

John R Engen

List of Publications by Year in descending order

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186
papers

13,229
citations

28274

55
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27406

106
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202
all docs

202
docs citations

202
times ranked

14208
citing authors

#	ARTICLE	IF	CITATIONS
1	Advances in Hydrogen/Deuterium Exchange Mass Spectrometry and the Pursuit of Challenging Biological Systems. <i>Chemical Reviews</i> , 2022, 122, 7562-7623.	47.7	109
2	The Conformational State of the BTK Substrate PLC β 3 Contributes to Ibrutinib Resistance. <i>Journal of Molecular Biology</i> , 2022, 434, 167422.	4.2	4
3	Protection of the Prodomain α 1-Helix Correlates with Latency in the Transforming Growth Factor- β 2 Family. <i>Journal of Molecular Biology</i> , 2022, 434, 167439.	4.2	2
4	Translocation of polyubiquitinated protein substrates by the hexameric Cdc48 ATPase. <i>Molecular Cell</i> , 2022, 82, 570-584.e8.	9.7	39
5	Allosteric control of Ubp6 and the proteasome via a bidirectional switch. <i>Nature Communications</i> , 2022, 13, 838.	12.8	15
6	Von Willebrand factor A1 domain stability and affinity for GPIb α are differentially regulated by its O-glycosylated N- and C-linker. <i>ELife</i> , 2022, 11, .	6.0	3
7	Structural basis for defective membrane targeting of mutant enzyme in human VLCAD deficiency. <i>Nature Communications</i> , 2022, 13, .	12.8	5
8	Simple and Fast Maximally Deuterated Control (maxD) Preparation for Hydrogen-Deuterium Exchange Mass Spectrometry Experiments. <i>Analytical Chemistry</i> , 2022, 94, 10142-10150.	6.5	14
9	Developments in Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2021, 93, 567-582.	6.5	63
10	The conformational stability of pro-apoptotic BAX is dictated by discrete residues of the protein core. <i>Nature Communications</i> , 2021, 12, 4932.	12.8	13
11	A Conservative Point Mutation in a Dynamic Antigen-binding Loop of Human Immunoglobulin λ 6 Light Chain Promotes Pathologic Amyloid Formation. <i>Journal of Molecular Biology</i> , 2021, 433, 167310.	4.2	9
12	Structure of the helicase core of Werner helicase, a key target in microsatellite instability cancers. <i>Life Science Alliance</i> , 2021, 4, e202000795.	2.8	12
13	A redox switch regulates the structure and function of anti-apoptotic BFL-1. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 781-789.	8.2	4
14	Combination of HDX-MS and in silico modeling to study enzymatic reactivity and stereo-selectivity at different solvent conditions. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2020, 182, 113141.	2.8	5
15	Cumulative deamidations of the major lens protein α -crystallin increase its aggregation during unfolding and oxidation. <i>Protein Science</i> , 2020, 29, 1945-1963.	7.6	25
16	Identification of a Structural Determinant for Selective Targeting of HDMX. <i>Structure</i> , 2020, 28, 847-857.e5.	3.3	2
17	Structure, function, and inhibitor targeting of HIV-1 Nef-effector kinase complexes. <i>Journal of Biological Chemistry</i> , 2020, 295, 15158-15171.	3.4	34
18	Targeting a helix-in-groove interaction between E1 and E2 blocks ubiquitin transfer. <i>Nature Chemical Biology</i> , 2020, 16, 1218-1226.	8.0	5

