

John R Engen

List of Publications by Year in descending order

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186
papers

13,229
citations

28242

55
h-index

27389

106
g-index

202
all docs

202
docs citations

202
times ranked

14208
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel mutant-selective EGFR kinase inhibitors against EGFR T790M. <i>Nature</i> , 2009, 462, 1070-1074.	13.7	886
2	Hydrogen exchange mass spectrometry for the analysis of protein dynamics. <i>Mass Spectrometry Reviews</i> , 2006, 25, 158-170.	2.8	767
3	Targeting Bcrâ€Abl by combining allosteric with ATP-binding-site inhibitors. <i>Nature</i> , 2010, 463, 501-506.	13.7	525
4	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
5	Analytical tools for characterizing biopharmaceuticals and the implications for biosimilars. <i>Nature Reviews Drug Discovery</i> , 2012, 11, 527-540.	21.5	441
6	Post-translational Modifications Differentially Affect IgG1 Conformation and Receptor Binding. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1716-1728.	2.5	355
7	The Utility of Hydrogen/Deuterium Exchange Mass Spectrometry in Biopharmaceutical Comparability Studies. <i>Journal of Pharmaceutical Sciences</i> , 2011, 100, 2071-2086.	1.6	324
8	Analysis of Protein Conformation and Dynamics by Hydrogen/Deuterium Exchange MS. <i>Analytical Chemistry</i> , 2009, 81, 7870-7875.	3.2	321
9	High-Speed and High-Resolution UPLC Separation at Zero Degrees Celsius. <i>Analytical Chemistry</i> , 2008, 80, 6815-6820.	3.2	309
10	Therapeutic Targeting of Oncogenic Kâ€Ras by a Covalent Catalytic Site Inhibitor. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 199-204.	7.2	262
11	Catalytic site remodelling of the DOT1L methyltransferase by selective inhibitors. <i>Nature Communications</i> , 2012, 3, 1288.	5.8	247
12	Semi-automated data processing of hydrogen exchange mass spectra using HX-Express. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 1700-1703.	1.2	234
13	Rpn1 provides adjacent receptor sites for substrate binding and deubiquitination by the proteasome. <i>Science</i> , 2016, 351, .	6.0	234
14	Substrate processing by the Cdc48 ATPase complex is initiated by ubiquitin unfolding. <i>Science</i> , 2019, 365, .	6.0	233
15	Force interacts with macromolecular structure in activation of TGF-Î². <i>Nature</i> , 2017, 542, 55-59.	13.7	222
16	Identification and characterization of EX1 kinetics in H/D exchange mass spectrometry by peak width analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 1498-1509.	1.2	209
17	Peer Reviewed: Investigating Protein Structure and Dynamics by Hydrogen Exchange MS. <i>Analytical Chemistry</i> , 2001, 73, 256 A-265 A.	3.2	203
18	Design of stapled antimicrobial peptides that are stable, nontoxic and kill antibiotic-resistant bacteria in mice. <i>Nature Biotechnology</i> , 2019, 37, 1186-1197.	9.4	187

