

Mikio Kataoka

List of Publications by Year in descending order

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130
papers

3,313
citations

156536

32
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162838

57
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132
docs citations

132
times ranked

3038
citing authors

#	ARTICLE	IF	CITATIONS
1	Expanding horizons of biosciences by light-control. <i>Biophysics and Physicobiology</i> , 2021, 18, 13-15.	0.5	0
2	Skeletal Structure of the Chromophore of Photoactive Yellow Protein in the Excited State Investigated by Ultraviolet Femtosecond Stimulated Raman Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2021, 125, 6154-6161.	1.2	5
3	Regulation of Photocycle Kinetics of Photoactive Yellow Protein by Modulating Flexibility of the β -Turn. <i>Journal of Physical Chemistry B</i> , 2020, 124, 1452-1459.	1.2	0
4	Biophysical Society of Japan, 45 years ago. <i>Biophysical Reviews</i> , 2020, 12, 207-208.	1.5	3
5	Rigidity of protein structure revealed by incoherent neutron scattering. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129536.	1.1	6
6	Spectroscopic and structural characteristics of a dual-light sensor protein, PYP-phytochrome related protein. <i>Biophysics and Physicobiology</i> , 2020, 17, 103-112.	0.5	1
7	Universality and Structural Implications of the Boson Peak in Proteins. <i>Biophysical Journal</i> , 2019, 117, 229-238.	0.2	3
8	Fifth-order time-domain Raman spectroscopy of photoactive yellow protein for visualizing vibrational coupling in its excited state. <i>Science Advances</i> , 2019, 5, eaau4490.	4.7	42
9	Mechanism of the light-driven proton pump of bacteriorhodopsin based on the consistency principle. <i>Biophysics and Physicobiology</i> , 2019, 16, 274-279.	0.5	5
10	How can we derive hydration water dynamics with incoherent neutron scattering and molecular dynamics simulation?. <i>Biophysics and Physicobiology</i> , 2019, 16, 213-219.	0.5	8
11	Statistical description of the denatured structure of a single protein, staphylococcal nuclease, by FRET analysis. <i>Biophysical Reviews</i> , 2018, 10, 145-152.	1.5	2
12	Probing the early stages of photoreception in photoactive yellow protein with ultrafast time-domain Raman spectroscopy. <i>Nature Chemistry</i> , 2017, 9, 660-666.	6.6	90
13	Active-Site pKa Determination for Photoactive Yellow Protein Rationalizes Slow Ground-State Recovery. <i>Biophysical Journal</i> , 2017, 112, 2109-2116.	0.2	5
14	Neutron crystallography of photoactive yellow protein reveals unusual protonation state of Arg52 in the crystal. <i>Scientific Reports</i> , 2017, 7, 9361.	1.6	19
15	VIPP1 Has a Disordered C-Terminal Tail Necessary for Protecting Photosynthetic Membranes against Stress. <i>Plant Physiology</i> , 2016, 171, 1983-1995.	2.3	50
16	Vibrational analysis on the revised potential energy curve of the low-barrier hydrogen bond in photoactive yellow protein. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 16-19.	1.9	6
17	Structure, Dynamics, and Function of Staphylococcal Nuclease. , 2016, , 151-161.		1
18	Watching a Signaling Protein Function in Real Time via Picosecond Time-Resolved Laue Crystallography. , 2016, , 65-85.		0

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19	Domain-Swapped Dimer of <i>Pseudomonas aeruginosa</i> Cytochrome c551: Structural Insights into Domain Swapping of Cytochrome c Family Proteins. PLoS ONE, 2015, 10, e0123653.	1.1	19
20	Time-Resolved Observation of Chiral-Index-Selective Wrapping on Single-Walled Carbon Nanotube with Non-Aromatic Polysilane. Journal of the American Chemical Society, 2013, 135, 2374-2383.	6.6	22
21	2P129 Translation diffusion dynamics of protein hydration water and its dynamical coupling with protein dynamics(07. Water & Hydration & Electrolyte,Poster). Seibutsu Butsuri, 2013, 53, S180.	0.0	0
22	2P253 Excited State Proton Transfer of Fluorescent Photoactive Yellow Protein Reconstituted with Hydroxycoumarin(18A. Photobiology: Vision & Photoreception,Poster). Seibutsu Butsuri, 2013, 53, S200.	0.0	0
23	3P019 The role of the flexible loop in Staphylococcal nuclease on its catalytic activity(01A. Protein:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.0	0
24	Structural Basis of β -Catenin Recognition by EspB from Enterohaemorrhagic <i>E. coli</i> Based on Hybrid Strategy Using Low-Resolution Structural and Protein Dissection. PLoS ONE, 2013, 8, e71618.	1.1	3
25	2P248 Analysis of interaction sites on the Photoactive Yellow Protein of <i>Rhodobacter capsulatus</i> (18A.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.0	0
26	2P055 Domain-Swapped Oligomerization and Molten Globule State of Cytochrome c(01C. Protein:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.0	0
27	Watching a signaling protein function in real time via 100-ps time-resolved Laue crystallography. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 19256-19261.	3.3	177
28	1E1534 Kinetics of hydrogen-bonding of protein hydration water and its dynamical coupling with protein dynamics(Proteins: Property I,Oral Presentation,The 50th Annual Meeting of the Biophysical) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.0	0
29	1PT124 The role of the flexible loop in Staphylococcal nuclease on its catalytic activity(The 50th) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.0	0
30	Development of Neutron Biophysics. Hamon, 2012, 22, 132-138.	0.0	0
31	1H1536 Classification of function element of dihydrofolate reductase by the systematic alanine insertion(Protein: Property 2,The 49th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2011, 51, S50.	0.0	0
32	2SJ-03 Cytochrome c polymerization by domain swapping(2SJ New developments in protein complex) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.0	0
33	Systematic alanine insertion reveals the essential regions that encode structure formation and activity of dihydrofolate reductase. Biophysics (Nagoya-shi, Japan), 2011, 7, 1-10.	0.4	4
34	Neutrons in Biological Research. Hamon, 2011, 21, 243-246.	0.0	0
35	Percolation of Hydration Water as a Control of Protein Dynamics. Journal of the Physical Society of Japan, 2010, 79, 083801.	0.7	40
36	1P268 Substitution effects of basic residues in the photoactive yellow protein of <i>Rhodobacter capsulatus</i> .(Photobiology:Vision & Photoreception,The 48th Annual Meeting of the Biophysical) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.0	0