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19	Hydrocarbon-Stitched Peptide Agonists of Glucagon-Like Peptide-1 Receptor. <i>ACS Chemical Biology</i> , 2020, 15, 1340-1348.	3.4	11
20	Identification of a Covalent Molecular Inhibitor of Anti-apoptotic BFL-1 by Disulfide Tethering. <i>Cell Chemical Biology</i> , 2020, 27, 647-656.e6.	5.2	28
21	Complementarity of Hydrogen/Deuterium Exchange Mass Spectrometry and Cryo-Electron Microscopy. <i>Trends in Biochemical Sciences</i> , 2020, 45, 906-918.	7.5	31
22	Homogeneous Oligomers of Pro-apoptotic BAX Reveal Structural Determinants of Mitochondrial Membrane Permeabilization. <i>Molecular Cell</i> , 2020, 79, 68-83.e7.	9.7	32
23	Site-Dependent Cysteine Lipidation Potentiates the Activation of Proapoptotic BAX. <i>Cell Reports</i> , 2020, 30, 3229-3239.e6.	6.4	15
24	Selective USP7 inhibition elicits cancer cell killing through a p53-dependent mechanism. <i>Scientific Reports</i> , 2020, 10, 5324.	3.3	69
25	Structural Basis for Lipid Binding and Function by an Evolutionarily Conserved Protein, Serum Amyloid A. <i>Journal of Molecular Biology</i> , 2020, 432, 1978-1995.	4.2	16
26	Structural analysis of lecithin:cholesterol acyltransferase bound to high density lipoprotein particles. <i>Communications Biology</i> , 2020, 3, 28.	4.4	30
27	The heme-regulatory motifs of heme oxygenase-2 contribute to the transfer of heme to the catalytic site for degradation. <i>Journal of Biological Chemistry</i> , 2020, 295, 5177-5191.	3.4	16
28	Considerations in the Analysis of Hydrogen Exchange Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2020, 2051, 407-435.	0.9	6
29	Mitochondrial ClpX activates an essential biosynthetic enzyme through partial unfolding. <i>ELife</i> , 2020, 9, .	6.0	21
30	Differential impact of BTK active site inhibitors on the conformational state of full-length BTK. <i>ELife</i> , 2020, 9, .	6.0	25
31	Design of stapled antimicrobial peptides that are stable, nontoxic and kill antibiotic-resistant bacteria in mice. <i>Nature Biotechnology</i> , 2019, 37, 1186-1197.	17.5	187
32	Structural basis of the atypical activation mechanism of KRASV14I. <i>Journal of Biological Chemistry</i> , 2019, 294, 13964-13972.	3.4	24
33	Substrate processing by the Cdc48 ATPase complex is initiated by ubiquitin unfolding. <i>Science</i> , 2019, 365, .	12.6	233
34	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
35	Hydrogen deuterium exchange mass spectrometry applied to chaperones and chaperone-assisted protein folding. <i>Expert Review of Proteomics</i> , 2019, 16, 613-625.	3.0	6
36	Dynamic and structural differences between heme oxygenase-1 and -2 are due to differences in their C-terminal regions. <i>Journal of Biological Chemistry</i> , 2019, 294, 8259-8272.	3.4	17

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37	Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755.	9.4	127
38	Remodeling of the Binding Site of Nucleoside Diphosphate Kinase Revealed by X-ray Structure and H/D Exchange. <i>Biochemistry</i> , 2019, 58, 1440-1449.	2.5	1
39	Lipid-targeting pleckstrin homology domain turns its autoinhibitory face toward the TEC kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21539-21544.	7.1	19
40	General structural features that regulate integrin affinity revealed by atypical Î±VÎ²8. <i>Nature Communications</i> , 2019, 10, 5481.	12.8	28
41	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.	9.7	45
42	Tolloid cleavage activates latent GDF8 by priming the proÎ± complex for dissociation. <i>EMBO Journal</i> , 2018, 37, 384-397.	7.8	27
43	Remodeling of HIV-1 Nef Structure by Src-Family Kinase Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 310-321.	4.2	18
44	Hydrogen-Deuterium Exchange Mass Spectrometry to Study Protein Complexes. <i>Methods in Molecular Biology</i> , 2018, 1764, 153-171.	0.9	33
45	The Src family kinase Fgr is a transforming oncoprotein that functions independently of SH3-SH2 domain regulation. <i>Science Signaling</i> , 2018, 11, .	3.6	22
46	Structure of the Cdc48 ATPase with its ubiquitin-binding cofactor Ufd1Î±Npl4. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 616-622.	8.2	82
47	Effects of Disease-Causing Mutations on the Conformation of Human Apolipoprotein A-I in Model Lipoproteins. <i>Biochemistry</i> , 2018, 57, 4583-4596.	2.5	7
48	Inhibition of Flaviviruses by Targeting a Conserved Pocket on the Viral Envelope Protein. <i>Cell Chemical Biology</i> , 2018, 25, 1006-1016.e8.	5.2	68
49	Fusion surface structure, function, and dynamics of gamete fusogen HAP2. <i>ELife</i> , 2018, 7, .	6.0	37
50	Force interacts with macromolecular structure in activation of TGF-Î². <i>Nature</i> , 2017, 542, 55-59.	27.8	222
51	Subzero Celsius separations in three-zone temperature controlled hydrogen deuterium exchange mass spectrometry. <i>Journal of Chromatography A</i> , 2017, 1523, 275-282.	3.7	24
52	Structural stability and local dynamics in disease-causing mutants of human apolipoprotein a-I: what makes the protein amyloidogenic?. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2017, 24, 11-12.	3.0	2
53	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.	5.2	149
54	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.	3.3	44

