

John R Engen

List of Publications by Year in descending order

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186
papers

13,229
citations

28274

55
h-index

27406

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. | 27.8 | 886 |
| 2 | Hydrogen exchange mass spectrometry for the analysis of protein dynamics. <i>Mass Spectrometry Reviews</i> , 2006, 25, 158-170. | 5.4 | 767 |
| 3 | Targeting Bcrâ€“Abl by combining allosteric with ATP-binding-site inhibitors. <i>Nature</i> , 2010, 463, 501-506. | 27.8 | 525 |
| 4 | 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 |
| 5 | Analytical tools for characterizing biopharmaceuticals and the implications for biosimilars. <i>Nature Reviews Drug Discovery</i> , 2012, 11, 527-540. | 46.4 | 441 |
| 6 | Post-translational Modifications Differentially Affect IgG1 Conformation and Receptor Binding. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1716-1728. | 3.8 | 355 |
| 7 | 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 |
| 8 | Analysis of Protein Conformation and Dynamics by Hydrogen/Deuterium Exchange MS. <i>Analytical Chemistry</i> , 2009, 81, 7870-7875. | 6.5 | 321 |
| 9 | High-Speed and High-Resolution UPLC Separation at Zero Degrees Celsius. <i>Analytical Chemistry</i> , 2008, 80, 6815-6820. | 6.5 | 309 |
| 10 | Therapeutic Targeting of Oncogenic Kâ€“Ras by a Covalent Catalytic Site Inhibitor. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 199-204. | 13.8 | 262 |
| 11 | Catalytic site remodelling of the DOT1L methyltransferase by selective inhibitors. <i>Nature Communications</i> , 2012, 3, 1288. | 12.8 | 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. | 2.8 | 234 |
| 13 | Rpn1 provides adjacent receptor sites for substrate binding and deubiquitination by the proteasome. <i>Science</i> , 2016, 351, . | 12.6 | 234 |
| 14 | Substrate processing by the Cdc48 ATPase complex is initiated by ubiquitin unfolding. <i>Science</i> , 2019, 365, . | 12.6 | 233 |
| 15 | Force interacts with macromolecular structure in activation of TGF-Î². <i>Nature</i> , 2017, 542, 55-59. | 27.8 | 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. | 2.8 | 209 |
| 17 | Peer Reviewed: Investigating Protein Structure and Dynamics by Hydrogen Exchange MS. <i>Analytical Chemistry</i> , 2001, 73, 256 A-265 A. | 6.5 | 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. | 17.5 | 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. | 6.4 | 176 |
| 20 | Characterization of IgG1 Conformation and Conformational Dynamics by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 2644-2651. | 6.5 | 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. | 3.7 | 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. | 2.8 | 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. | 5.2 | 149 |
| 24 | 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 |
| 25 | Chemically Induced Degradation of the Oncogenic Transcription Factor BCL6. <i>Cell Reports</i> , 2017, 20, 2860-2875. | 6.4 | 133 |
| 26 | Applications of Hydrogen/Deuterium Exchange MS from 2012 to 2014. <i>Analytical Chemistry</i> , 2015, 87, 99-118. | 6.5 | 131 |
| 27 | Tissue-Specific Oncogenic Activity of KRASA146T. <i>Cancer Discovery</i> , 2019, 9, 738-755. | 9.4 | 127 |
| 28 | GroEL/ES Chaperonin Modulates the Mechanism and Accelerates the Rate of TIM-Barrel Domain Folding. <i>Cell</i> , 2014, 157, 922-934. | 28.9 | 116 |
| 29 | Inhibition of Pro-Apoptotic BAX by a Noncanonical Interaction Mechanism. <i>Molecular Cell</i> , 2015, 57, 873-886. | 9.7 | 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. | 3.4 | 112 |
| 31 | Analytical Aspects of Hydrogen Exchange Mass Spectrometry. <i>Annual Review of Analytical Chemistry</i> , 2015, 8, 127-148. | 5.4 | 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. | 2.3 | 111 |
| 33 | 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 |
| 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. | 2.8 | 102 |
| 35 | 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 |
| 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. | 6.5 | 89 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Structure and Dynamic Regulation of Abl Kinases*. Journal of Biological Chemistry, 2013, 288, 5443-5450. | 3.4 | 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. | 2.5 | 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. | 8.2 | 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. | 3.3 | 84 |
| 41 | Structure of the Cdc48 ATPase with its ubiquitin-binding cofactor Ufd1. Nature Structural and Molecular Biology, 2018, 25, 616-622. | 8.2 | 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. | 5.9 | 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. | 2.8 | 76 |
| 44 | Hydrogen Exchange Shows Peptide Binding Stabilizes Motions in Hck SH2. Biochemistry, 1999, 38, 8926-8935. | 2.5 | 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. | 2.8 | 72 |
