

# Munehito Arai

## List of Publications by Year in descending order

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75  
papers

3,117  
citations

201385

27  
h-index

155451

55  
g-index

78  
all docs

78  
docs citations

78  
times ranked

3161  
citing authors

#	ARTICLE	IF	CITATIONS
1	Rational design of a helical peptide inhibitor targeting c-Myb-KIX interaction. <i>Scientific Reports</i> , 2022, 12, 816.	1.6	9
2	Intron-Encoded Domain of Herstatin, An Autoinhibitor of Human Epidermal Growth Factor Receptors, Is Intrinsically Disordered. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 862910.	1.6	2
3	A comparative study of unpasteurized and pasteurized frozen whole hen eggs using size-exclusion chromatography and small-angle X-ray scattering. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
4	The Wako-Saito-Muoz-Eaton Model for Predicting Protein Folding and Dynamics. <i>Molecules</i> , 2022, 27, 4460.	1.7	5
5	Repressor Activity of SqrR, a Master Regulator of Persulfide-Responsive Genes, Is Regulated by Heme Coordination. <i>Plant and Cell Physiology</i> , 2021, 62, 100-110.	1.5	3
6	Changes in dynamic and static structures of the HIV p24 capsid protein domain caused by amino acid substitution are associated with its viral viability. <i>Protein Science</i> , 2021, 30, 2233-2245.	3.1	1
7	Biophysical Research in the Fight Against Viral Diseases. <i>Seibutsu Butsuri</i> , 2021, 61, 081-081.	0.0	0
8	Electrostatic interactions at the interface of two enzymes are essential for two-step alkane biosynthesis in cyanobacteria. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 228-237.	0.6	10
9	Determining Binding Kinetics of Intrinsically Disordered Proteins by NMR Spectroscopy. <i>Methods in Molecular Biology</i> , 2020, 2141, 663-681.	0.4	3
10	Editorial. <i>Biophysics and Physicobiology</i> , 2020, 17, 155-155.	0.5	0
11	Identification of non-conserved residues essential for improving the hydrocarbon-producing activity of cyanobacterial aldehyde-deformylating oxygenase. <i>Biotechnology for Biofuels</i> , 2019, 12, 89.	6.2	24
12	Mutational analysis of a catalytically important loop containing active site and substrate-binding site in <i>Escherichia coli</i> phytase AppA. <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 860-868.	0.6	2
13	The retrograde signaling protein GUN1 regulates tetrapyrrole biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24900-24906.	3.3	48
14	Improving hydrocarbon production by engineering cyanobacterial acyl-(acyl carrier protein) reductase. <i>Biotechnology for Biofuels</i> , 2019, 12, 291.	6.2	10
15	Production and characterization of recombinant P1 adhesin essential for adhesion, gliding, and antigenic variation in the human pathogenic bacterium, <i>Mycoplasma pneumoniae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 508, 1050-1055.	1.0	16
16	Conformational diversity in the intrinsically disordered HIV-1 Tat protein induced by zinc and pH. <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 564-569.	1.0	7
17	Unified understanding of folding and binding mechanisms of globular and intrinsically disordered proteins. <i>Biophysical Reviews</i> , 2018, 10, 163-181.	1.5	46
18	Interaction of the GntR-family transcription factor Sll1961 with thioredoxin in the cyanobacterium <i>Synechocystis</i> sp. PCC 6803. <i>Scientific Reports</i> , 2018, 8, 6666.	1.6	6

