2016, 5, e12095.	2.8	74
24	The angiopoietin-like protein ANGPTL4 catalyzes unfolding of the hydrolase domain in lipoprotein lipase and the endothelial membrane protein GPIHBP1 counteracts this unfolding. <i>ELife</i> , 2016, 5, .	2.8	78
25	Effect of Metals in Biomimetic Dimetal Complexes on Affinity and Gas-Phase Protection of Phosphate Esters. <i>Analytical Chemistry</i> , 2015, 87, 7060-7068.	3.2	7
26	Conformational Analysis of Large and Highly Disulfide-Stabilized Proteins by Integrating Online Electrochemical Reduction into an Optimized H/D Exchange Mass Spectrometry Workflow. <i>Analytical Chemistry</i> , 2015, 87, 8880-8888.	3.2	44
27	A Phosphorylation Tag for Uranyl Mediated Protein Purification and Photo Assisted Tag Removal. <i>PLoS ONE</i> , 2014, 9, e91138.	1.1	6
28	Measuring the Hydrogen/Deuterium Exchange of Proteins at High Spatial Resolution by Mass Spectrometry: Overcoming Gas-Phase Hydrogen/Deuterium Scrambling. <i>Accounts of Chemical Research</i> , 2014, 47, 3018-3027.	7.6	81
29	Co-existence of Two Different β -Synuclein Oligomers with Different Core Structures Determined by Hydrogen/Deuterium Exchange Mass Spectrometry (<i>Angew. Chem.</i> 29/2014). <i>Angewandte Chemie</i> , 2014, 126, 7808-7808.	1.6	0
30	Local Transient Unfolding of Native State PAI-1 Associated with Serpin Metastability. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 9751-9754.	7.2	29
31	Ion source parameters and hydrogen scrambling in the ECD of selectively deuterated peptides. <i>International Journal of Mass Spectrometry</i> , 2014, 367, 21-27.	0.7	2
32	Co-existence of Two Different β -Synuclein Oligomers with Different Core Structures Determined by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 7560-7563.	7.2	103
33	Dissecting the Effect of RNA Aptamer Binding on the Dynamics of Plasminogen Activator Inhibitor 1 Using Hydrogen/Deuterium Exchange Mass Spectrometry. <i>ACS Chemical Biology</i> , 2014, 9, 174-182.	1.6	32
34	Activity-regulating structural changes and autoantibody epitopes in transglutaminase 2 assessed by hydrogen/deuterium exchange. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17146-17151.	3.3	51
35	On the photostability of peptides after selective photoexcitation of the backbone: prompt versus slow dissociation. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 15831-15838.	1.3	22
36	Affinity Capture of Biotinylated Proteins at Acidic Conditions to Facilitate Hydrogen/Deuterium Exchange Mass Spectrometry Analysis of Multimeric Protein Complexes. <i>Analytical Chemistry</i> , 2013, 85, 7052-7059.	3.2	13

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37	Improved PET Imaging of uPAR Expression Using new ⁶⁴ Cu-labeled Cross-Bridged Peptide Ligands: Comparative in vitro and in vivo Studies. <i>Theranostics</i> , 2013, 3, 618-632.	4.6	50
38	A Flexible Multidomain Structure Drives the Function of the Urokinase-type Plasminogen Activator Receptor (uPAR)*. <i>Journal of Biological Chemistry</i> , 2012, 287, 34304-34315.	1.6	43
39	Spatially Resolved Protein Hydrogen Exchange Measured by Subzero-Cooled Chip-Based Nanoelectrospray Ionization Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 4467-4473.	3.2	41
40	Hydrogen/Deuterium Exchange Mass Spectrometry Reveals Specific Changes in the Local Flexibility of Plasminogen Activator Inhibitor 1 upon Binding to the Somatomedin B Domain of Vitronectin. <i>Biochemistry</i> , 2012, 51, 8256-8266.	1.2	29
41	Spatially Resolved Protein Hydrogen Exchange Measured by Matrix-Assisted Laser Desorption Ionization In-Source Decay. <i>Analytical Chemistry</i> , 2011, 83, 8859-8862.	3.2	35
42	Investigation of amide hydrogen back-exchange in Asp and His repeats measured by hydrogen (¹ H/ ² H) exchange mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 110-115.	0.7	28
43	Loss of Ammonia during Electron-Transfer Dissociation of Deuterated Peptides as an Inherent Gauge of Gas-Phase Hydrogen Scrambling. <i>Analytical Chemistry</i> , 2010, 82, 9755-9762.	3.2	40
