

# Thomas J D JÃ,rgensen

## List of Publications by Year in descending order

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65  
papers

3,521  
citations

147801

31  
h-index

144013

57  
g-index

71  
all docs

71  
docs citations

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times ranked

3632  
citing authors

#	ARTICLE	IF	CITATIONS
1	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	19.0	452
2	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.	7.1	273
3	Protein Hydrogen Exchange Measured at Single-Residue Resolution by Electron Transfer Dissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5577-5584.	6.5	204
4	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.	13.7	167
5	Intramolecular Migration of Amide Hydrogens in Protonated Peptides upon Collisional Activation. <i>Journal of the American Chemical Society</i> , 2005, 127, 2785-2793.	13.7	161
6	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.	13.7	158
7	Structure and allosteric effects of low-molecular-weight activators on the protein kinase PDK1. <i>Nature Chemical Biology</i> , 2009, 5, 758-764.	8.0	134
8	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.	1.3	127
9	Coexistence of Two Different $\beta$ -Synuclein Oligomers with Different Core Structures Determined by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 7560-7563.	13.8	103
10	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.	15.6	81
11	Characterization of the Functional Epitope on the Urokinase Receptor. <i>Journal of Biological Chemistry</i> , 2006, 281, 19260-19272.	3.4	78
12	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, .	6.0	78
13	Development of a Peptide Probe for the Occurrence of Hydrogen ( $^1\text{H}/^2\text{H}$ ) Scrambling upon Gas-Phase Fragmentation. <i>Analytical Chemistry</i> , 2007, 79, 8686-8693.	6.5	77
14	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.	6.0	74
15	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.	7.1	56
16	Dynamics of Urokinase Receptor Interaction with Peptide Antagonists Studied by Amide Hydrogen Exchange and Mass Spectrometry. <i>Biochemistry</i> , 2004, 43, 15044-15057.	2.5	54
17	Allosteric Activation of Coagulation Factor VIIa Visualized by Hydrogen Exchange. <i>Journal of Biological Chemistry</i> , 2006, 281, 23018-23024.	3.4	52
18	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.	7.1	51

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19	A disordered acidic domain in GPIHBP1 harboring a sulfated tyrosine regulates lipoprotein lipase. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6020-E6029.	7.1	51
20	Improved PET Imaging of uPAR Expression Using new <sup>64</sup> Cu-labeled Cross-Bridged Peptide Ligands: Comparative in vitro and in vivo Studies. Theranostics, 2013, 3, 618-632.	10.0	50
21	Conformational Analysis of Large and Highly Disulfide-Stabilized Proteins by Integrating Online Electrochemical Reduction into an Optimized H/D Exchange Mass Spectrometry Workflow. Analytical Chemistry, 2015, 87, 8880-8888.	6.5	44
22	Analysis of subsecond protein dynamics by amide hydrogen exchange and mass spectrometry using a quenched-flow setup. Protein Science, 2005, 14, 626-632.	7.6	43
23	A Flexible Multidomain Structure Drives the Function of the Urokinase-type Plasminogen Activator Receptor (uPAR)*. Journal of Biological Chemistry, 2012, 287, 34304-34315.	3.4	43
24	Spatially Resolved Protein Hydrogen Exchange Measured by Subzero-Cooled Chip-Based Nanoelectrospray Ionization Tandem Mass Spectrometry. Analytical Chemistry, 2012, 84, 4467-4473.	6.5	41
25	Loss of Ammonia during Electron-Transfer Dissociation of Deuterated Peptides as an Inherent Gauge of Gas-Phase Hydrogen Scrambling. Analytical Chemistry, 2010, 82, 9755-9762.	6.5	40
26	Removal of N-Linked Glycosylations at Acidic pH by PNGase A Facilitates Hydrogen/Deuterium Exchange Mass Spectrometry Analysis of N-Linked Glycoproteins. Analytical Chemistry, 2016, 88, 12479-12488.	6.5	38
27	Mass spectrometric analysis of protein interactions. Current Opinion in Chemical Biology, 2005, 9, 509-516.	6.1	36
28	Collisional Activation by MALDI Tandem Time-of-flight Mass Spectrometry Induces Intramolecular Migration of Amide Hydrogens in Protonated Peptides. Molecular and Cellular Proteomics, 2005, 4, 1910-1919.	3.8	36
29	Gas-Phase Fragmentation of Peptides by MALDI in-Source Decay with Limited Amide Hydrogen (<sup>1</sup>H/<sup>2</sup>H) Scrambling. Analytical Chemistry, 2008, 80, 6431-6435.	6.5	35
30	Spatially Resolved Protein Hydrogen Exchange Measured by Matrix-Assisted Laser Desorption Ionization In-Source Decay. Analytical Chemistry, 2011, 83, 8859-8862.	6.5	35
31	Solution structure of recombinant somatomedin B domain from vitronectin produced in <i>Pichia pastoris</i>. Protein Science, 2007, 16, 1934-1945.	7.6	32
32	Dissecting the Effect of RNA Aptamer Binding on the Dynamics of Plasminogen Activator Inhibitor 1 Using Hydrogen/Deuterium Exchange Mass Spectrometry. ACS Chemical Biology, 2014, 9, 174-182.	3.4	32
33	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. Biochemistry, 2012, 51, 8256-8266.	2.5	29
34	Local Transient Unfolding of Native State PAI-1 Associated with Serpin Metastability. Angewandte Chemie - International Edition, 2014, 53, 9751-9754.	13.8	29
35	The intrinsic instability of the hydrolase domain of lipoprotein lipase facilitates its inactivation by ANGPTL4-catalyzed unfolding. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	29
36	The Origins of Enhanced Activity in Factor VIIa Analogs and the Interplay between Key Allosteric Sites Revealed by Hydrogen Exchange Mass Spectrometry. Journal of Biological Chemistry, 2008, 283, 13378-13387.	3.4	28