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19	Hydrogen/deuterium exchange mass spectrometry for probing higher order structure of protein therapeutics: methodology and applications. <i>Drug Discovery Today</i> , 2014, 19, 95-102.	3.2	176
20	Characterization of IgG1 Conformation and Conformational Dynamics by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 2644-2651.	3.2	174
21	Hydrogen exchange mass spectrometry: what is it and what can it tell us?. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 397, 967-972.	1.9	166
22	Analysis of Overlapped and Noisy Hydrogen/Deuterium Exchange Mass Spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1906-1912.	1.2	150
23	Structure-Guided Development of a Potent and Selective Non-covalent Active-Site Inhibitor of USP7. <i>Cell Chemical Biology</i> , 2017, 24, 1490-1500.e11.	2.5	149
24	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
25	Chemically Induced Degradation of the Oncogenic Transcription Factor BCL6. <i>Cell Reports</i> , 2017, 20, 2860-2875.	2.9	133
26	Applications of Hydrogen/Deuterium Exchange MS from 2012 to 2014. <i>Analytical Chemistry</i> , 2015, 87, 99-118.	3.2	131
27	Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755.	7.7	127
28	GroEL/ES Chaperonin Modulates the Mechanism and Accelerates the Rate of TIM-Barrel Domain Folding. <i>Cell</i> , 2014, 157, 922-934.	13.5	116
29	Inhibition of Pro-Apoptotic BAX by a Noncanonical Interaction Mechanism. <i>Molecular Cell</i> , 2015, 57, 873-886.	4.5	116
30	Src Family Kinases Phosphorylate the Bcr-Abl SH3-SH2 Region and Modulate Bcr-Abl Transforming Activity. <i>Journal of Biological Chemistry</i> , 2006, 281, 30907-30916.	1.6	112
31	Analytical Aspects of Hydrogen Exchange Mass Spectrometry. <i>Annual Review of Analytical Chemistry</i> , 2015, 8, 127-148.	2.8	112
32	Assessing the reproducibility and specificity of pepsin and other aspartic proteases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1222-1229.	1.1	111
33	Advances in Hydrogen/Deuterium Exchange Mass Spectrometry and the Pursuit of Challenging Biological Systems. <i>Chemical Reviews</i> , 2022, 122, 7562-7623.	23.0	109
34	Hydrogen Exchange Mass Spectrometry: Are We Out of the Quicksand?. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1003-1010.	1.2	102
35	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
36	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

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37	Structure and Dynamic Regulation of Abl Kinases*. Journal of Biological Chemistry, 2013, 288, 5443-5450.	1.6	89
38	Identification and Localization of Slow, Natural, Cooperative Unfolding in the Hematopoietic Cell Kinase SH3 Domain by Amide Hydrogen Exchange and Mass Spectrometry. Biochemistry, 1997, 36, 14384-14391.	1.2	88
39	Antibody mechanics on a membrane-bound HIV segment essential for GP41-targeted viral neutralization. Nature Structural and Molecular Biology, 2011, 18, 1235-1243.	3.6	86
40	Investigating Monoclonal Antibody Aggregation Using a Combination of H/DX-MS and Other Biophysical Measurements. Journal of Pharmaceutical Sciences, 2013, 102, 4315-4329.	1.6	84
41	Structure of the Cdc48 ATPase with its ubiquitin-binding cofactor Ufd1. Nature Structural and Molecular Biology, 2018, 25, 616-622.	3.6	82
42	Phosphorylation and structure-based functional studies reveal a positive and a negative role for the activation loop of the c-Abl tyrosine kinase. Oncogene, 2001, 20, 8075-8084.	2.6	80
43	Ultra performance liquid chromatography (UPLC) further improves hydrogen/deuterium exchange mass spectrometry. Journal of the American Society for Mass Spectrometry, 2006, 17, 163-167.	1.2	76
44	Hydrogen Exchange Shows Peptide Binding Stabilizes Motions in Hck SH2. Biochemistry, 1999, 38, 8926-8935.	1.2	72
45	ETD in a Traveling Wave Ion Guide at Tuned Z-Spray Ion Source Conditions Allows for Site-Specific Hydrogen/Deuterium Exchange Measurements. Journal of the American Society for Mass Spectrometry, 2011, 22, 1784-93.	1.2	72
46	Selective USP7 inhibition elicits cancer cell killing through a p53-dependent mechanism. Scientific Reports, 2020, 10, 5324.	1.6	69
47	Conformational disturbance in Abl kinase upon mutation and deregulation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1386-1391.	3.3	68
48	Inhibition of Flaviviruses by Targeting a Conserved Pocket on the Viral Envelope Protein. Cell Chemical Biology, 2018, 25, 1006-1016.e8.	2.5	68
49	Analysis of protein complexes with hydrogen exchange and mass spectrometry. Analyst, The, 2003, 128, 623.	1.7	66
50	Conformational Transitions in the Membrane Scaffold Protein of Phospholipid Bilayer Nanodiscs. Molecular and Cellular Proteomics, 2011, 10, M111.010876.	2.5	66
51	Partial Unfolding of Diverse SH3 Domains on a Wide Timescale. Journal of Molecular Biology, 2006, 357, 1592-1604.	2.0	63
52	Ion mobility adds an additional dimension to mass spectrometric analysis of solution-phase hydrogen/deuterium exchange. Rapid Communications in Mass Spectrometry, 2008, 22, 2898-2904.	0.7	63
53	Allosteric Interactions between the Myristate- and ATP-Site of the Abl Kinase. PLoS ONE, 2011, 6, e15929.	1.1	63
54	Developments in Hydrogen/Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2021, 93, 567-582.	3.2	63

