

J Patrick Loria

List of Publications by Year in descending order

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72
papers

5,275
citations

126708

33
h-index

88477

70
g-index

75
all docs

75
docs citations

75
times ranked

4268
citing authors

#	ARTICLE	IF	CITATIONS
1	MptpA Kinetics Enhanced by Allosteric Control of an Active Conformation. <i>Journal of Molecular Biology</i> , 2022, 434, 167540.	2.0	7
2	A simple method to determine changes in the affinity between HisF and HisH in the Imidazole Glycerol Phosphate Synthase heterodimer. <i>PLoS ONE</i> , 2022, 17, e0267536.	1.1	0
3	Phosphorylation of a Human Microprotein Promotes Dissociation of Biomolecular Condensates. <i>Journal of the American Chemical Society</i> , 2021, 143, 12675-12687.	6.6	20
4	Significant Loop Motions in the SsoPTP Protein Tyrosine Phosphatase Allow for Dual General Acid Functionality. <i>Biochemistry</i> , 2021, 60, 2888-2901.	1.2	5
5	Role of a high centrality residue in protein dynamics and thermal stability. <i>Journal of Structural Biology</i> , 2021, 213, 107773.	1.3	3
6	A deubiquitylase with an unusually high-affinity ubiquitin-binding domain from the scrub typhus pathogen <i>Orientia tsutsugamushi</i> . <i>Nature Communications</i> , 2020, 11, 2343.	5.8	22
7	Allosteric Impact of the Variable Insert Loop in <i>Vaccinia</i> H1-Related (VHR) Phosphatase. <i>Biochemistry</i> , 2020, 59, 1896-1908.	1.2	5
8	Allosteric Control of Enzyme Activity: From Ancient Origins to Recent Gene-Editing Technologies. <i>Biochemistry</i> , 2020, 59, 1711-1712.	1.2	3
9	Reaching the sparse-sampling limit for reconstructing a single peak in a 2D NMR spectrum using iterated maps. <i>Journal of Biomolecular NMR</i> , 2019, 73, 545-560.	1.6	3
10	Uncovering the Molecular Interactions in the Catalytic Loop That Modulate the Conformational Dynamics in Protein Tyrosine Phosphatase 1B. <i>Journal of the American Chemical Society</i> , 2019, 141, 12634-12647.	6.6	40
11	Accelerating 2D NMR relaxation dispersion experiments using iterated maps. <i>Journal of Biomolecular NMR</i> , 2019, 73, 561-576.	1.6	5
12	Nanosecond Dynamics Regulate the MIF α -Induced Activity of CD74. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7116-7119.	7.2	32
13	Eigenvector centrality for characterization of protein allosteric pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E12201-E12208.	3.3	145
14	I260Q DNA polymerase β highlights precatalytic conformational rearrangements critical for fidelity. <i>Nucleic Acids Research</i> , 2018, 46, 10740-10756.	6.5	8
15	A YopH PTP1B Chimera Shows the Importance of the WPD-Loop Sequence to the Activity, Structure, and Dynamics of Protein Tyrosine Phosphatases. <i>Biochemistry</i> , 2018, 57, 5315-5326.	1.2	20
16	Glutamine Hydrolysis by Imidazole Glycerol Phosphate Synthase Displays Temperature Dependent Allosteric Activation. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 4.	1.6	25
17	Nanosecond Dynamics Regulate the MIF α -Induced Activity of CD74. <i>Angewandte Chemie</i> , 2018, 130, 7234-7237.	1.6	2
18	Altering the allosteric pathway in IGPS suppresses millisecond motions and catalytic activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3414-E3423.	3.3	55

