

Ryo Kitahara

List of Publications by Year in descending order

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46
papers

1,275
citations

361413

20
h-index

361022

35
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all docs

46
docs citations

46
times ranked

1040
citing authors

#	ARTICLE	IF	CITATIONS
1	Amplification of the Specific Conformational Fluctuation of Proteins by Site-Specific Mutagenesis and Hydrostatic Pressure. <i>Journal of Physical Chemistry B</i> , 2022, 126, 1868-1875.	2.6	0
2	Pressure tolerance of brine shrimp (<i>Artemia</i>). <i>High Pressure Research</i> , 2021, 41, 109-117.	1.2	0
3	Pressure and Temperature Phase Diagram for Liquid-Liquid Phase Separation of the RNA-Binding Protein Fused in Sarcoma. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6821-6829.	2.6	30
4	Pressure Effects on the Binding of 1,4-Dioxane to Amide Naphthotubes in Water. <i>Review of High Pressure Science and Technology/Koatsuryoku No Kagaku To Gijutsu</i> , 2021, 31, 90-95.	0.0	0
5	Pressure-Jump Kinetics of Liquid-Liquid Phase Separation: Comparison of Two Different Condensed Phases of the RNA-Binding Protein, Fused in Sarcoma. <i>Journal of the American Chemical Society</i> , 2021, 143, 19697-19702.	13.7	13
6	Dynamic aspects of pressure and temperature-stabilized intermediates of outer surface protein A. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 1423-1433.	2.6	1
7	Volumetric Properties for the Binding of 1,4-Dioxane to Amide Naphthotubes in Water. <i>Journal of Physical Chemistry B</i> , 2020, 124, 9175-9181.	2.6	5
8	é«~âœšăš»ăĒè»ç™1/2è³ăă«ăšă1/4ă™ă1/2±éÿj. <i>Kagaku To Seibutsu</i> , 2020, 58, 579-584.	0.0	0
9	Rational design using sequence information only produces a peptide that binds to the intrinsically disordered region of p53. <i>Scientific Reports</i> , 2019, 9, 8584.	3.3	16
10	Paramagnetic relaxation enhancement-assisted structural characterization of a partially disordered conformation of ubiquitin. <i>Protein Science</i> , 2019, 28, 1993-2003.	7.6	7
11	Pressure accelerates the circadian clock of cyanobacteria. <i>Scientific Reports</i> , 2019, 9, 12395.	3.3	11
12	How internal cavities destabilize a protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21031-21036.	7.1	44
13	Gene delivery to cone photoreceptors by subretinal injection of rAAV2/6 in the mouse retina. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 222-227.	2.1	4
14	Characterization of low-lying excited states of proteins by high-pressure NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 350-358.	2.3	29
15	Nuclear magnetic resonance-based determination of dioxygen binding sites in protein cavities. <i>Protein Science</i> , 2018, 27, 769-779.	7.6	2
16	Water-Protein Interactions Coupled with Protein Conformational Transition. <i>Biophysical Journal</i> , 2018, 115, 981-987.	0.5	4
17	Analysis of O ₂ -binding Sites in Proteins Using Gas-Pressure NMR Spectroscopy: Outer Surface Protein A. <i>Biophysical Journal</i> , 2017, 112, 1820-1828.	0.5	8
18	Interactions Controlling the Slow Dynamic Conformational Motions of Ubiquitin. <i>Molecules</i> , 2017, 22, 1414.	3.8	3