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55	Chemically Induced Degradation of the Oncogenic Transcription Factor BCL6. <i>Cell Reports</i> , 2017, 20, 2860-2875.	6.4	133
56	Mechanism of Enzyme Repair by the AAA+ Chaperone Rubisco Activase. <i>Molecular Cell</i> , 2017, 67, 744-756.e6.	9.7	47
57	KRAS G12C Drug Development: Discrimination between Switch II Pocket Configurations Using Hydrogen/Deuterium-Exchange Mass Spectrometry. <i>Structure</i> , 2017, 25, 1442-1448.e3.	3.3	27
58	Structures of PGAM5 Provide Insight into Active Site Plasticity and Multimeric Assembly. <i>Structure</i> , 2017, 25, 1089-1099.e3.	3.3	27
59	Engineering Aglycosylated IgG Variants with Wild-Type or Improved Binding Affinity to Human Fc Gamma RIIA and Fc Gamma RIIIAs. <i>Journal of Molecular Biology</i> , 2017, 429, 2528-2541.	4.2	13
60	Allosteric sensitization of proapoptotic BAX. <i>Nature Chemical Biology</i> , 2017, 13, 961-967.	8.0	40
61	Characterization of Aggregation Propensity of a Human Fc-Fusion Protein Therapeutic by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 795-802.	2.8	20
62	Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. <i>PLoS Computational Biology</i> , 2016, 12, e1004826.	3.2	40
63	Dynamics of the <sc>T</sc> family tyrosine kinase <sc>SH</sc>3 domains. <i>Protein Science</i> , 2016, 25, 852-864.	7.6	8
64	Hydrogen Exchange Mass Spectrometry of Related Proteins with Divergent Sequences: A Comparative Study of HIV-1 Nef Allelic Variants. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1048-1061.	2.8	11
65	Allosteric inhibition of antiapoptotic MCL-1. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 600-607.	8.2	46
66	Conformational insight into multi-protein signaling assemblies by hydrogenâ€“deuterium exchange mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2016, 41, 187-193.	5.7	57
67	Structural Dynamics in Ras and Related Proteins upon Nucleotide Switching. <i>Journal of Molecular Biology</i> , 2016, 428, 4723-4735.	4.2	30
68	c-Abl Tyrosine Kinase Adopts Multiple Active Conformational States in Solution. <i>Biochemistry</i> , 2016, 55, 3251-3260.	2.5	8
69	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.	2.8	34
70	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.	4.2	47
71	Rpn1 provides adjacent receptor sites for substrate binding and deubiquitination by the proteasome. <i>Science</i> , 2016, 351, .	12.6	234
72	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.	2.5	12

