

Kasper D Rand

List of Publications by Year in descending order

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96
papers

3,869
citations

134610

34
h-index

162838

57
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103
all docs

103
docs citations

103
times ranked

4789
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	2.0	7
2	The dopamine transporter antiports potassium to increase the uptake of dopamine. <i>Nature Communications</i> , 2022, 13, 2446.	5.8	10
3	Revealing the Dynamic Allosteric Changes Required for Formation of the Cysteine Synthase Complex by Hydrogen-Deuterium Exchange MS. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100098.	2.5	1
4	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.	1.2	11
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	Epitope Mapping of Polyclonal Antibodies by Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS). <i>Analytical Chemistry</i> , 2021, 93, 11669-11678.	3.2	19
7	Hydrogen-Deuterium Exchange Mass Spectrometry with Integrated Size-Exclusion Chromatography for Analysis of Complex Protein Samples. <i>Analytical Chemistry</i> , 2021, 93, 11406-11414.	3.2	16
8	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.	3.2	17
9	Conformational dynamics of free and membrane-bound human Hsp70 in model cytosolic and endo-lysosomal environments. <i>Communications Biology</i> , 2021, 4, 1369.	2.0	8
10	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.	2.9	9
11	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.	2.6	12
12	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.	2.0	18
13	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
14	Probing the conformational impact of detergents on the integral membrane protein LeuT by global HDX-MS. <i>Journal of Proteomics</i> , 2020, 225, 103845.	1.2	9
15	An intact C-terminal end of albumin is required for its long half-life in humans. <i>Communications Biology</i> , 2020, 3, 181.	2.0	40
16	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.	2.6	22
17	Molecular Basis of the Mechanisms Controlling MASTL. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 326-343.	2.5	7
18	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.	1.9	8

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19	Conformational heterogeneity of Savinase from NMR, HDX-MS and X-ray diffraction analysis. PeerJ, 2020, 8, e9408.	0.9	2
20	Investigating the Conformational Response of the Sortilin Receptor upon Binding Endogenous Peptide- and Protein Ligands by HDX-MS. Structure, 2019, 27, 1103-1113.e3.	1.6	12
21	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	9.0	452
22	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
23	Circularized and solubility-enhanced <scp>MSP</scp>s facilitate simple and high-yield production of stable nanodiscs for studies of membrane proteins in solution. FEBS Journal, 2019, 286, 1734-1751.	2.2	36
24	Improving the Sequence Coverage of Integral Membrane Proteins during Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. Analytical Chemistry, 2019, 91, 10970-10978.	3.2	22
25	Substrate-induced conformational dynamics of the dopamine transporter. Nature Communications, 2019, 10, 2714.	5.8	46
26	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Analytical Chemistry, 2019, 91, 6953-6961.	3.2	100
27	Interlaboratory Comparison of Hydrogen-Deuterium Exchange Mass Spectrometry Measurements of the Fab Fragment of NISTmAb. Analytical Chemistry, 2019, 91, 7336-7345.	3.2	44
28	A post-translational modification of human Norovirus capsid protein attenuates glycan binding. Nature Communications, 2019, 10, 1320.	5.8	50
29	Molecular architecture of the Jumonji C family histone demethylase KDM5B. Scientific Reports, 2019, 9, 4019.	1.6	16
30	Conformational dynamics of the human serotonin transporter during substrate and drug binding. Nature Communications, 2019, 10, 1687.	5.8	57
31	Substrate-Induced Conformational Dynamics of the Dopamine Transporter. Biophysical Journal, 2019, 116, 346a.	0.2	0
32	Probing the Dissociation of Protein Complexes by Means of Gas-Phase H/D Exchange Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2019, 30, 45-57.	1.2	16
33	Thiol-ene Microfluidic Chip for Performing Hydrogen/Deuterium Exchange of Proteins at Subsecond Time Scales. Analytical Chemistry, 2019, 91, 1309-1317.	3.2	25
34	Structure and Dynamics of a Promiscuous Xanthan Lyase from Paenibacillus nanensis and the Design of Variants with Increased Stability and Activity. Cell Chemical Biology, 2019, 26, 191-202.e6.	2.5	13
35	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.	1.6	3
36	Glycine Perturbs Local and Global Conformational Flexibility of a Transmembrane Helix. Biochemistry, 2018, 57, 1326-1337.	1.2	41

