

Kasper D Rand

List of Publications by Year in descending order

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96
papers

3,869
citations

117625

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144013

57
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103
all docs

103
docs citations

103
times ranked

4329
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	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
3	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
4	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
5	Conformational Analysis of Membrane Proteins in Phospholipid Bilayer Nanodiscs by Hydrogen Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 5415-5419.	6.5	133
6	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	6.5	100
7	False EX1 signatures caused by sample carryover during HX MS analyses. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 19-25.	1.5	94
8	Gas-Phase Hydrogen/Deuterium Exchange in a Traveling Wave Ion Guide for the Examination of Protein Conformations. <i>Analytical Chemistry</i> , 2009, 81, 10019-10028.	6.5	89
9	Antibody mechanics on a membrane-bound HIV segment essential for GP41-targeted viral neutralization. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1235-1243.	8.2	86
10	Conformational analysis of complex protein states by hydrogen/deuterium exchange mass spectrometry (HDX-MS): Challenges and emerging solutions. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 106, 125-138.	11.4	83
11	Investigating the Interaction between the Neonatal Fc Receptor and Monoclonal Antibody Variants by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 148-161.	3.8	82
12	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
13	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.	6.5	77
14	ETD in a Traveling Wave Ion Guide at Tuned Z-Spray Ion Source Conditions Allows for Site-Specific Hydrogen/Deuterium Exchange Measurements. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1784-93.	2.8	72
15	A Poly-ADP-Ribose Trigger Releases the Auto-Inhibition of a Chromatin Remodeling Oncogene. <i>Molecular Cell</i> , 2017, 68, 860-871.e7.	9.7	70
16	Conformational Transitions in the Membrane Scaffold Protein of Phospholipid Bilayer Nanodiscs. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010876.	3.8	66
17	Site-Specific Analysis of Gas-Phase Hydrogen/Deuterium Exchange of Peptides and Proteins by Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2012, 84, 1931-1940.	6.5	61
18	Conformational dynamics of the human serotonin transporter during substrate and drug binding. <i>Nature Communications</i> , 2019, 10, 1687.	12.8	57

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19	Molecular Analysis of the Interaction between the Hematopoietic Master Transcription Factors GATA-1 and PU.1. <i>Journal of Biological Chemistry</i> , 2006, 281, 28296-28306.	3.4	53
20	Getting to the core of protein pharmaceuticals – Comprehensive structure analysis by mass spectrometry. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2015, 93, 95-109.	4.3	53
21	Allosteric Activation of Coagulation Factor VIIa Visualized by Hydrogen Exchange. <i>Journal of Biological Chemistry</i> , 2006, 281, 23018-23024.	3.4	52
22	Rapid and simple preparation of thiol-ene emulsion-templated monoliths and their application as enzymatic microreactors. <i>Lab on A Chip</i> , 2015, 15, 2162-2172.	6.0	51
23	A post-translational modification of human Norovirus capsid protein attenuates glycan binding. <i>Nature Communications</i> , 2019, 10, 1320.	12.8	50
24	Substrate-modulated unwinding of transmembrane helices in the NSS transporter LeuT. <i>Science Advances</i> , 2018, 4, eaar6179.	10.3	47
25	Substrate-induced conformational dynamics of the dopamine transporter. <i>Nature Communications</i> , 2019, 10, 2714.	12.8	46
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.	6.5	44
27	Interlaboratory Comparison of Hydrogen-Deuterium Exchange Mass Spectrometry Measurements of the Fab Fragment of NISTmAb. <i>Analytical Chemistry</i> , 2019, 91, 7336-7345.	6.5	44
28	Thiol-ene Monolithic Pepsin Microreactor with a 3D-Printed Interface for Efficient UPLC-MS Peptide Mapping Analyses. <i>Analytical Chemistry</i> , 2017, 89, 4573-4580.	6.5	41
29	Glycine Perturbs Local and Global Conformational Flexibility of a Transmembrane Helix. <i>Biochemistry</i> , 2018, 57, 1326-1337.	2.5	41
30	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.	6.5	40
31	An intact C-terminal end of albumin is required for its long half-life in humans. <i>Communications Biology</i> , 2020, 3, 181.	4.4	40
32	Crystal Structure of a Prolactin Receptor Antagonist Bound to the Extracellular Domain of the Prolactin Receptor. <i>Journal of Biological Chemistry</i> , 2008, 283, 19085-19094.	3.4	38
33	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.	6.5	38
34	Probing the Binding Interfaces of Protein Complexes Using Gas-Phase H/D Exchange Mass Spectrometry. <i>Structure</i> , 2016, 24, 310-318.	3.3	38
35	Construct design, production, and characterization of <i>Plasmodium falciparum</i> 48/45 R0.6C subunit protein produced in <i>Lactococcus lactis</i> as candidate vaccine. <i>Microbial Cell Factories</i> , 2017, 16, 97.	4.0	37
36	Circularized and solubility-enhanced MSPs facilitate simple and high-yield production of stable nanodiscs for studies of membrane proteins in solution. <i>FEBS Journal</i> , 2019, 286, 1734-1751.	4.7	36