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73	Noncognate γ -family DNA damage prevents the formation of the active conformation of the γ -family DNA polymerases DinB and DNA polymerase β . FEBS Journal, 2015, 282, 2646-2660.	4.7	12
74	Utilizing Microchip Capillary Electrophoresis Electrospray Ionization for Hydrogen Exchange Mass Spectrometry. Analytical Chemistry, 2015, 87, 6280-6287.	6.5	30
75	Tag and Capture Flow Hydrogen Exchange Mass Spectrometry with a Fluorous-Immobilized Probe. Analytical Chemistry, 2015, 87, 6349-6356.	6.5	1
76	Replication in bioanalytical studies with HDX MS: aim as high as possible. Bioanalysis, 2015, 7, 1065-1067.	1.5	16
77	Inhibition of Pro-Apoptotic BAX by a Noncanonical Interaction Mechanism. Molecular Cell, 2015, 57, 873-886.	9.7	116
78	Analytical Aspects of Hydrogen Exchange Mass Spectrometry. Annual Review of Analytical Chemistry, 2015, 8, 127-148.	5.4	112
79	Membrane-Associated Conformation of HIV-1 Nef Investigated with Hydrogen Exchange Mass Spectrometry at a Langmuir Monolayer. Analytical Chemistry, 2015, 87, 7030-7035.	6.5	14
80	Hydrogen/deuterium exchange mass spectrometry applied to IL-23 interaction characteristics: potential impact for therapeutics. Expert Review of Proteomics, 2015, 12, 159-169.	3.0	28
81	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.	2.8	15
82	Hydrogen Exchange Mass Spectrometry of Proteins at Langmuir Monolayers. Analytical Chemistry, 2015, 87, 7022-7029.	6.5	19
83	Applications of Hydrogen/Deuterium Exchange MS from 2012 to 2014. Analytical Chemistry, 2015, 87, 99-118.	6.5	131
84	Differential Sensitivity of Src-Family Kinases to Activation by SH3 Domain Displacement. PLoS ONE, 2014, 9, e105629.	2.5	35
85	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.	2.8	17
86	Conformational Analysis of Processivity Clamps in Solution Demonstrates that Tertiary Structure Does Not Correlate with Protein Dynamics. Structure, 2014, 22, 572-581.	3.3	30
87	GroEL/ES Chaperonin Modulates the Mechanism and Accelerates the Rate of TIM-Barrel Domain Folding. Cell, 2014, 157, 922-934.	28.9	116
88	Hydrogen/deuterium exchange mass spectrometry for probing higher order structure of protein therapeutics: methodology and applications. Drug Discovery Today, 2014, 19, 95-102.	6.4	176
89	Therapeutic Targeting of Oncogenic Ras by a Covalent Catalytic Site Inhibitor. Angewandte Chemie - International Edition, 2014, 53, 199-204.	13.8	262
90	A Conformational Investigation of Propeptide Binding to the Integral Membrane Protein β -Glutamyl Carboxylase Using Nanodisc Hydrogen Exchange Mass Spectrometry. Biochemistry, 2014, 53, 1511-1520.	2.5	47

