PatrickÂ L Wintrode

List of Publications by Year
in descending order

63	3,081	201674 27	168389 53
papers	citations	h-index	g-index

64	64	64	4914
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	19.0	452
2	How enzymes adapt: lessons from directed evolution. Trends in Biochemical Sciences, 2001, 26, 100-106.	7.5	351
3	Directed evolution study of temperature adaptation in a psychrophilic enzyme 1 1Edited by J. A. Wells. Journal of Molecular Biology, 2000, 297, 1015-1026.	4.2	243
4	beta-Sheet core of human prion protein amyloid fibrils as determined by hydrogen/deuterium exchange. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1510-1515.	7.1	218
5	Thermodynamics of ubiquitin unfolding. Proteins: Structure, Function and Bioinformatics, 1994, 18, 246-253.	2.6	170
6	Cold Adaptation of a Mesophilic Subtilisin-like Protease by Laboratory Evolution. Journal of Biological Chemistry, 2000, 275, 31635-31640.	3.4	128
7	Protein Dynamics in a Family of Laboratory Evolved Thermophilic Enzymes. Journal of Molecular Biology, 2003, 327, 745-757.	4.2	96
8	Energetics of target peptide recognition by calmodulin: A calorimetric study. Journal of Molecular Biology, 1997, 266, 1050-1062.	4.2	93
9	Hydrogen/Deuterium Exchange-Mass Spectrometry: A Powerful Tool for Probing Protein Structure, Dynamics and Interactions. Current Medicinal Chemistry, 2007, 14, 2344-2358.	2.4	93
10	Conformational dynamics of a neurotransmitter:sodium symporter in a lipid bilayer. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1786-E1795.	7.1	76
11	Folding mechanism of the metastable serpin Î± ₁ -antitrypsin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4467-4472.	7.1	67
12	Crystal Structures of the Toll/Interleukin-1 Receptor (TIR) Domains from the Brucella Protein TcpB and Host Adaptor TIRAP Reveal Mechanisms of Molecular Mimicry. Journal of Biological Chemistry, 2014, 289, 669-679.	3.4	66
13	Successes and challenges in simulating the folding of large proteins. Journal of Biological Chemistry, 2020, 295, 15-33.	3.4	56
14	Effects of glycosylation on the stability and flexibility of a metastable protein: The human serpin Î±1-antitrypsin. International Journal of Mass Spectrometry, 2011, 302, 69-75.	1.5	54
15	Complementary Structural Mass Spectrometry Techniques Reveal Local Dynamics in Functionally Important Regions of a Metastable Serpin. Structure, 2008, 16, 38-51.	3.3	48
16	IL-1 Family Cytokines Use Distinct Molecular Mechanisms to Signal through Their Shared Co-receptor. Immunity, 2017, 47, 510-523.e4.	14.3	48
17	A Dimer Interface Mutation in Glyceraldehyde-3-Phosphate Dehydrogenase Regulates Its Binding to AU-rich RNA. Journal of Biological Chemistry, 2015, 290, 1770-1785.	3.4	47
18	The Helicobacter pylori adhesin protein HopQ exploits the dimer interface of human CEACAMs to facilitate translocation of the oncoprotein CagA. EMBO Journal, 2018, 37, .	7.8	47