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37	Gas-Phase Fragmentation of Peptides by MALDI in-Source Decay with Limited Amide Hydrogen (¹H/²H) Scrambling. <i>Analytical Chemistry</i> , 2008, 80, 6431-6435.	6.5	35
38	Spatially Resolved Protein Hydrogen Exchange Measured by Matrix-Assisted Laser Desorption Ionization In-Source Decay. <i>Analytical Chemistry</i> , 2011, 83, 8859-8862.	6.5	35
39	Conformational Destabilization of Immunoglobulin G Increases the Low pH Binding Affinity with the Neonatal Fc Receptor. <i>Journal of Biological Chemistry</i> , 2016, 291, 1817-1825.	3.4	35
40	Simple Setup for Gas-Phase H/D Exchange Mass Spectrometry Coupled to Electron Transfer Dissociation and Ion Mobility for Analysis of Polypeptide Structure on a Liquid Chromatographic Time Scale. <i>Analytical Chemistry</i> , 2014, 86, 11868-11876.	6.5	34
41	UV Photodissociation Mass Spectrometry Accurately Localize Sites of Backbone Deuteration in Peptides. <i>Analytical Chemistry</i> , 2018, 90, 1077-1080.	6.5	32
42	A Two-pronged Binding Mechanism of IgG to the Neonatal Fc Receptor Controls Complex Stability and IgG Serum Half-life. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 451-456.	3.8	31
43	A combined structural dynamics approach identifies a putative switch in factor VIIa employed by tissue factor to initiate blood coagulation. <i>Protein Science</i> , 2007, 16, 671-682.	7.6	30
44	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.	3.4	28
45	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
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.	2.8	27
47	Substrate- and Cofactor-independent Inhibition of Histone Demethylase KDM4C. <i>ACS Chemical Biology</i> , 2014, 9, 2131-2138.	3.4	25
48	Thiol-ene Microfluidic Chip for Performing Hydrogen/Deuterium Exchange of Proteins at Subsecond Time Scales. <i>Analytical Chemistry</i> , 2019, 91, 1309-1317.	6.5	25
49	A simple sheathless CE-MS interface with a sub-micrometer electrical contact fracture for sensitive analysis of peptide and protein samples. <i>Analytica Chimica Acta</i> , 2016, 936, 157-167.	5.4	24
50	Pinpointing changes in higher-order protein structure by hydrogen/deuterium exchange coupled to electron transfer dissociation mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2013, 338, 2-10.	1.5	22
51	Improving the Sequence Coverage of Integral Membrane Proteins during Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. <i>Analytical Chemistry</i> , 2019, 91, 10970-10978.	6.5	22
52	Hydrogen/deuterium exchange mass spectrometry with improved electrochemical reduction enables comprehensive epitope mapping of a therapeutic antibody to the cysteine-knot containing vascular endothelial growth factor. <i>Analytica Chimica Acta</i> , 2020, 1115, 41-51.	5.4	22
53	Conformational Dynamics of the Escherichia coli DNA Polymerase Manager Proteins UmuD and UmuD ² . <i>Journal of Molecular Biology</i> , 2010, 398, 40-53.	4.2	20
54	Sites Involved in Intra- and Interdomain Allostery Associated with the Activation of Factor VIIa Pinpointed by Hydrogen-Deuterium Exchange and Electron Transfer Dissociation Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2014, 289, 35388-35396.	3.4	20