| 46 | Selective USP7 inhibition elicits cancer cell killing through a p53-dependent mechanism. Scientific Reports, 2020, 10, 5324. | 3.3 | 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. | 7.1 | 68 |
| 48 | Inhibition of Flaviviruses by Targeting a Conserved Pocket on the Viral Envelope Protein. Cell Chemical Biology, 2018, 25, 1006-1016.e8. | 5.2 | 68 |
| 49 | Analysis of protein complexes with hydrogen exchange and mass spectrometry. Analyst, The, 2003, 128, 623. | 3.5 | 66 |
| 50 | Conformational Transitions in the Membrane Scaffold Protein of Phospholipid Bilayer Nanodiscs. Molecular and Cellular Proteomics, 2011, 10, M111.010876. | 3.8 | 66 |
| 51 | Partial Unfolding of Diverse SH3 Domains on a Wide Timescale. Journal of Molecular Biology, 2006, 357, 1592-1604. | 4.2 | 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. | 1.5 | 63 |
| 53 | Allosteric Interactions between the Myristate- and ATP-Site of the Abl Kinase. PLoS ONE, 2011, 6, e15929. | 2.5 | 63 |
| 54 | Developments in Hydrogen/Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2021, 93, 567-582. | 6.5 | 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. | 6.5 | 60 |
| 56 | Conformational Locking upon Cooperative Assembly of Notch Transcription Complexes. <i>Structure</i> , 2012, 20, 340-349. | 3.3 | 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. | 3.3 | 59 |
| 58 | Considerations in the Analysis of Hydrogen Exchange Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2013, 1007, 263-288. | 0.9 | 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. | 5.7 | 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. | 2.8 | 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. | 3.4 | 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. | 4.2 | 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. | 2.5 | 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. | 4.2 | 47 |
| 67 | Mechanism of Enzyme Repair by the AAA+ Chaperone Rubisco Activase. <i>Molecular Cell</i> , 2017, 67, 744-756.e6. | 9.7 | 47 |
| 68 | Allosteric inhibition of antiapoptotic MCL-1. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 600-607. | 8.2 | 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. | 9.7 | 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. | 3.3 | 44 |
| 71 | Sulfonyl Fluoride Inhibitors of Fatty Acid Amide Hydrolase. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 10074-10089. | 6.4 | 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. | 6.5 | 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. | 7.6 | 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. | 4.7 | 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. | 4.2 | 41 |
| 76 | Fetal alcohol exposure alters neurosteroid levels in the developing rat brain. <i>Journal of Neurochemistry</i> , 2004, 90, 1530-1539. | 3.9 | 41 |
| 77 | Activation of the Src Family Kinase Hck without SH3-Linker Release. <i>Journal of Biological Chemistry</i> , 2005, 280, 40832-40837. | 3.4 | 41 |
| 78 | <i>Escherichia coli</i> Processivity Clamp $\hat{\tau}^2$ from DNA Polymerase III Is Dynamic in Solution. <i>Biochemistry</i> , 2011, 50, 5958-5968. | 2.5 | 40 |
| 79 | Dynamic Allostery Mediated by a Conserved Tryptophan in the Tec Family Kinases. <i>PLoS Computational Biology</i> , 2016, 12, e1004826. | 3.2 | 40 |
| 80 | Allosteric sensitization of proapoptotic BAX. <i>Nature Chemical Biology</i> , 2017, 13, 961-967. | 8.0 | 40 |
| 81 | Characterization of IgG1 Conformation and Conformational Dynamics by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5966-5966. | 6.5 | 39 |
| 82 | Translocation of polyubiquitinated protein substrates by the hexameric Cdc48 ATPase. <i>Molecular Cell</i> , 2022, 82, 570-584.e8. | 9.7 | 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. | 4.2 | 38 |
| 84 | 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 |
| 85 | Fusion surface structure, function, and dynamics of gamete fusogen HAP2. <i>ELife</i> , 2018, 7, . | 6.0 | 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. | 2.3 | 36 |
| 87 | Conformational Analysis of Recombinant Monoclonal Antibodies with Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 988, 269-289. | 0.9 | 35 |
| 88 | Differential Sensitivity of Src-Family Kinases to Activation by SH3 Domain Displacement. <i>PLoS ONE</i> , 2014, 9, e105629. | 2.5 | 35 |
| 89 | Electron Transfer Control in Soluble Methane Monooxygenase. <i>Journal of the American Chemical Society</i> , 2014, 136, 9754-9762. | 13.7 | 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. | 4.2 | 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. | 7.6 | 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. | 2.8 | 34 |
| 93 | 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 |
| 94 | Hydrogen-Deuterium Exchange Mass Spectrometry to Study Protein Complexes. <i>Methods in Molecular Biology</i> , 2018, 1764, 153-171. | 0.9 | 33 |
| 95 | 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 |