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19	Exploring protein structure and dynamics through a project-oriented biochemistry laboratory module. <i>Biochemistry and Molecular Biology Education</i> , 2017, 45, 403-410.	0.5	10
20	Characterization of Protein Tyrosine Phosphatase 1B Inhibition by Chlorogenic Acid and Cichoric Acid. <i>Biochemistry</i> , 2017, 56, 96-106.	1.2	18
21	Allostery in enzyme catalysis. <i>Current Opinion in Structural Biology</i> , 2017, 47, 123-130.	2.6	60
22	Leveraging Reciprocity to Identify and Characterize Unknown Allosteric Sites in Protein Tyrosine Phosphatases. <i>Journal of Molecular Biology</i> , 2017, 429, 2360-2372.	2.0	47
23	Allosteric Communication Disrupted by a Small Molecule Binding to the Imidazole Glycerol Phosphate Synthase Protein-Protein Interface. <i>Biochemistry</i> , 2016, 55, 6484-6494.	1.2	33
24	Dissecting Dynamic Allosteric Pathways Using Chemically Related Small-Molecule Activators. <i>Structure</i> , 2016, 24, 1155-1166.	1.6	38
25	Induced Fit in the Selection of Correct versus Incorrect Nucleotides by DNA Polymerase β . <i>Biochemistry</i> , 2016, 55, 382-395.	1.2	16
26	Using NMR spectroscopy to elucidate the role of molecular motions in enzyme function. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2016, 92-93, 1-17.	3.9	42
27	Solution NMR Spectroscopy for the Study of Enzyme Allostery. <i>Chemical Reviews</i> , 2016, 116, 6323-6369.	23.0	106
28	Movement and Specificity in a Modular DNA Binding Protein. <i>Structure</i> , 2015, 23, 973-974.	1.6	1
29	Complexity of Protein Energy Landscapes Studied by Solution NMR Relaxation Dispersion Experiments. <i>Journal of Physical Chemistry B</i> , 2015, 119, 3743-3754.	1.2	9
30	^1H , ^{15}N , and ^{13}C backbone resonance assignments for the yersinia protein tyrosine phosphatase YopH. <i>Biomolecular NMR Assignments</i> , 2014, 8, 387-389.	0.4	4
31	MoD-QM/MM Structural Refinement Method: Characterization of Hydrogen Bonding in the <i>Oxytricha nova</i> G-Quadruplex. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 5125-5135.	2.3	16
32	Enzyme Architecture: The Effect of Replacement and Deletion Mutations of Loop 6 on Catalysis by Triosephosphate Isomerase. <i>Biochemistry</i> , 2014, 53, 3486-3501.	1.2	23
33	Conformational Motions Regulate Phosphoryl Transfer in Related Protein Tyrosine Phosphatases. <i>Science</i> , 2013, 341, 899-903.	6.0	168
34	What's in Your Buffer? Solute Altered Millisecond Motions Detected by Solution NMR. <i>Biochemistry</i> , 2013, 52, 6548-6558.	1.2	18
35	Accelerating multidimensional NMR and MRI experiments using iterated maps. <i>Journal of Magnetic Resonance</i> , 2013, 237, 100-109.	1.2	23
36	Solution NMR and Computational Methods for Understanding Protein Allostery. <i>Journal of Physical Chemistry B</i> , 2013, 117, 3063-3073.	1.2	40

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37	NMR insights into protein allostery. Archives of Biochemistry and Biophysics, 2012, 519, 223-231.	1.4	73
38	Substrate-Dependent Millisecond Domain Motions in DNA Polymerase β . Journal of Molecular Biology, 2012, 419, 171-182.	2.0	22
39	Allosteric pathways in imidazole glycerol phosphate synthase. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1428-36.	3.3	192
40	Alteration of Hydrogen Bonding in the Vicinity of Histidine 48 Disrupts Millisecond Motions in RNase A. Biochemistry, 2011, 50, 1723-1730.	1.2	31
41	Reengineering Rate-Limiting, Millisecond Enzyme Motions by Introduction of an Unnatural Amino Acid. Biophysical Journal, 2011, 101, 411-420.	0.2	28
42	Nanometer Propagation of Millisecond Motions in V-Type Allostery. Structure, 2010, 18, 1596-1607.	1.6	67
43	The crystal structure of ribonuclease A in complex with thymidine β -monophosphate provides further insight into ligand binding. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2459-2468.	1.5	16
44	Millisecond dynamics in the allosteric enzyme imidazole glycerol phosphate synthase (IGPS) from <i>Thermotoga maritima</i> . Journal of Biomolecular NMR, 2009, 45, 73-84.	1.6	30
45	Helix Stabilization Precedes Aqueous and Bilayer-Catalyzed Fiber Formation in Islet Amyloid Polypeptide. Journal of Molecular Biology, 2009, 393, 383-396.	2.0	170
46	The Flexibility of a Distant Loop Modulates Active Site Motion and Product Release in Ribonuclease A. Biochemistry, 2009, 48, 7160-7168.	1.2	91
47	Monitoring Molecular Interactions by NMR. Methods in Molecular Biology, 2009, 490, 115-134.	0.4	8
48	^1H , ^{15}N and ^{13}C resonance assignment of imidazole glycerol phosphate (IGP) synthase protein HisF from <i>Thermotoga maritima</i> . Biomolecular NMR Assignments, 2008, 2, 219-221.	0.4	12
49	Characterization of Enzyme Motions by Solution NMR Relaxation Dispersion. Accounts of Chemical Research, 2008, 41, 214-221.	7.6	155
50	The mechanism of rate-limiting motions in enzyme function. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11981-11986.	3.3	146
51	Dynamic Requirements for a Functional Protein Hinge. Journal of Molecular Biology, 2007, 368, 131-149.	2.0	77
52	Value of a Hydrogen Bond in Triosephosphate Isomerase Loop Motion. Biochemistry, 2007, 46, 6001-6010.	1.2	35
53	The effects of cosolutes on protein dynamics: The reversal of denaturant-induced protein fluctuations by trimethylamineN-oxide. Protein Science, 2007, 16, 20-29.	3.1	38
54	Enzyme Dynamics along the Reaction Coordinate: Critical Role of a Conserved Residue. Biochemistry, 2006, 45, 2636-2647.	1.2	72