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19	Common coding variant in SERPINA1 increases the risk for large artery stroke. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3613-3618.	7.1	46
20	Bacterial flagellar capping proteins adopt diverse oligomeric states. ELife, 2016, 5, .	6.0	46
21	Interlaboratory Comparison of Hydrogenâ€“Deuterium Exchange Mass Spectrometry Measurements of the Fab Fragment of NISTmAb. Analytical Chemistry, 2019, 91, 7336-7345.	6.5	44
22	Allosteric Suppression of HIV-1 Reverse Transcriptase Structural Dynamics upon Inhibitor Binding. Biophysical Journal, 2011, 100, 144-153.	0.5	41
23	Multi-state Unfolding of the Alpha Subunit of Tryptophan Synthase, a TIM Barrel Protein: Insights into the Secondary Structure of the Stable Equilibrium Intermediates by Hydrogen Exchange Mass Spectrometry. Journal of Molecular Biology, 2004, 341, 241-253.	4.2	32
24	The Structural Basis of Serpin Polymerization Studied by Hydrogen/Deuterium Exchange and Mass Spectrometry. Journal of Biological Chemistry, 2008, 283, 30804-30811.	3.4	31
25	Serpin latency transition at atomic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15414-15419.	7.1	31
26	Solution Structural Dynamics of HIV-1 Reverse Transcriptase Heterodimer. Biochemistry, 2009, 48, 7646-7655.	2.5	30
27	Structure and dynamics of an Î±-fucosidase reveal a mechanism for highly efficient IgG transfucosylation. Nature Communications, 2020, 11, 6204.	12.8	29
28	Structure and Dynamics of FosA-Mediated Fosfomycin Resistance in Klebsiella pneumoniae and Escherichia coli. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	28
29	Structural energetics of barstar studied by differential scanning microcalorimetry. Protein Science, 1995, 4, 1528-1534.	7.6	27
30	An Obligatory Intermediate Controls the Folding of the Î±-Subunit of Tryptophan Synthase, a TIM Barrel Protein. Journal of Molecular Biology, 2005, 347, 911-919.	4.2	27
31	Molecular Basis of Broad Spectrum N-Glycan Specificity and Processing of Therapeutic IgG Monoclonal Antibodies by Endoglycosidase S2. ACS Central Science, 2019, 5, 524-538.	11.3	27
32	Early Hydrophobic Collapse of Î±1-Antitrypsin Facilitates Formation of a Metastable State: Insights from Oxidative Labeling and Mass Spectrometry. Journal of Molecular Biology, 2012, 423, 789-799.	4.2	24
33	Antigen-Induced Allosteric Changes in a Human IgG1 Fc Increase Low-Affinity FcÎ³ Receptor Binding. Structure, 2020, 28, 516-527.e5.	3.3	23
34	Cooperative Unfolding of a Metastable Serpin to a Molten Globule Suggests a Link Between Functional and Folding Energy Landscapes. Journal of Molecular Biology, 2007, 371, 245-255.	4.2	22
35	Enhanced Molecular Mobility of Ordinarily Structured Regions Drives Polyglutamine Disease. Journal of Biological Chemistry, 2015, 290, 24190-24200.	3.4	22
36	Hydrogen/Deuterium Exchange Kinetics Demonstrate Long Range Allosteric Effects of Thumb Site 2 Inhibitors of Hepatitis C Viral RNA-dependent RNA Polymerase. Journal of Biological Chemistry, 2016, 291, 10078-10088.	3.4	22