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91	A Conserved Isoleucine Maintains the Inactive State of Bruton's Tyrosine Kinase. <i>Journal of Molecular Biology</i> , 2014, 426, 3656-3669.	4.2	10
92	Electron Transfer Control in Soluble Methane Monooxygenase. <i>Journal of the American Chemical Society</i> , 2014, 136, 9754-9762.	13.7	35
93	Considerations in the Analysis of Hydrogen Exchange Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2013, 1007, 263-288.	0.9	58
94	Conformational Analysis of Recombinant Monoclonal Antibodies with Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 988, 269-289.	0.9	35
95	Analysis of Overlapped and Noisy Hydrogen/Deuterium Exchange Mass Spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1906-1912.	2.8	150
96	Conformational Transition of Membrane-Associated Terminally Acylated HIV-1 Nef. <i>Structure</i> , 2013, 21, 1822-1833.	3.3	29
97	Assessing the reproducibility and specificity of pepsin and other aspartic proteases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1222-1229.	2.3	111
98	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.	4.2	26
99	Active-Site Inhibitors Modulate the Dynamic Properties of Human Monoacylglycerol Lipase: A Hydrogen Exchange Mass Spectrometry Study. <i>Biochemistry</i> , 2013, 52, 5016-5026.	2.5	17
100	Hydrogen Exchange-Mass Spectrometry Measures Stapled Peptide Conformational Dynamics and Predicts Pharmacokinetic Properties. <i>Analytical Chemistry</i> , 2013, 85, 11185-11188.	6.5	21
101	Membrane phospholipid bilayer as a determinant of monoacylglycerol lipase kinetic profile and conformational repertoire. <i>Protein Science</i> , 2013, 22, 774-787.	7.6	37
102	Activation Loop Dynamics Determine the Different Catalytic Efficiencies of B Cell- and T Cell-Specific Tec Kinases. <i>Science Signaling</i> , 2013, 6, ra76.	3.6	27
103	Structure and Dynamic Regulation of Abl Kinases*. <i>Journal of Biological Chemistry</i> , 2013, 288, 5443-5450.	3.4	89
104	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.	3.4	14
105	Investigating Monoclonal Antibody Aggregation Using a Combination of H/DX-MS and Other Biophysical Measurements. <i>Journal of Pharmaceutical Sciences</i> , 2013, 102, 4315-4329.	3.3	84
106	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.	3.4	29
107	Partial cooperative unfolding in proteins as observed by hydrogen exchange mass spectrometry. <i>International Reviews in Physical Chemistry</i> , 2013, 32, 96-127.	2.3	36
108	Conformational analysis of processivity clamps demonstrates that tertiary structure does not correlate with structural dynamics. <i>FASEB Journal</i> , 2013, 27, 541.1.	0.5	0

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109	Sulfonyl Fluoride Inhibitors of Fatty Acid Amide Hydrolase. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 10074-10089.	6.4	43
110	Endocannabinoid Enzyme Engineering: Soluble Human Thio-Monoacylglycerol Lipase (sol-S-hMGL). <i>ACS Chemical Neuroscience</i> , 2012, 3, 393-399.	3.5	9
111	Analytical tools for characterizing biopharmaceuticals and the implications for biosimilars. <i>Nature Reviews Drug Discovery</i> , 2012, 11, 527-540.	46.4	441
112	The Natural Product Cucurbitacin E Inhibits Depolymerization of Actin Filaments. <i>ACS Chemical Biology</i> , 2012, 7, 1502-1508.	3.4	51
113	Catalytic site remodelling of the DOT1L methyltransferase by selective inhibitors. <i>Nature Communications</i> , 2012, 3, 1288.	12.8	247
114	Pepsin Immobilized on High-Strength Hybrid Particles for Continuous Flow Online Digestion at 10 ⁶ psi. <i>Analytical Chemistry</i> , 2012, 84, 7256-7262.	6.5	60
115	Hydrogen Exchange Mass Spectrometry: Are We Out of the Quicksand?. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1003-1010.	2.8	102
116	Conformational Locking upon Cooperative Assembly of Notch Transcription Complexes. <i>Structure</i> , 2012, 20, 340-349.	3.3	60
117	HIV-1 Nef interaction influences the ATP-binding site of the Src-family kinase, Hck. <i>BMC Chemical Biology</i> , 2012, 12, 1.	1.6	18
118	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.	2.8	53
119	Effects of HIV-1 Nef on Human <i>N</i> -Myristoyltransferase 1. <i>Biochemistry</i> , 2011, 50, 3394-3403.	2.5	20
120	<i>Escherichia coli</i> Processivity Clamp β^2 from DNA Polymerase III Is Dynamic in Solution. <i>Biochemistry</i> , 2011, 50, 5958-5968.	2.5	40
121	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
122	On the Solution Conformation and Dynamics of the HIV-1 Viral Infectivity Factor. <i>Journal of Molecular Biology</i> , 2011, 410, 1008-1022.	4.2	25
123	Allosteric Interactions between the Myristate- and ATP-Site of the Abl Kinase. <i>PLoS ONE</i> , 2011, 6, e15929.	2.5	63
124	Evidence for Increased Exposure of the Notch1 Metalloprotease Cleavage Site upon Conversion to an Activated Conformation. <i>Structure</i> , 2011, 19, 546-554.	3.3	59
125	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
126	The Utility of Hydrogen/Deuterium Exchange Mass Spectrometry in Biopharmaceutical Comparability Studies. <i>Journal of Pharmaceutical Sciences</i> , 2011, 100, 2071-2086.	3.3	324