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55	Pepsin Immobilized on High-Strength Hybrid Particles for Continuous Flow Online Digestion at 10 ⁶ psi. <i>Analytical Chemistry</i> , 2012, 84, 7256-7262.	3.2	60
56	Conformational Locking upon Cooperative Assembly of Notch Transcription Complexes. <i>Structure</i> , 2012, 20, 340-349.	1.6	60
57	Evidence for Increased Exposure of the Notch1 Metalloprotease Cleavage Site upon Conversion to an Activated Conformation. <i>Structure</i> , 2011, 19, 546-554.	1.6	59
58	Considerations in the Analysis of Hydrogen Exchange Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2013, 1007, 263-288.	0.4	58
59	Conformational insight into multi-protein signaling assemblies by hydrogen-deuterium exchange mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2016, 41, 187-193.	2.6	57
60	Using Hydrogen/Deuterium Exchange Mass Spectrometry to Study Conformational Changes in Granulocyte Colony Stimulating Factor upon PEGylation. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 498-504.	1.2	53
61	Investigating the Higher Order Structure of Proteins: Hydrogen Exchange, Proteolytic Fragmentation, and Mass Spectrometry. , 2000, 146, 95-112.		52
62	Investigating Solution-Phase Protein Structure and Dynamics by Hydrogen Exchange Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2009, 58, Unit 17.6.1-17.	2.8	51
63	The Natural Product Cucurbitacin E Inhibits Depolymerization of Actin Filaments. <i>ACS Chemical Biology</i> , 2012, 7, 1502-1508.	1.6	51
64	Conformational Differences Between Arrestin2 and Pre-activated Mutants as Revealed by Hydrogen Exchange Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2005, 351, 865-878.	2.0	49
65	A Conformational Investigation of Propeptide Binding to the Integral Membrane Protein \hat{I}^3 -Glutamyl Carboxylase Using Nanodisc Hydrogen Exchange Mass Spectrometry. <i>Biochemistry</i> , 2014, 53, 1511-1520.	1.2	47
66	Structural Stability and Local Dynamics in Disease-Causing Mutants of Human Apolipoprotein A-I: What Makes the Protein Amyloidogenic?. <i>Journal of Molecular Biology</i> , 2016, 428, 449-462.	2.0	47
67	Mechanism of Enzyme Repair by the AAA+ Chaperone Rubisco Activase. <i>Molecular Cell</i> , 2017, 67, 744-756.e6.	4.5	47
68	Allosteric inhibition of antiapoptotic MCL-1. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 600-607.	3.6	46
69	Dynamic Regulation of Long-Chain Fatty Acid Oxidation by a Noncanonical Interaction between the MCL-1 BH3 Helix and VLCAD. <i>Molecular Cell</i> , 2018, 69, 729-743.e7.	4.5	45
70	Achieving a Graded Immune Response: BTK Adopts a Range of Active/Inactive Conformations Dictated by Multiple Interdomain Contacts. <i>Structure</i> , 2017, 25, 1481-1494.e4.	1.6	44
71	Sulfonyl Fluoride Inhibitors of Fatty Acid Amide Hydrolase. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 10074-10089.	2.9	43
72	Extensive Deuterium Back-Exchange in Certain Immobilized Pepsin Columns Used for H/D Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 1719-1723.	3.2	42