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19	Cyanobacterial Enzymes for Bioalkane Production. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1080, 119-154.	0.8	7
20	Highly Heterogeneous Nature of the Native and Unfolded States of the B Domain of Protein A Revealed by Two-Dimensional Fluorescence Lifetime Correlation Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2017, 121, 5463-5473.	1.2	20
21	Sustainable Bioenergy Production Using Cyanobacteria With Multifarious Strategies. <i>Kagaku To Seibutsu</i> , 2017, 55, 88-97.	0.0	0
22	Formation of the chaperonin complex studied by 2D NMR spectroscopy. <i>PLoS ONE</i> , 2017, 12, e0187022.	1.1	0
23	Mapping the interactions of adenoviral E1A proteins with the p160 nuclear receptor coactivator binding domain of CBP. <i>Protein Science</i> , 2016, 25, 2256-2267.	3.1	18
24	Comparison of aldehyde-producing activities of cyanobacterial acyl-(acyl carrier protein) reductases. <i>Biotechnology for Biofuels</i> , 2016, 9, 234.	6.2	19
25	Development of the Line Confocal System for the Single Molecule Tracking of Fast Folding Dynamics of Proteins. <i>Biophysical Journal</i> , 2015, 108, 50a-51a.	0.2	0
26	Two-Dimensional Fluorescence Lifetime Correlation Spectroscopy on the Folding Mechanism of B Domain of Protein A. <i>Biophysical Journal</i> , 2015, 108, 501a.	0.2	0
27	Conformational propensities of intrinsically disordered proteins influence the mechanism of binding and folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9614-9619.	3.3	222
28	Complexity of the Folding Transition of the B Domain of Protein A Revealed by the High-Speed Tracking of Single-Molecule Fluorescence Time Series. <i>Journal of Physical Chemistry B</i> , 2015, 119, 6081-6091.	1.2	18
29	Role of Cysteine Residues in the Structure, Stability, and Alkane Producing Activity of Cyanobacterial Aldehyde Deformylating Oxygenase. <i>PLoS ONE</i> , 2015, 10, e0122217.	1.1	27
30	Flexible and rigid structures in HIV-1 p17 matrix protein monitored by relaxation and amide proton exchange with NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 520-526.	1.1	6
31	2P056 Interaction of the intrinsically disordered HIV-1 Tat protein with the KIX domain of the transcriptional coactivator CBP(01C. Protein: Property,Poster,The 52nd Annual Meeting of the Tj ETQq1 1 0.7843 140rgBT /Overlock 1		
32	3P067 Toward the construction of the cyanobacterial mutants that produce high amounts of alkanes(01D. Protein: Function,Poster,The 52nd Annual Meeting of the Biophysical Society of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 217		
33	Microsecond dynamics of an unfolded protein by a line confocal tracking of single molecule fluorescence. <i>Scientific Reports</i> , 2013, 3, 2151.	1.6	29
34	Quantitative Analysis of Protein-Ligand Interactions by NMR. <i>Seibutsu Butsuri</i> , 2013, 53, 305-308.	0.0	1
35	Quantitative Analysis of Multisite Protein-Ligand Interactions by NMR: Binding of Intrinsically Disordered p53 Transactivation Subdomains with the TAZ2 Domain of CBP. <i>Journal of the American Chemical Society</i> , 2012, 134, 3792-3803.	6.6	123
36	Microsecond Subdomain Folding in Dihydrofolate Reductase. <i>Journal of Molecular Biology</i> , 2011, 410, 329-342.	2.0	33

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37	Leu628 of the KIX domain of CBP is a key residue for the interaction with the MLL transactivation domain. <i>FEBS Letters</i> , 2010, 584, 4500-4504.	1.3	32
38	3P040 Mapping the Interactions of the Intrinsically Disordered p53 Transactivation Subdomains with the TAZ2 Domain of CBP by NMR(Protein: Structure & Function,The 48th Annual Meeting of the) Tj ETQq0 0 0 rgBT0,0verlock10 Tf 50 6		
39	Graded enhancement of p53 binding to CREB-binding protein (CBP) by multisite phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19290-19295.	3.3	188
40	Probing the roles of conserved arginine-44 of Escherichia coli dihydrofolate reductase in its function and stability by systematic sequence perturbation analysis. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 1703-1707.	1.0	10
41	Cooperative regulation of p53 by modulation of ternary complex formation with CBP/p300 and HDM2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6591-6596.	3.3	197
42	Mapping the Interactions of the p53 Transactivation Domain with the KIX Domain of CBP. <i>Biochemistry</i> , 2009, 48, 2115-2124.	1.2	109
43	Asymmetry of the GroEL-GroES Complex under Physiological Conditions as Revealed by Small-Angle X-Ray Scattering. <i>Biophysical Journal</i> , 2008, 94, 1392-1402.	0.2	18
44	Stabilization of Hyperactive Dihydrofolate Reductase by Cyanocysteine-mediated Backbone Cyclization. <i>Journal of Biological Chemistry</i> , 2007, 282, 9420-9429.	1.6	16
45	Microsecond Hydrophobic Collapse in the Folding of Escherichia coli Dihydrofolate Reductase, an $\alpha/\beta$ -Type Protein. <i>Journal of Molecular Biology</i> , 2007, 368, 219-229.	2.0	75
46	The allosteric transition of the chaperonin groel from escherichia coli as studied by solution X-ray scattering. <i>Macromolecular Research</i> , 2006, 14, 166-172.	1.0	1
47	Peptide fragment studies on the folding elements of dihydrofolate reductase from Escherichia coli. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 399-410.	1.5	3
48	Characterization of Kinetic Folding Intermediates of Recombinant Canine Milk Lysozyme by Stopped-Flow Circular Dichroism. <i>Biochemistry</i> , 2005, 44, 6685-6692.	1.2	17
49	Probing the Interactions between the Folding Elements Early in the Folding of Escherichia coli Dihydrofolate Reductase by Systematic Sequence Perturbation Analysis. <i>Journal of Molecular Biology</i> , 2005, 347, 337-353.	2.0	29
50	Helical and Expanded Conformation of Equine $\beta$ -Lactoglobulin in the Cold-denatured State. <i>Journal of Molecular Biology</i> , 2005, 350, 338-348.	2.0	24
51	Oligomeric Hsp33 with Enhanced Chaperone Activity. <i>Journal of Biological Chemistry</i> , 2004, 279, 55760-55769.	1.6	27
52	Unification of the Folding Mechanisms of Non-two-state and Two-state Proteins. <i>Journal of Molecular Biology</i> , 2004, 339, 951-965.	2.0	81
53	Localized Nature of the Transition-state Structure in Goat $\beta$ -Lactalbumin Folding. <i>Journal of Molecular Biology</i> , 2004, 341, 589-604.	2.0	27
54	Denaturation and reassembly of chaperonin GroEL studied by solution X-ray scattering. <i>Protein Science</i> , 2003, 12, 672-680.	3.1	20