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127	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
128	Conformational Transitions in the Membrane Scaffold Protein of Phospholipid Bilayer Nanodiscs. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010876.	3.8	66
129	Conformational and dynamic characterization of the <i>Escherichia coli</i> DNA polymerase III beta processivity clamp. <i>FASEB Journal</i> , 2011, 25, 880.2.	0.5	0
130	Hydrogen exchange mass spectrometry: what is it and what can it tell us?. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 397, 967-972.	3.7	166
131	Targeting Bcr-Abl by combining allosteric with ATP-binding-site inhibitors. <i>Nature</i> , 2010, 463, 501-506.	27.8	525
132	Neutron Reflectometry Study of the Conformation of HIV Nef Bound to Lipid Membranes. <i>Biophysical Journal</i> , 2010, 99, 1940-1948.	0.5	22
133	Post-translational Modifications Differentially Affect IgG1 Conformation and Receptor Binding. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1716-1728.	3.8	355
134	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
135	Conformational Dynamics of the <i>Escherichia coli</i> DNA Polymerase Manager Proteins UmuD and UmuC. <i>Journal of Molecular Biology</i> , 2010, 398, 40-53.	4.2	20
136	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.	4.2	21
137	The DNA damage inducible protein UmuD inhibits replication. <i>FASEB Journal</i> , 2010, 24, 492.2.	0.5	0
138	Conformational disturbance in Abl kinase upon mutation and deregulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1386-1391.	7.1	68
139	Novel mutant-selective EGFR kinase inhibitors against EGFR T790M. <i>Nature</i> , 2009, 462, 1070-1074.	27.8	886
140	Characterization of IgG1 Conformation and Conformational Dynamics by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5966-5966.	6.5	39
141	Characterization of IgG1 Conformation and Conformational Dynamics by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 2644-2651.	6.5	174
142	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
143	Aspartic proteinases in Antarctic fish. <i>Marine Genomics</i> , 2009, 2, 1-10.	1.1	16
144	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

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145	Analysis of Protein Conformation and Dynamics by Hydrogen/Deuterium Exchange MS. Analytical Chemistry, 2009, 81, 7870-7875.	6.5	321
146	Regulation of DNA damage responses by the polymerase manager proteins UmuD and UmuD ² . FASEB Journal, 2009, 23, 837.1.	0.5	0
147	Ion mobility adds an additional dimension to mass spectrometric analysis of solution ² phase hydrogen/deuterium exchange. Rapid Communications in Mass Spectrometry, 2008, 22, 2898-2904.	1.5	63
148	High-Speed and High-Resolution UPLC Separation at Zero Degrees Celsius. Analytical Chemistry, 2008, 80, 6815-6820.	6.5	309
149	Tyrosine Phosphorylation in the SH3 Domain Disrupts Negative Regulatory Interactions within the c-Abl Kinase Core. Journal of Molecular Biology, 2008, 383, 414-423.	4.2	38
150	Abl N-Terminal Cap Stabilization of SH3 Domain Dynamics. Biochemistry, 2008, 47, 5795-5803.	2.5	20
151	Chapter 4 Protein Analysis with Hydrogen ² Deuterium Exchange Mass Spectrometry. Comprehensive Analytical Chemistry, 2008, 52, 83-102.	1.3	0
152	Dynamics of the polymerase manager protein UmuD: DNA damage tolerance in E. coli. FASEB Journal, 2008, 22, 591.4.	0.5	0
153	Functional Characterization and Conformational Analysis of the Herpesvirus saimiri Tip-C484 Protein. Journal of Molecular Biology, 2007, 366, 1282-1293.	4.2	21
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155	Purification and characterization of pepsins ² A1 and A2 from the Antarctic rock cod <i>Trematomus bernacchii</i> . FEBS Journal, 2007, 274, 6152-6166.	4.7	42
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