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73	An examination of dynamics crosstalk between SH2 and SH3 domains by hydrogen/deuterium exchange and mass spectrometry. <i>Protein Science</i> , 2006, 15, 65-73.	3.1	42
74	Purification and characterization of pepsinsâ€fA1 and A2 from the Antarctic rock cod <i>Trematomus bernacchii</i>. <i>FEBS Journal</i> , 2007, 274, 6152-6166.	2.2	42
75	Comparison of SH3 and SH2 domain dynamics when expressed alone or in an SH(3 + 2) construct: the role of protein dynamics in functional regulation. <i>Journal of Molecular Biology</i> , 1999, 287, 645-656.	2.0	41
76	Fetal alcohol exposure alters neurosteroid levels in the developing rat brain. <i>Journal of Neurochemistry</i> , 2004, 90, 1530-1539.	2.1	41
77	Activation of the Src Family Kinase Hck without SH3-Linker Release. <i>Journal of Biological Chemistry</i> , 2005, 280, 40832-40837.	1.6	41
78	<i>Escherichia coli</i> Processivity Clamp \hat{p}^2 from DNA Polymerase III Is Dynamic in Solution. <i>Biochemistry</i> , 2011, 50, 5958-5968.	1.2	40
79	Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. <i>PLoS Computational Biology</i> , 2016, 12, e1004826.	1.5	40
80	Allosteric sensitization of proapoptotic BAX. <i>Nature Chemical Biology</i> , 2017, 13, 961-967.	3.9	40
81	Characterization of IgG1 Conformation and Conformational Dynamics by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5966-5966.	3.2	39
82	Translocation of polyubiquitinated protein substrates by the hexameric Cdc48 ATPase. <i>Molecular Cell</i> , 2022, 82, 570-584.e8.	4.5	39
83	Tyrosine Phosphorylation in the SH3 Domain Disrupts Negative Regulatory Interactions within the c-Abl Kinase Core. <i>Journal of Molecular Biology</i> , 2008, 383, 414-423.	2.0	38
84	Membrane phospholipid bilayer as a determinant of monoacylglycerol lipase kinetic profile and conformational repertoire. <i>Protein Science</i> , 2013, 22, 774-787.	3.1	37
85	Fusion surface structure, function, and dynamics of gamete fusogen HAP2. <i>ELife</i> , 2018, 7, .	2.8	37
86	Partial cooperative unfolding in proteins as observed by hydrogen exchange mass spectrometry. <i>International Reviews in Physical Chemistry</i> , 2013, 32, 96-127.	0.9	36
87	Conformational Analysis of Recombinant Monoclonal Antibodies with Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 988, 269-289.	0.4	35
88	Differential Sensitivity of Src-Family Kinases to Activation by SH3 Domain Displacement. <i>PLoS ONE</i> , 2014, 9, e105629.	1.1	35
89	Electron Transfer Control in Soluble Methane Monooxygenase. <i>Journal of the American Chemical Society</i> , 2014, 136, 9754-9762.	6.6	35
90	Allosteric Loss-of-function Mutations in HIV-1 Nef from a Long-term Non-progressor. <i>Journal of Molecular Biology</i> , 2007, 374, 121-129.	2.0	34