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37	Investigation of amide hydrogen back-exchange in Asp and His repeats measured by hydrogen (1H/2H) exchange mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 110-115.	1.5	28
38	Rapid desalting of protein samples for on-line microflow electrospray ionization mass spectrometry. <i>Analytical Biochemistry</i> , 2005, 342, 160-162.	2.4	27
39	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.	2.8	27
40	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.	2.8	26
41	Dissecting the interaction between transglutaminase 2 and fibronectin. <i>Amino Acids</i> , 2017, 49, 489-500.	2.7	23
42	Benefits of 2.94 $\mu$ m infrared matrix-assisted laser desorption/ionization for analysis of labile molecules by Fourier transform mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2000, 14, 578-584.		22
43	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.	2.8	22
44	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.	6.5	22
45	Epitope-dependent Functional Effects of Celiac Disease Autoantibodies on Transglutaminase 2. <i>Journal of Biological Chemistry</i> , 2016, 291, 25542-25552.	3.4	20
46	Mass spectrometric characterization of conformational preludes to $\beta$ 2-microglobulin aggregation. <i>International Journal of Mass Spectrometry</i> , 2007, 268, 207-216.	1.5	16
47	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.	2.8	16
48	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.	9.4	15
49	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.	6.5	13
50	Lipid Peroxidation Products HNE and ONE Promote and Stabilize Alpha-Synuclein Oligomers by Chemical Modifications. <i>Biochemistry</i> , 2021, 60, 3644-3658.	2.5	13
51	Copper(II) Ions Increase Plasminogen Activator Inhibitor Type 1 Dynamics in Key Structural Regions That Govern Stability. <i>Biochemistry</i> , 2016, 55, 4386-4398.	2.5	11
52	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.	3.3	11
53	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.	3.4	11
54	Uranyl Photocleavage of Phosphopeptides Yields Truncated C-Terminally Amidated Peptide Products. <i>ChemBioChem</i> , 2017, 18, 1117-1122.	2.6	9

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55	The T-Cell Receptor Can Bind to the Peptide-Bound Major Histocompatibility Complex and Uncomplexed $\hat{I}^2$ -Microglobulin through Distinct Binding Sites. <i>Biochemistry</i> , 2017, 56, 3945-3961.	2.5	8
56	Ultraviolet Photodissociation of Protonated Peptides and Proteins Can Proceed with H/D Scrambling. <i>Analytical Chemistry</i> , 2021, 93, 691-696.	6.5	8
57	Effect of Metals in Biomimetic Dimetal Complexes on Affinity and Gas-Phase Protection of Phosphate Esters. <i>Analytical Chemistry</i> , 2015, 87, 7060-7068.	6.5	7
58	An RNA Aptamer Inhibits a Mutation-Induced Inactivating Misfolding of a Serpin. <i>Cell Chemical Biology</i> , 2016, 23, 700-708.	5.2	7
59	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.	6.5	7
60	A Phosphorylation Tag for Uranyl Mediated Protein Purification and Photo Assisted Tag Removal. <i>PLoS ONE</i> , 2014, 9, e91138.	2.5	6
61	Structural Basis for Dityrosine-Mediated Inhibition of $\hat{I}^{\pm}$ -Synuclein Fibrillization. <i>Journal of the American Chemical Society</i> , 2022, 144, 11949-11954.	13.7	6
62	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.	2.5	3
63	Ion source parameters and hydrogen scrambling in the ECD of selectively deuterated peptides. <i>International Journal of Mass Spectrometry</i> , 2014, 367, 21-27.	1.5	2
64	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.	3.5	2
65	Co-existence of Two Different $\hat{I}^{\pm}$ -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.	2.0	0