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55	Conformational characterization of nerve growth factor- β reveals that its regulatory pro-part domain stabilizes three loop regions in its mature part. <i>Journal of Biological Chemistry</i> , 2017, 292, 16665-16676.	3.4	20
56	Dissecting the Binding Mode of Low Affinity Phage Display Peptide Ligands to Protein Targets by Hydrogen/Deuterium Exchange Coupled to Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 11734-11741.	6.5	19
57	Epitope Mapping of Polyclonal Antibodies by Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS). <i>Analytical Chemistry</i> , 2021, 93, 11669-11678.	6.5	19
58	Discovery of Highly Active Recombinant PNGase H+ Variants Through the Rational Exploration of Unstudied Acidobacterial Genomes. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 741.	4.1	18
59	Hydrogen/Deuterium Exchange Mass Spectrometry with Integrated Electrochemical Reduction and Microchip-Enabled Deglycosylation for Epitope Mapping of Heavily Glycosylated and Disulfide-Bonded Proteins. <i>Analytical Chemistry</i> , 2021, 93, 16330-16340.	6.5	17
60	Probing the Conformational and Functional Consequences of Disulfide Bond Engineering in Growth Hormone by Hydrogen-Deuterium Exchange Mass Spectrometry Coupled to Electron Transfer Dissociation. <i>Analytical Chemistry</i> , 2015, 87, 5973-5980.	6.5	16
61	Molecular architecture of the Jumonji C family histone demethylase KDM5B. <i>Scientific Reports</i> , 2019, 9, 4019.	3.3	16
62	Probing the Dissociation of Protein Complexes by Means of Gas-Phase H/D Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 45-57.	2.8	16
63	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
64	Hydrogen-Deuterium Exchange Mass Spectrometry with Integrated Size-Exclusion Chromatography for Analysis of Complex Protein Samples. <i>Analytical Chemistry</i> , 2021, 93, 11406-11414.	6.5	16
65	Conformational Analysis of Proteins in Highly Concentrated Solutions by Dialysis-Coupled Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 669-676.	2.8	15
66	Side-chain moieties from the N-terminal region of $\text{A}\beta$ are involved in an oligomer-stabilizing network of interactions. <i>PLoS ONE</i> , 2018, 13, e0201761.	2.5	14
67	Structure and Dynamics of a Promiscuous Xanthan Lyase from <i>Paenibacillus nanensis</i> and the Design of Variants with Increased Stability and Activity. <i>Cell Chemical Biology</i> , 2019, 26, 191-202.e6.	5.2	13
68	Rapid Conformational Analysis of Protein Drugs in Formulation by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of Pharmaceutical Sciences</i> , 2016, 105, 3269-3277.	3.3	12
69	Structural Dynamics and Catalytic Properties of a Multimodular Xanthanase. <i>ACS Catalysis</i> , 2018, 8, 6021-6034.	11.2	12
70	Investigating the Conformational Response of the Sortilin Receptor upon Binding Endogenous Peptide- and Protein Ligands by HDX-MS. <i>Structure</i> , 2019, 27, 1103-1113.e3.	3.3	12
71	Thiol-ene microfluidic chip for fast on-chip sample clean-up, separation and ESI mass spectrometry of peptides and proteins. <i>Analytica Chimica Acta</i> , 2020, 1140, 168-177.	5.4	12
72	Fully Automated Electro Membrane Extraction Autosampler for LC-MS Systems Allowing Soft Extractions for High-Throughput Applications. <i>Analytical Chemistry</i> , 2016, 88, 6797-6804.	6.5	11