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91	The Abl SH2-kinase linker naturally adopts a conformation competent for SH3 domain binding. <i>Protein Science</i> , 2007, 16, 572-581.	3.1	34
92	Tuning a High Transmission Ion Guide to Prevent Gas-Phase Proton Exchange During H/D Exchange MS Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 662-668.	1.2	34
93	Structure, function, and inhibitor targeting of HIV-1 Nef-effector kinase complexes. <i>Journal of Biological Chemistry</i> , 2020, 295, 15158-15171.	1.6	34
94	Hydrogen-Deuterium Exchange Mass Spectrometry to Study Protein Complexes. <i>Methods in Molecular Biology</i> , 2018, 1764, 153-171.	0.4	33
95	Homogeneous Oligomers of Pro-apoptotic BAX Reveal Structural Determinants of Mitochondrial Membrane Permeabilization. <i>Molecular Cell</i> , 2020, 79, 68-83.e7.	4.5	32
96	Complementarity of Hydrogen/Deuterium Exchange Mass Spectrometry and Cryo-Electron Microscopy. <i>Trends in Biochemical Sciences</i> , 2020, 45, 906-918.	3.7	31
97	Conformational Analysis of Processivity Clamps in Solution Demonstrates that Tertiary Structure Does Not Correlate with Protein Dynamics. <i>Structure</i> , 2014, 22, 572-581.	1.6	30
98	Utilizing Microchip Capillary Electrophoresis Electrospray Ionization for Hydrogen Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 6280-6287.	3.2	30
99	Structural Dynamics in Ras and Related Proteins upon Nucleotide Switching. <i>Journal of Molecular Biology</i> , 2016, 428, 4723-4735.	2.0	30
100	Structural analysis of lecithin:cholesterol acyltransferase bound to high density lipoprotein particles. <i>Communications Biology</i> , 2020, 3, 28.	2.0	30
101	Conformational Transition of Membrane-Associated Terminally Acylated HIV-1 Nef. <i>Structure</i> , 2013, 21, 1822-1833.	1.6	29
102	Enhanced SH3/Linker Interaction Overcomes Abl Kinase Activation by Gatekeeper and Myristic Acid Binding Pocket Mutations and Increases Sensitivity to Small Molecule Inhibitors*. <i>Journal of Biological Chemistry</i> , 2013, 288, 6116-6129.	1.6	29
103	Hydrogen/deuterium exchange mass spectrometry applied to IL-23 interaction characteristics: potential impact for therapeutics. <i>Expert Review of Proteomics</i> , 2015, 12, 159-169.	1.3	28
104	General structural features that regulate integrin affinity revealed by atypical β^28 . <i>Nature Communications</i> , 2019, 10, 5481.	5.8	28
105	Identification of a Covalent Molecular Inhibitor of Anti-apoptotic BFL-1 by Disulfide Tethering. <i>Cell Chemical Biology</i> , 2020, 27, 647-656.e6.	2.5	28
106	Activation Loop Dynamics Determine the Different Catalytic Efficiencies of B Cell- and T Cell-Specific Tec Kinases. <i>Science Signaling</i> , 2013, 6, ra76.	1.6	27
107	KRAS G12C Drug Development: Discrimination between Switch II Pocket Configurations Using Hydrogen/Deuterium-Exchange Mass Spectrometry. <i>Structure</i> , 2017, 25, 1442-1448.e3.	1.6	27
108	Structures of PGAM5 Provide Insight into Active Site Plasticity and Multimeric Assembly. <i>Structure</i> , 2017, 25, 1089-1099.e3.	1.6	27