| 96 | Complementarity of Hydrogen/Deuterium Exchange Mass Spectrometry and Cryo-Electron Microscopy. <i>Trends in Biochemical Sciences</i> , 2020, 45, 906-918. | 7.5 | 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. | 3.3 | 30 |
| 98 | Utilizing Microchip Capillary Electrophoresis Electrospray Ionization for Hydrogen Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 6280-6287. | 6.5 | 30 |
| 99 | Structural Dynamics in Ras and Related Proteins upon Nucleotide Switching. <i>Journal of Molecular Biology</i> , 2016, 428, 4723-4735. | 4.2 | 30 |
| 100 | Structural analysis of lecithin:cholesterol acyltransferase bound to high density lipoprotein particles. <i>Communications Biology</i> , 2020, 3, 28. | 4.4 | 30 |
| 101 | Conformational Transition of Membrane-Associated Terminally Acylated HIV-1 Nef. <i>Structure</i> , 2013, 21, 1822-1833. | 3.3 | 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. | 3.4 | 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. | 3.0 | 28 |
| 104 | General structural features that regulate integrin affinity revealed by atypical β 28. <i>Nature Communications</i> , 2019, 10, 5481. | 12.8 | 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. | 5.2 | 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. | 3.6 | 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. | 3.3 | 27 |
| 108 | Structures of PGAM5 Provide Insight into Active Site Plasticity and Multimeric Assembly. <i>Structure</i> , 2017, 25, 1089-1099.e3. | 3.3 | 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. | 7.8 | 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. | 4.2 | 26 |
| 111 | Using Stable-Isotope-Labeled Proteins for Hydrogen Exchange Studies in Complex Mixtures. <i>Analytical Chemistry</i> , 2002, 74, 1680-1686. | 6.5 | 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. | 4.2 | 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. | 7.6 | 25 |
| 114 | Differential impact of BTK active site inhibitors on the conformational state of full-length BTK. <i>ELife</i> , 2020, 9, . | 6.0 | 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. | 2.5 | 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. | 3.7 | 24 |
| 117 | Structural basis of the atypical activation mechanism of KRASV14I. <i>Journal of Biological Chemistry</i> , 2019, 294, 13964-13972. | 3.4 | 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. | 2.5 | 23 |
| 119 | Neutron Reflectometry Study of the Conformation of HIV Nef Bound to α Lipid Membranes. <i>Biophysical Journal</i> , 2010, 99, 1940-1948. | 0.5 | 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, . | 3.6 | 22 |
| 121 | Functional Characterization and Conformational Analysis of the Herpesvirus saimiri Tip-C484 Protein. <i>Journal of Molecular Biology</i> , 2007, 366, 1282-1293. | 4.2 | 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. | 4.2 | 21 |
| 123 | Hydrogen Exchange-Mass Spectrometry Measures Stapled Peptide Conformational Dynamics and Predicts Pharmacokinetic Properties. <i>Analytical Chemistry</i> , 2013, 85, 11185-11188. | 6.5 | 21 |
| 124 | Mitochondrial ClpX activates an essential biosynthetic enzyme through partial unfolding. <i>ELife</i> , 2020, 9, . | 6.0 | 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. | 3.3 | 20 |
| 126 | Abl N-Terminal Cap Stabilization of SH3 Domain Dynamics. <i>Biochemistry</i> , 2008, 47, 5795-5803. | 2.5 | 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. | 4.2 | 20 |
| 128 | Effects of HIV-1 Nef on Human N-Myristoyltransferase 1. Biochemistry, 2011, 50, 3394-3403. | 2.5 | 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. | 2.8 | 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. | 1.8 | 19 |
| 131 | Hydrogen Exchange Mass Spectrometry of Proteins at Langmuir Monolayers. Analytical Chemistry, 2015, 87, 7022-7029. | 6.5 | 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. | 7.1 | 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. | 4.2 | 18 |
| 136 | Active-Site Inhibitors Modulate the Dynamic Properties of Human Monoacylglycerol Lipase: A Hydrogen Exchange Mass Spectrometry Study. Biochemistry, 2013, 52, 5016-5026. | 2.5 | 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. | 2.8 | 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. | 3.4 | 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. | 13.7 | 16 |
| 140 | Aspartic proteinases in Antarctic fish. Marine Genomics, 2009, 2, 1-10. | 1.1 | 16 |
| 141 | Replication in bioanalytical studies with HDX MS: aim as high as possible. Bioanalysis, 2015, 7, 1065-1067. | 1.5 | 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. | 4.2 | 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. | 3.4 | 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. | 2.8 | 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. | 6.4 | 15 |
| 146 | Allosteric control of Ubp6 and the proteasome via a bidirectional switch. <i>Nature Communications</i> , 2022, 13, 838. | 12.8 | 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. | 7.6 | 14 |
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