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37	UV Photodissociation Mass Spectrometry Accurately Localize Sites of Backbone Deuteration in Peptides. <i>Analytical Chemistry</i> , 2018, 90, 1077-1080.	3.2	32
38	Substrate-modulated unwinding of transmembrane helices in the NSS transporter LeuT. <i>Science Advances</i> , 2018, 4, eaar6179.	4.7	47
39	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.	1.9	10
40	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.	5.8	83
41	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.	1.4	8
42	Structural Dynamics and Catalytic Properties of a Multimodular Xanthanase. <i>ACS Catalysis</i> , 2018, 8, 6021-6034.	5.5	12
43	Side-chain moieties from the N-terminal region of A β 2 are Involved in an oligomer-stabilizing network of interactions. <i>PLoS ONE</i> , 2018, 13, e0201761.	1.1	14
44	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.	2.5	31
45	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.	3.2	41
46	Mapping the Interactions of Selective Biochemical Probes of Antibody Conformation by Hydrogen-Deuterium Exchange Mass Spectrometry. <i>ChemBioChem</i> , 2017, 18, 1016-1021.	1.3	7
47	Conformational characterization of nerve growth factor- β 2 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.	1.6	20
48	A Poly-ADP-Ribose Trigger Releases the Auto-Inhibition of a Chromatin Remodeling Oncogene. <i>Molecular Cell</i> , 2017, 68, 860-871.e7.	4.5	70
49	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.	1.2	8
50	Construct design, production, and characterization of Plasmodium falciparum 48/45 R0.6C subunit protein produced in Lactococcus lactis as candidate vaccine. <i>Microbial Cell Factories</i> , 2017, 16, 97.	1.9	37
51	Expression, Purification and Characterization of GMZ2 TM .10C, a Complex Disulphide-Bonded Fusion Protein Vaccine Candidate against the Asexual and Sexual Life-Stages of the Malaria-Causing Plasmodium falciparum Parasite. <i>Pharmaceutical Research</i> , 2017, 34, 1970-1983.	1.7	10
52	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.	3.1	8
53	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.	1.6	35
54	Rapid Conformational Analysis of Protein Drugs in Formulation by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of Pharmaceutical Sciences</i> , 2016, 105, 3269-3277.	1.6	12

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55	Applications of Mass Spectrometry in Drug Development Science. <i>Advances in Delivery Science and Technology</i> , 2016, , 253-289.	0.4	3
56	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.	0.7	10
57	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.	2.6	24
58	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
59	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.	3.2	11
60	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.	1.2	15
61	Investigating the Role of Artemin Glycosylation. <i>Pharmaceutical Research</i> , 2016, 33, 1383-1398.	1.7	10
62	Probing the Binding Interfaces of Protein Complexes Using Gas-Phase H/D Exchange Mass Spectrometry. <i>Structure</i> , 2016, 24, 310-318.	1.6	38
63	Direct coupling of a flow-flow electromembrane extraction probe to LC-MS. <i>Analytica Chimica Acta</i> , 2016, 905, 93-99.	2.6	10
64	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.	3.2	16
65	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.	2.5	82
66	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.	3.1	51
67	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.	2.0	53
68	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
69	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
70	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.	3.2	34
71	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.	1.6	20
72	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.	3.2	19

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73	Substrate- and Cofactor-independent Inhibition of Histone Demethylase KDM4C. <i>ACS Chemical Biology</i> , 2014, 9, 2131-2138.	1.6	25
74	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.	0.7	22
75	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.	3.2	61
76	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
77	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.	3.6	86
78	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.	0.7	28
79	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.	1.2	72
80	False EX1 signatures caused by sample carryover during HX MS analyses. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 19-25.	0.7	94
81	Conformational Transitions in the Membrane Scaffold Protein of Phospholipid Bilayer Nanodiscs. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010876.	2.5	66
82	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
83	Conformational Analysis of Membrane Proteins in Phospholipid Bilayer Nanodiscs by Hydrogen Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 5415-5419.	3.2	133
84	Conformational Dynamics of the Escherichia coli DNA Polymerase Manager Proteins UmuD and UmuD ² . <i>Journal of Molecular Biology</i> , 2010, 398, 40-53.	2.0	20
85	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
86	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.	3.2	89
87	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
88	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
89	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.	3.2	35
90	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

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91	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.	1.6	38
92	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
93	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
94	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.	3.1	30
95	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.	1.6	53
96	Allosteric Activation of Coagulation Factor VIIa Visualized by Hydrogen Exchange. <i>Journal of Biological Chemistry</i> , 2006, 281, 23018-23024.	1.6	52