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109	Tolloid cleavage activates latent GDF8 by priming the pro- α complex for dissociation. <i>EMBO Journal</i> , 2018, 37, 384-397.	3.5	27
110	Insights into Notch3 Activation and Inhibition Mediated by Antibodies Directed against Its Negative Regulatory Region. <i>Journal of Molecular Biology</i> , 2013, 425, 3192-3204.	2.0	26
111	Using Stable-Isotope-Labeled Proteins for Hydrogen Exchange Studies in Complex Mixtures. <i>Analytical Chemistry</i> , 2002, 74, 1680-1686.	3.2	25
112	On the Solution Conformation and Dynamics of the HIV-1 Viral Infectivity Factor. <i>Journal of Molecular Biology</i> , 2011, 410, 1008-1022.	2.0	25
113	Cumulative deamidations of the major lens protein α -crystallin increase its aggregation during unfolding and oxidation. <i>Protein Science</i> , 2020, 29, 1945-1963.	3.1	25
114	Differential impact of BTK active site inhibitors on the conformational state of full-length BTK. <i>ELife</i> , 2020, 9, .	2.8	25
115	Regulation of c-Fes Tyrosine Kinase Activity by Coiled-Coil and SH2 Domains: α Analysis with <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2003, 42, 3567-3574.	1.2	24
116	Subzero Celsius separations in three-zone temperature controlled hydrogen deuterium exchange mass spectrometry. <i>Journal of Chromatography A</i> , 2017, 1523, 275-282.	1.8	24
117	Structural basis of the atypical activation mechanism of KRASV14I. <i>Journal of Biological Chemistry</i> , 2019, 294, 13964-13972.	1.6	24
118	Conformational Features of the Full-Length HIV and SIV Nef Proteins Determined by Mass Spectrometry α . <i>Biochemistry</i> , 2006, 45, 7733-7739.	1.2	23
119	Neutron Reflectometry Study of the Conformation of HIV Nef Bound to α Lipid Membranes. <i>Biophysical Journal</i> , 2010, 99, 1940-1948.	0.2	22
120	The Src family kinase Fgr is a transforming oncoprotein that functions independently of SH3-SH2 domain regulation. <i>Science Signaling</i> , 2018, 11, .	1.6	22
121	Functional Characterization and Conformational Analysis of the Herpesvirus saimiri Tip-C484 Protein. <i>Journal of Molecular Biology</i> , 2007, 366, 1282-1293.	2.0	21
122	Molecular Insight into the Conformational Dynamics of the Elongin BC Complex and Its Interaction with HIV-1 Vif. <i>Journal of Molecular Biology</i> , 2010, 402, 892-904.	2.0	21
123	Hydrogen Exchange-Mass Spectrometry Measures Stapled Peptide Conformational Dynamics and Predicts Pharmacokinetic Properties. <i>Analytical Chemistry</i> , 2013, 85, 11185-11188.	3.2	21
124	Mitochondrial ClpX activates an essential biosynthetic enzyme through partial unfolding. <i>ELife</i> , 2020, 9, .	2.8	21
125	Determining the Site of Spin Trapping of the Equine Myoglobin Radical by Combined Use of EPR, Electrophoretic Purification, and Mass Spectrometry. <i>Chemical Research in Toxicology</i> , 2002, 15, 1589-1594.	1.7	20
126	Abl N-Terminal Cap Stabilization of SH3 Domain Dynamics. <i>Biochemistry</i> , 2008, 47, 5795-5803.	1.2	20

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127	Conformational Dynamics of the Escherichia coli DNA Polymerase Manager Proteins UmuD and UmuD ² . Journal of Molecular Biology, 2010, 398, 40-53.	2.0	20
128	Effects of HIV-1 Nef on Human N-Myristoyltransferase 1. Biochemistry, 2011, 50, 3394-3403.	1.2	20
129	Characterization of Aggregation Propensity of a Human Fc-Fusion Protein Therapeutic by Hydrogen/Deuterium Exchange Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2017, 28, 795-802.	1.2	20
130	Intramolecular Binding of a Proximal PP _{II} Helix to an SH3 Domain in the Fusion Protein SH3 _{Hck} : PP _{II} _{hGAP} . Cell Biochemistry and Biophysics, 2001, 35, 115-126.	0.9	19
131	Hydrogen Exchange Mass Spectrometry of Proteins at Langmuir Monolayers. Analytical Chemistry, 2015, 87, 7022-7029.	3.2	19
132	Lipid-targeting pleckstrin homology domain turns its autoinhibitory face toward the TEC kinases. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21539-21544.	3.3	19
133	Protein Interactions Probed With Mass Spectrometry. , 2006, 316, 179-197.		18
134	HIV-1 Nef interaction influences the ATP-binding site of the Src-family kinase, Hck. BMC Chemical Biology, 2012, 12, 1.	1.6	18
135	Remodeling of HIV-1 Nef Structure by Src-Family Kinase Binding. Journal of Molecular Biology, 2018, 430, 310-321.	2.0	18
136	Active-Site Inhibitors Modulate the Dynamic Properties of Human Monoacylglycerol Lipase: A Hydrogen Exchange Mass Spectrometry Study. Biochemistry, 2013, 52, 5016-5026.	1.2	17
137	The Influence of Adnectin Binding on the Extracellular Domain of Epidermal Growth Factor Receptor. Journal of the American Society for Mass Spectrometry, 2014, 25, 2093-2102.	1.2	17
138	Dynamic and structural differences between heme oxygenase-1 and -2 are due to differences in their C-terminal regions. Journal of Biological Chemistry, 2019, 294, 8259-8272.	1.6	17
139	l-Canavanine Is a Time-Controlled Mechanism-Based Inhibitor of Pseudomonas aeruginosa Arginine Deiminase. Journal of the American Chemical Society, 2005, 127, 16412-16413.	6.6	16
140	Aspartic proteinases in Antarctic fish. Marine Genomics, 2009, 2, 1-10.	0.4	16
141	Replication in bioanalytical studies with HDX MS: aim as high as possible. Bioanalysis, 2015, 7, 1065-1067.	0.6	16
142	Structural Basis for Lipid Binding and Function by an Evolutionarily Conserved Protein, Serum Amyloid A. Journal of Molecular Biology, 2020, 432, 1978-1995.	2.0	16
143	The heme-regulatory motifs of heme oxygenase-2 contribute to the transfer of heme to the catalytic site for degradation. Journal of Biological Chemistry, 2020, 295, 5177-5191.	1.6	16
144	Steric gate residues of Y-family DNA polymerases DinB and pol kappa are crucial for dNTP-induced conformational change. DNA Repair, 2015, 29, 65-73.	1.3	15