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55	Equilibrium and Kinetics of the Allosteric Transition of GroEL Studied by Solution X-ray Scattering and Fluorescence Spectroscopy. <i>Journal of Molecular Biology</i> , 2003, 327, 183-191.	2.0	28
56	Testing the Relationship Between Foldability and the Early Folding Events of Dihydrofolate Reductase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2003, 328, 273-288.	2.0	30
57	The Allosteric Transition of GroEL Induced by Metal Fluoride-ADP Complexes. <i>Journal of Molecular Biology</i> , 2003, 329, 121-134.	2.0	19
58	Effects of the Difference in the Unfolded-state Ensemble on the Folding of <i>Escherichia coli</i> Dihydrofolate Reductase. <i>Journal of Molecular Biology</i> , 2003, 329, 779-791.	2.0	26
59	Reversible and Fast Association Equilibria of a Molecular Chaperone, gp57A, of Bacteriophage T4. <i>Biophysical Journal</i> , 2003, 85, 2606-2618.	0.2	32
60	Folding mechanism of canine milk lysozyme studied by circular dichroism and fluorescence spectroscopy. <i>Spectroscopy</i> , 2003, 17, 183-193.	0.8	7
61	Fast Compaction of $\beta$ -Lactalbumin During Folding Studied by Stopped-flow X-ray Scattering. <i>Journal of Molecular Biology</i> , 2002, 321, 121-132.	2.0	100
62	The Use of the Time-Resolved X-Ray Solution Scattering for Studies of Globular Proteins. <i>Spectroscopy</i> , 2002, 16, 127-138.	0.8	3
63	Refolding of $\beta$ -lactoglobulin studied by stopped-flow circular dichroism at subzero temperatures. <i>FEBS Letters</i> , 2001, 507, 299-302.	1.3	15
64	Folding-unfolding of goat $\beta$ -lactalbumin studied by stopped-flow circular dichroism and molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 49-65.	1.5	18
65	Is folding of $\beta$ -lactoglobulin non-hierarchical? intermediate with native-like $\beta$ -sheet and non-native $\beta$ -helix 1 Edited by C. R. Matthews. <i>Journal of Molecular Biology</i> , 2000, 296, 1039-1051.	2.0	95
66	Folding of Green Fluorescent Protein and the Cycle3 Mutant. <i>Biochemistry</i> , 2000, 39, 12025-12032.	1.2	183
67	Role of the molten globule state in protein folding. <i>Advances in Protein Chemistry</i> , 2000, 53, 209-282.	4.4	404
68	Equilibrium and Kinetic Studies on Folding of the Authentic and Recombinant Forms of Human $\beta$ -Lactalbumin by Circular Dichroism Spectroscopy. <i>Biochemistry</i> , 2000, 39, 15643-15651.	1.2	41
69	Effect of an Alternative Disulfide Bond on the Structure, Stability, and Folding of Human Lysozyme. <i>Biochemistry</i> , 2000, 39, 3472-3479.	1.2	14
70	Folding~Unfolding Equilibrium and Kinetics of Equine $\beta$ -Lactoglobulin:~Equivalence between the Equilibrium Molten Globule State and a Burst-Phase Folding Intermediate. <i>Biochemistry</i> , 1999, 38, 4455-4463.	1.2	64
71	Effect of the Extra N-terminal Methionine Residue on the Stability and Folding of Recombinant $\beta$ -Lactalbumin Expressed in <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1999, 285, 1179-1194.	2.0	90
72	Chaperonin-affected refolding of $\beta$ -lactalbumin: effects of nucleotides and the co-chaperonin GroES. <i>Journal of Molecular Biology</i> , 1999, 293, 125-137.	2.0	28

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73	Kinetic refolding of $\hat{1}^2$ -lactoglobulin. Studies by synchrotron X-ray scattering, and circular dichroism, absorption and fluorescence spectroscopy 1 Edited by P. E. Wright. Journal of Molecular Biology, 1998, 275, 149-162.	2.0	114
74	Equilibrium and kinetics of the folding of equine lysozyme studied by circular dichroism spectroscopy. Journal of Molecular Biology, 1998, 283, 265-277.	2.0	64
75	Rapid formation of a molten globule intermediate in refolding of $\hat{1}^{\pm}$ -lactalbumin. Folding & Design, 1996, 1, 275-287.	4.5	146