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	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
2	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
3	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
4	Modeling the native ensemble of PhuS using enhanced sampling MD and HDX-ensemble reweighting. Biophysical Journal, 2021, 120, 5141-5157.	0.5	7
5	Successes and challenges in simulating the folding of large proteins. Journal of Biological Chemistry, 2020, 295, 15-33.	3.4	56
6	Structure and dynamics of an Î±-fucosidase reveal a mechanism for highly efficient IgG transfucosylation. Nature Communications, 2020, 11, 6204.	12.8	29
7	Antigen-Induced Allosteric Changes in a Human IgG1 Fc Increase Low-Affinity FcÎ³ Receptor Binding. Structure, 2020, 28, 516-527.e5.	3.3	23
8	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. Nature Methods, 2019, 16, 595-602.	19.0	452
9	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
10	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
11	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
12	Interlaboratory Comparison of Hydrogenâ€“Deuterium Exchange Mass Spectrometry Measurements of the Fab Fragment of NISTmAb. Analytical Chemistry, 2019, 91, 7336-7345.	6.5	44
13	Monitoring dendrimer conformational transition using 19 F and 1 H 2 O NMR. Magnetic Resonance in Chemistry, 2019, 57, 861-872.	1.9	10
14	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
15	Determination of the Mechanism of RNA Regulation by CPSF30 Utilizing Both Biophysical and Structural Approaches. Biophysical Journal, 2019, 116, 503a.	0.5	0
16	Small-Molecule Inhibitor of FosA Expands Fosfomycin Activity to Multidrug-Resistant Gram-Negative Pathogens. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	11
17	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
18	Neurotransmitter Transporter Conformational Dynamics using HDX-MS and Molecular Dynamics Simulation. Biophysical Journal, 2018, 114, 207a.	0.5	2

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19	All-Atom Simulations Reveal How Single-Point Mutations Promote Serpin Misfolding. Biophysical Journal, 2018, 114, 2083-2094.	0.5	19
20	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
21	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
22	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
23	IL-1 Family Cytokines Use Distinct Molecular Mechanisms to Signal through Their Shared Co-receptor. Immunity, 2017, 47, 510-523.e4.	14.3	48
24	Remodeling KRAS. Structure, 2017, 25, 1323-1324.	3.3	0
25	Structure and Dynamics of FosA-Mediated Fosfomycin Resistance in Klebsiella pneumoniae and Escherichia coli. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	28
26	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
27	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
28	Bacterial flagellar capping proteins adopt diverse oligomeric states. ELife, 2016, 5, .	6.0	46
29	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
30	Enhanced Molecular Mobility of Ordinarily Structured Regions Drives Polyglutamine Disease. Journal of Biological Chemistry, 2015, 290, 24190-24200.	3.4	22
31	Thumb II Site Inhibitor Allosterically Suppresses the Dynamics of HCV NS5B RNAâ€Dependent RNA Polymerase. FASEB Journal, 2015, 29, LB81.	0.5	0
32	The Z Mutation Alters the Global Structural Dynamics of Î±1-Antitrypsin. PLoS ONE, 2014, 9, e102617.	2.5	18
33	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
34	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
35	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
36	Mass spectrometry in structural biology. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1187.	2.3	3

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37	Does Changing the Predicted Dynamics of a Phospholipase C Alter Activity and Membrane Binding?. Biophysical Journal, 2013, 104, 185-195.	0.5	11
38	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
39	HIV-1 Reverse Transcriptase Monomers Adopt Multiple Conformations inÂSolution. Biophysical Journal, 2012, 102, 46a-47a.	0.5	0
40	Anchoring of PI-PLC to DMPC Bilayers Involves Specific Cation-PI Interactions. Biophysical Journal, 2012, 102, 78a-79a.	0.5	0
41	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
42	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
43	Allosteric Suppression of HIV-1 Reverse Transcriptase Structural Dynamics upon Inhibitor Binding. Biophysical Journal, 2011, 100, 144-153.	0.5	41
44	Local Conformational Flexibility Provides a Basis for Facile Polymer Formation in Human Neuroserpin. Biophysical Journal, 2011, 101, 1758-1765.	0.5	13
45	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
46	Probing Serpin Conformational Change Using Mass Spectrometry and Related Methods. Methods in Enzymology, 2011, 501, 325-350.	1.0	5
47	Solution Structural Dynamics of HIV-1 Reverse Transcriptase Heterodimer. Biochemistry, 2009, 48, 7646-7655.	2.5	30
48	Structural Changes in Monomeric HIV-RT Upon Binding the NNRTI Efavirenz. Biophysical Journal, 2009, 96, 446a.	0.5	0
49	Complementary Structural Mass Spectrometry Techniques Reveal Local Dynamics in Functionally Important Regions of a Metastable Serpin. Structure, 2008, 16, 38-51.	3.3	48
50	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
51	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
52	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
53	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
54	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

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55	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
56	Protein Dynamics in a Family of Laboratory Evolved Thermophilic Enzymes. Journal of Molecular Biology, 2003, 327, 745-757.	4.2	96
57	How enzymes adapt: lessons from directed evolution. Trends in Biochemical Sciences, 2001, 26, 100-106.	7.5	351
58	Cold Adaptation of a Mesophilic Subtilisin-like Protease by Laboratory Evolution. Journal of Biological Chemistry, 2000, 275, 31635-31640.	3.4	128
59	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
60	Energetics of target peptide recognition by calmodulin: A calorimetric study. Journal of Molecular Biology, 1997, 266, 1050-1062.	4.2	93
61	Structural energetics of barstar studied by differential scanning microcalorimetry. Protein Science, 1995, 4, 1528-1534.	7.6	27
62	Thermodynamics of ubiquitin unfolding. Proteins: Structure, Function and Bioinformatics, 1994, 18, 246-253.	2.6	170
63	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