44	Structure and allosteric effects of low-molecular-weight activators on the protein kinase PDK1. <i>Nature Chemical Biology</i> , 2009, 5, 758-764.	3.9	134
45	Protein Hydrogen Exchange Measured at Single-Residue Resolution by Electron Transfer Dissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5577-5584.	3.2	204
46	Hydrogen atom scrambling in selectively labeled anionic peptides upon collisional activation by MALDI tandem time-of-flight mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1719-1725.	1.2	27
47	Electron Transfer Dissociation Facilitates the Measurement of Deuterium Incorporation into Selectively Labeled Peptides with Single Residue Resolution. <i>Journal of the American Chemical Society</i> , 2008, 130, 17453-17459.	6.6	158
48	Gas-Phase Fragmentation of Peptides by MALDI in-Source Decay with Limited Amide Hydrogen (¹ H/ ² H) Scrambling. <i>Analytical Chemistry</i> , 2008, 80, 6431-6435.	3.2	35
49	Electron Capture Dissociation Proceeds with a Low Degree of Intramolecular Migration of Peptide Amide Hydrogens. <i>Journal of the American Chemical Society</i> , 2008, 130, 1341-1349.	6.6	167
50	The Origins of Enhanced Activity in Factor VIIa Analogs and the Interplay between Key Allosteric Sites Revealed by Hydrogen Exchange Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2008, 283, 13378-13387.	1.6	28
51	Development of a Peptide Probe for the Occurrence of Hydrogen (¹ H/ ² H) Scrambling upon Gas-Phase Fragmentation. <i>Analytical Chemistry</i> , 2007, 79, 8686-8693.	3.2	77
52	Solution structure of recombinant somatomedin B domain from vitronectin produced in <i>Pichia pastoris</i> . <i>Protein Science</i> , 2007, 16, 1934-1945.	3.1	32
53	Mass spectrometric characterization of conformational preludes to β 2-microglobulin aggregation. <i>International Journal of Mass Spectrometry</i> , 2007, 268, 207-216.	0.7	16
54	Characterization of the Functional Epitope on the Urokinase Receptor. <i>Journal of Biological Chemistry</i> , 2006, 281, 19260-19272.	1.6	78

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55	Allosteric Activation of Coagulation Factor VIIa Visualized by Hydrogen Exchange. <i>Journal of Biological Chemistry</i> , 2006, 281, 23018-23024.	1.6	52
56	Rapid desalting of protein samples for on-line microflow electrospray ionization mass spectrometry. <i>Analytical Biochemistry</i> , 2005, 342, 160-162.	1.1	27
57	Mass spectrometric analysis of protein interactions. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 509-516.	2.8	36
58	Analysis of subsecond protein dynamics by amide hydrogen exchange and mass spectrometry using a quenched-flow setup. <i>Protein Science</i> , 2005, 14, 626-632.	3.1	43
59	Collisional Activation by MALDI Tandem Time-of-flight Mass Spectrometry Induces Intramolecular Migration of Amide Hydrogens in Protonated Peptides. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1910-1919.	2.5	36
60	Intramolecular Migration of Amide Hydrogens in Protonated Peptides upon Collisional Activation. <i>Journal of the American Chemical Society</i> , 2005, 127, 2785-2793.	6.6	161
61	Dynamics of Urokinase Receptor Interaction with Peptide Antagonists Studied by Amide Hydrogen Exchange and Mass Spectrometry. <i>Biochemistry</i> , 2004, 43, 15044-15057.	1.2	54
62	The combination of an electrospray ion source and an electrostatic storage ring for lifetime and spectroscopy experiments on biomolecules. <i>Review of Scientific Instruments</i> , 2002, 73, 1284-1287.	0.6	127
63	Molecular identification of the insect adipokinetic hormone receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 3446-3451.	3.3	273
64	Electron loss from multiply protonated lysozyme ions in high energy collisions with molecular oxygen. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 889-893.	1.2	26
65	Benefits of 2.94 μm infrared matrix-assisted laser desorption/ionization for analysis of labile molecules by Fourier transform mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2000, 35, 578-584.		22