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145	Site-Dependent Cysteine Lipidation Potentiates the Activation of Proapoptotic BAX. <i>Cell Reports</i> , 2020, 30, 3229-3239.e6.	2.9	15
146	Allosteric control of Ubp6 and the proteasome via a bidirectional switch. <i>Nature Communications</i> , 2022, 13, 838.	5.8	15
147	Altered dynamics in Lck SH3 upon binding to the LBD1 domain of Herpesvirus saimiri Tip. <i>Protein Science</i> , 2006, 15, 2402-2410.	3.1	14
148	Noncanonical Role of the PDZ4 Domain of the Adaptor Protein PDZK1 in the Regulation of the Hepatic High Density Lipoprotein Receptor Scavenger Receptor Class B, Type I (SR-BI). <i>Journal of Biological Chemistry</i> , 2013, 288, 19845-19860.	1.6	14
149	Membrane-Associated Conformation of HIV-1 Nef Investigated with Hydrogen Exchange Mass Spectrometry at a Langmuir Monolayer. <i>Analytical Chemistry</i> , 2015, 87, 7030-7035.	3.2	14
150	Simple and Fast Maximally Deuterated Control (maxD) Preparation for Hydrogen-Deuterium Exchange Mass Spectrometry Experiments. <i>Analytical Chemistry</i> , 2022, 94, 10142-10150.	3.2	14
151	Engineering Aglycosylated IgG Variants with Wild-Type or Improved Binding Affinity to Human Fc Gamma RIIA and Fc Gamma RIIBs. <i>Journal of Molecular Biology</i> , 2017, 429, 2528-2541.	2.0	13
152	The conformational stability of pro-apoptotic BAX is dictated by discrete residues of the protein core. <i>Nature Communications</i> , 2021, 12, 4932.	5.8	13
153	Subtle Dynamic Changes Accompany Hck Activation by HIV-1 Nef and are Reversed by an Antiretroviral Kinase Inhibitor. <i>Biochemistry</i> , 2015, 54, 6382-6391.	1.2	12
154	Noncognate DNA damage prevents the formation of the active conformation of the family DNA polymerases DinB and DNA polymerase β . <i>FEBS Journal</i> , 2015, 282, 2646-2660.	2.2	12
155	Structure of the helicase core of Werner helicase, a key target in microsatellite instability cancers. <i>Life Science Alliance</i> , 2021, 4, e202000795.	1.3	12
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