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19	Detecting O2 binding sites in protein cavities. <i>Scientific Reports</i> , 2016, 6, 20534.	3.3	18
20	Aberrant increase of NMR signal in hydrogen exchange experiments. Observation and explanation. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 1185-1188.	2.1	2
21	Zinc Ion-binding Activity of an Anti-ZnO VHH Antibody, 4F2. <i>Chemistry Letters</i> , 2015, 44, 1309-1311.	1.3	1
22	Cavity as a Source of Conformational Fluctuation and High-Energy State: High-Pressure NMR Study of a Cavity-Enlarged Mutant of T4Lysozyme. <i>Biophysical Journal</i> , 2015, 108, 133-145.	0.5	36
23	High-Pressure NMR Spectroscopy Reveals Functional Sub-states of Ubiquitin and Ubiquitin-Like Proteins. <i>Sub-Cellular Biochemistry</i> , 2015, 72, 199-214.	2.4	4
24	Is pressure-induced signal loss in NMR spectra for the Leu99Ala cavity mutant of T4 lysozyme due to unfolding?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E923-E923.	7.1	5
25	Close Identity between Alternatively Folded State N ₂ of Ubiquitin and the Conformation of the Protein Bound to the Ubiquitin-Activating Enzyme. <i>Biochemistry</i> , 2014, 53, 447-449.	2.5	19
26	Pressure-induced chemical shifts as probes for conformational fluctuations in proteins. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2013, 71, 35-58.	7.5	52
27	Exploring the folding energy landscape with pressure. <i>Archives of Biochemistry and Biophysics</i> , 2013, 531, 110-115.	3.0	69
28	Solution Structure of the Q41N Variant of Ubiquitin as a Model for the Alternatively Folded N ₂ State of Ubiquitin. <i>Biochemistry</i> , 2013, 52, 1874-1885.	2.5	26
29	Aberrant Assembly of RNA Recognition Motif 1 Links to Pathogenic Conversion of TAR DNA-binding Protein of 43 kDa (TDP-43). <i>Journal of Biological Chemistry</i> , 2013, 288, 14886-14905.	3.4	65
30	Design Strategy for High Free-Energy States of Proteins Based on High-Pressure NMR Study: Alternatively Folded Conformation of Ubiquitin. <i>Biophysical Journal</i> , 2012, 102, 25a.	0.5	0
31	A Delicate Interplay of Structure, Dynamics, and Thermodynamics for Function: A High Pressure NMR Study of Outer Surface Protein A. <i>Biophysical Journal</i> , 2012, 102, 916-926.	0.5	36
32	Structural plasticity of staphylococcal nuclease probed by perturbation with pressure and pH. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1293-1305.	2.6	28
33	Pressure-dependent ¹³ C chemical shifts in proteins: origins and applications. <i>Journal of Biomolecular NMR</i> , 2009, 44, 25-33.	2.8	13
34	Pressure-Dependent Structure Changes in Barnase on Ligand Binding Reveal Intermediate Rate Fluctuations. <i>Biophysical Journal</i> , 2009, 97, 1482-1490.	0.5	21
35	Basic Folded and Low-Populated Locally Disordered Conformers of SUMO-2 Characterized by NMR Spectroscopy at Varying Pressures. <i>Biochemistry</i> , 2008, 47, 30-39.	2.5	14
36	Evolutionally Conserved Intermediates Between Ubiquitin and NEDD8. <i>Journal of Molecular Biology</i> , 2006, 363, 395-404.	4.2	31

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37	S1c2-4 Probing energy landscape of ubiquitin-like proteins with variable-pressure NMR(S1-c2: "Protein) Tj ETQq1 1	0.784314	14
		0.1	0
38	Cold denaturation of ubiquitin at high pressure. <i>Magnetic Resonance in Chemistry</i> , 2006, 44, S108-S113.	1.9	41
39	NMR Snapshots of a Fluctuating Protein Structure: Ubiquitin at 30 barâ€“3 kbar. <i>Journal of Molecular Biology</i> , 2005, 347, 277-285.	4.2	153
40	High-pressure NMR spectroscopy for characterizing folding intermediates and denatured states of proteins. <i>Methods</i> , 2004, 34, 133-143.	3.8	81
41	High-pressure 1H NMR study of pressure-induced structural changes in the heme environments of metcyanomyoglobins. <i>Protein Science</i> , 2003, 12, 207-217.	7.6	8
42	Close identity of a pressure-stabilized intermediate with a kinetic intermediate in protein folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 3167-3172.	7.1	101
43	High Pressure NMR Reveals that Apomyoglobin is an Equilibrium Mixture from the Native to the Unfolded. <i>Journal of Molecular Biology</i> , 2002, 320, 311-319.	4.2	81
44	Equilibrium and Pressure-jump Relaxation Studies of the Conformational Transitions of P13MTCP1. <i>Journal of Molecular Biology</i> , 2002, 320, 609-628.	4.2	51
45	Two Folded Conformers of Ubiquitin Revealed by High-Pressure NMRâ€“. <i>Biochemistry</i> , 2001, 40, 13556-13563.	2.5	63
46	High Pressure NMR Reveals Active-Site Hinge Motion of Folate-Bound Escherichia coli Dihydrofolate Reductase. <i>Biochemistry</i> , 2000, 39, 12789-12795.	2.5	79