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73	Epitope and Paratope Mapping by HDX-MS Combined with SPR Elucidates the Difference in Bactericidal Activity of Two Anti-NadA Monoclonal Antibodies. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1575-1582.	2.8	11
74	The Impact of the "Austrian"™ Mutation of the Amyloid Precursor Protein Transmembrane Helix is Communicated to the Hinge Region. <i>ChemistrySelect</i> , 2016, 1, 4408-4412.	1.5	10
75	Investigating the Role of Artemin Glycosylation. <i>Pharmaceutical Research</i> , 2016, 33, 1383-1398.	3.5	10
76	Direct coupling of a flow-flow electromembrane extraction probe to LC-MS. <i>Analytica Chimica Acta</i> , 2016, 905, 93-99.	5.4	10
77	Expression, Purification and Characterization of GMZ2™.10C, a Complex Disulphide-Bonded Fusion Protein Vaccine Candidate against the Asexual and Sexual Life-Stages of the Malaria-Causing <i>Plasmodium falciparum</i> Parasite. <i>Pharmaceutical Research</i> , 2017, 34, 1970-1983.	3.5	10
78	Installation, validation, and application examples of two instrumental setups for gas-phase HDX-MS analysis of peptides and proteins. <i>Methods</i> , 2018, 144, 113-124.	3.8	10
79	The dopamine transporter antiports potassium to increase the uptake of dopamine. <i>Nature Communications</i> , 2022, 13, 2446.	12.8	10
80	Benzothiazolinone Derivatives as Potent Allosteric Monoacylglycerol Lipase Inhibitors That Functionally Mimic Sulfenylation of Regulatory Cysteines. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 1261-1280.	6.4	9
81	Probing the conformational impact of detergents on the integral membrane protein LeuT by global HDX-MS. <i>Journal of Proteomics</i> , 2020, 225, 103845.	2.4	9
82	The T-Cell Receptor Can Bind to the Peptide-Bound Major Histocompatibility Complex and Uncomplexed β_2 -Microglobulin through Distinct Binding Sites. <i>Biochemistry</i> , 2017, 56, 3945-3961.	2.5	8
83	Investigating the utility of minimized sample preparation and high-resolution mass spectrometry for quantification of monoclonal antibody drugs. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 159, 384-392.	2.8	8
84	The extraordinary thermal stability of EstA from <i>S. islandicus</i> is independent of post translational modifications. <i>Protein Science</i> , 2017, 26, 1819-1827.	7.6	8
85	Investigating surrogate cerebrospinal fluid matrix compositions for use in quantitative LC-MS analysis of therapeutic antibodies in the cerebrospinal fluid. <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 1653-1661.	3.7	8
86	Conformational dynamics of free and membrane-bound human Hsp70 in model cytosolic and endo-lysosomal environments. <i>Communications Biology</i> , 2021, 4, 1369.	4.4	8
87	Mapping the Interactions of Selective Biochemical Probes of Antibody Conformation by Hydrogen-Deuterium Exchange Mass Spectrometry. <i>ChemBioChem</i> , 2017, 18, 1016-1021.	2.6	7
88	Molecular Basis of the Mechanisms Controlling MASTL. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 326-343.	3.8	7
89	Probing the Impact of Temperature and Substrates on the Conformational Dynamics of the Neurotransmitter:Sodium symporter LeuT. <i>Journal of Molecular Biology</i> , 2022, 434, 167356.	4.2	7
90	Applications of Mass Spectrometry in Drug Development Science. <i>Advances in Delivery Science and Technology</i> , 2016, , 253-289.	0.4	3

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91	Unusual Self-Assembly of the Recombinant Chlamydia trachomatis Major Outer Membrane Protein-Based Fusion Antigen CTH522 Into Protein Nanoparticles. Journal of Pharmaceutical Sciences, 2018, 107, 1690-1700.	3.3	3
92	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.	1.2	3
93	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. Biochemistry, 2021, 60, 859-872.	2.5	3
94	Conformational heterogeneity of Savinase from NMR, HDX-MS and X-ray diffraction analysis. PeerJ, 2020, 8, e9408.	2.0	2
95	Revealing the Dynamic Allosteric Changes Required for Formation of the Cysteine Synthase Complex by Hydrogen-Deuterium Exchange MS. Molecular and Cellular Proteomics, 2021, 20, 100098.	3.8	1
96	Substrate-Induced Conformational Dynamics of the Dopamine Transporter. Biophysical Journal, 2019, 116, 346a.	0.5	0