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37	Identification of a Region in the N-Terminus of Escherichia coli Lon That Affects ATPase, Substrate Translocation and Proteolytic Activity. Journal of Molecular Biology, 2012, 418, 208-225.	4.2	21
38	All-Atom Simulations Reveal How Single-Point Mutations Promote Serpin Misfolding. Biophysical Journal, 2018, 114, 2083-2094.	0.5	19
39	The Z Mutation Alters the Global Structural Dynamics of Î±1-Antitrypsin. PLoS ONE, 2014, 9, e102617.	2.5	18
40	Ligand-induced allostery in the interaction of the Pseudomonas aeruginosa heme binding protein with heme oxygenase. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3421-3426.	7.1	18
41	Local Conformational Flexibility Provides a Basis for Facile Polymer Formation in Human Neuroserpin. Biophysical Journal, 2011, 101, 1758-1765.	0.5	13
42	Does Changing the Predicted Dynamics of a Phospholipase C Alter Activity and Membrane Binding?. Biophysical Journal, 2013, 104, 185-195.	0.5	11
43	Imatinib binding to human c-Src is coupled to inter-domain allostery and suggests a novel kinase inhibition strategy. Scientific Reports, 2016, 6, 30832.	3.3	11
44	Small-Molecule Inhibitor of FosA Expands Fosfomycin Activity to Multidrug-Resistant Gram-Negative Pathogens. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	11
45	Monitoring dendrimer conformational transition using 19 F and 1 H 2 O NMR. Magnetic Resonance in Chemistry, 2019, 57, 861-872.	1.9	10
46	A temperature-dependent conformational shift in p38Î± MAPK substrateâ€“binding region associated with changes in substrate phosphorylation profile. Journal of Biological Chemistry, 2019, 294, 12624-12637.	3.4	9
47	Conformational transition of a non-associative fluorinated amphiphile in aqueous solution. II. Conformational transition vs. supramolecular assembly. RSC Advances, 2019, 9, 1956-1966.	3.6	9
48	Modeling the native ensemble of PhuS using enhanced sampling MD and HDX-ensemble reweighting. Biophysical Journal, 2021, 120, 5141-5157.	0.5	7
49	Probing Serpin Conformational Change Using Mass Spectrometry and Related Methods. Methods in Enzymology, 2011, 501, 325-350.	1.0	5
50	Mass spectrometry in structural biology. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1187.	2.3	3
51	Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS) Centroid Data Measured between 3.6 Â°C and 25.4 Â°C for the Fab Fragment of NISTmAb. Journal of Research of the National Institute of Standards and Technology, 2019, 124, 1-7.	1.2	3
52	Interpreting hydrogen-deuterium exchange experiments with molecular simulations: Tutorials and applications of the HDXer ensemble reweighting software [Article v1.0]. Living Journal of Computational Molecular Science, 2022, 3, .	6.4	3
53	Neurotransmitter Transporter Conformational Dynamics using HDX-MS and Molecular Dynamics Simulation. Biophysical Journal, 2018, 114, 207a.	0.5	2
54	Characterization of interaction between blood coagulation factor <scp>VIII</scp> and <scp>LRP1</scp> suggests dynamic binding by alternating complex contacts. Journal of Thrombosis and Haemostasis, 0, , .	3.8	2

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55	A structure and function relationship study to identify the impact of the R721G mutation in the human mitochondrial lon protease. Archives of Biochemistry and Biophysics, 2021, 710, 108983.	3.0	1
56	Structural Changes in Monomeric HIV-RT Upon Binding the NNRTI Efavirenz. Biophysical Journal, 2009, 96, 446a.	0.5	0
57	HIV-1 Reverse Transcriptase Monomers Adopt Multiple Conformations inÂSolution. Biophysical Journal, 2012, 102, 46a-47a.	0.5	0
58	Anchoring of PI-PLC to DMPC Bilayers Involves Specific Cation-PI Interactions. Biophysical Journal, 2012, 102, 78a-79a.	0.5	0
59	Cation-PI Interactions as Specific Anchors for B. Thurigiensis Phosphoinositol-Specific Phospholipase-C Binding to Phosphatidylcholine Bilayer. Biophysical Journal, 2013, 104, 536a.	0.5	0
60	Remodeling KRAS. Structure, 2017, 25, 1323-1324.	3.3	0
61	Determination of the Mechanism of RNA Regulation by CPSF30 Utilizing Both Biophysical and Structural Approaches. Biophysical Journal, 2019, 116, 503a.	0.5	0
62	HDX-MS Guided Ensemble Reweighting Approach Characterizes a Large Conformational Rearrangement in the Cytoplasmic Heme Binding Protein PhuS. Biophysical Journal, 2021, 120, 127a.	0.5	0
63	Thumb II Site Inhibitor Allosterically Suppresses the Dynamics of HCV NS5B RNAâ€Ðependent RNA Polymerase. FASEB Journal, 2015, 29, LB81.	0.5	0