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55	Faithful estimation of dynamics parameters from CPMG relaxation dispersion measurements. <i>Journal of Magnetic Resonance</i> , 2006, 180, 93-104.	1.2	78
56	Characterization of the Transition State of Functional Enzyme Dynamics. <i>Journal of the American Chemical Society</i> , 2006, 128, 7724-7725.	6.6	37
57	Crystallization and characterization of the thallium form of the <i>Oxytricha nova</i> G-quadruplex. <i>Nucleic Acids Research</i> , 2006, 34, 4506-4514.	6.5	49
58	Conservation of $\frac{1}{4}$ ms Enzyme Motions in the Apo- and Substrate-Mimicked State. <i>Journal of the American Chemical Society</i> , 2005, 127, 9167-9176.	6.6	146
59	205Tl NMR Methods for the Characterization of Monovalent Cation Binding to Nucleic Acids. <i>Journal of the American Chemical Society</i> , 2005, 127, 16723-16732.	6.6	69
60	Solution Structure and Dynamics of LuxU from <i>Vibrio harveyi</i> , a Phosphotransferase Protein Involved in Bacterial Quorum Sensing. <i>Journal of Molecular Biology</i> , 2005, 347, 297-307.	2.0	20
61	Letter to the Editor: ^1H , ^{15}N , and ^{13}C chemical shift assignments of the <i>Vibrio harveyi</i> histidine phosphotransferase protein LuxU. <i>Journal of Biomolecular NMR</i> , 2004, 29, 551-552.	1.6	1
62	Measurement of Intermediate Exchange Phenomena. , 2004, 278, 185-232.		24
63	Multiple Time Scale Backbone Dynamics of Homologous Thermophilic and Mesophilic Ribonuclease HI Enzymes. <i>Journal of Molecular Biology</i> , 2004, 339, 855-871.	2.0	76
64	Protein Dynamics from Solution NMR. <i>Cell Biochemistry and Biophysics</i> , 2003, 37, 187-212.	0.9	73
65	FAST-Modelfree: a program for rapid automated analysis of solution NMR spin-relaxation data. <i>Journal of Biomolecular NMR</i> , 2003, 26, 203-213.	1.6	194
66	Off-Resonance TROSY ($R_{1\rho}$) for Quantitation of Fast Exchange Processes in Large Proteins. <i>Journal of the American Chemical Society</i> , 2003, 125, 12064-12065.	6.6	27
67	Temperature Dependence of the Backbone Dynamics of Ribonuclease A in the Ground State and Bound to the Inhibitor 5'-Phosphothymidine (3'- γ -Pyrophosphate Adenosine 3'-Phosphate. <i>Biochemistry</i> , 2003, 42, 5279-5291.		43
68	Evidence for Flexibility in the Function of Ribonuclease A. <i>Biochemistry</i> , 2002, 41, 6072-6081.	1.2	123
69	Nuclear Magnetic Resonance Methods for Quantifying Microsecond-to-Millisecond Motions in Biological Macromolecules. <i>Methods in Enzymology</i> , 2001, 339, 204-238.	0.4	823
70	The Static Magnetic Field Dependence of Chemical Exchange Linebroadening Defines the NMR Chemical Shift Time Scale. <i>Journal of the American Chemical Society</i> , 2000, 122, 2867-2877.	6.6	316
71	A TROSY CPMG sequence for characterizing chemical exchange in large proteins. <i>Journal of Biomolecular NMR</i> , 1999, 15, 151-155.	1.6	217
72	A Relaxation-Compensated Carr-Purcell-Meiboom-Gill Sequence for Characterizing Chemical Exchange by NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 1999, 121, 2331-2332.	6.6	624