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37	3P038 Intrinsically Less-ordered Bacterial Effectors : A Case of EspB from Enterohaemorrhagic Escherichia coli(Protein: Structure & Function,The 48th Annual Meeting of the Biophysical Society of) Tj ETQq1 1 0.784314 rgBT /Overlock	0.0	0
38	2P064 Classification of the functional element of dihydrofolate reductase (DHFR) by the systematic alanine insertion(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S93.	0.0	0
39	2P244 Effects of trehalose on the structures and dynamics of lipid membranes(The 48th Annual) Tj ETQq1 1 0.784314 rgBT /Overlock	0.0	0
40	3P023 Cytochrome c polymerization by successive domain swapping at the C-terminal helix(Protein:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf S149.	0.0	0
41	3P063 The investigation of the relationship between non-local interaction and the effect of single alanine insertion in staphylococcal nuclease(Protein: Property,The 48th Annual Meeting of the) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.0	0
42	1P017 Urea denaturation of staphylococcal nuclease monitored by tryptophan-cysteine distance(Protein:Structure,The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S21-S22.	0.0	0
43	2P012 Solution structural analysis of Drosophila GGA(The 48th Annual Meeting of the Biophysical) Tj ETQq1 1 0.784314 rgBT /Overlock	0.0	0
44	Effect of conformational states on protein dynamical transition. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2010, 1804, 27-33.	1.1	25
45	Nonlocal Interactions Are Responsible for Tertiary Structure Formation in Staphylococcal Nuclease. Biophysical Journal, 2010, 98, 678-686.	0.2	7
46	Self-Assembly and Enhanced Magnetic Properties of Three-Dimensional Superlattice Structures Composed of Cube-Shaped EuS Nanocrystals. Chemistry of Materials, 2010, 22, 1776-1781.	3.2	40
47	Introduction to the Special Articles "Japan-Originated Biophysics". Seibutsu Butsuri, 2010, 50, 004-005.	0.0	0
48	Low-barrier hydrogen bond in photoactive yellow protein. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 440-444.	3.3	191
49	3P-049 Structural Characterization of the Intrinsically Disordered Mutants of Staphylococcal Nuclease by Electron Paramagnetic Resonance Spectroscopy(Protein:Property,The 47th Annual) Tj ETQq1 1 0.784314 rgBT /Overlock	0.0	0
50	Effect of hydration on protein dynamics by incoherent neutron inelastic scattering. Hamon, 2009, 19, 91-94.	0.0	0
51	Mechanism of induced folding: Both folding before binding and binding before folding can be realized in staphylococcal nuclease mutants. Proteins: Structure, Function and Bioinformatics, 2008, 72, 837-847.	1.5	48
52	Role of the N-terminal Region in the Function of the Photosynthetic Bacterium Transcription Regulator PpsR<sup></sup>. Photochemistry and Photobiology, 2008, 84, 839-844.	1.3	4
53	The Photoreaction of the Photoactive Yellow Protein Domain in the Light Sensor Histidine Kinase Ppr is Influenced by the C-terminal Domains<sup></sup>. Photochemistry and Photobiology, 2008, 84, 895-902.	1.3	5
54	Introduction to the Symposium "Print on Photoreceptors and Signal Transduction in Honor of Professor Fumio Tokunaga. Photochemistry and Photobiology, 2008, 84, 821-822.	1.3	0

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55	Hydration Effect on Low-Frequency Protein Dynamics Observed in Simulated Neutron Scattering Spectra. Biophysical Journal, 2008, 94, 4435-4443.	0.2	27
56	Diverse Roles of Glycine Residues Conserved in Photoactive Yellow Proteins. Biophysical Journal, 2008, 94, 3620-3628.	0.2	10
57	3P-116 Structure and dynamics of the protein hydration water at the protein dynamical transition(The) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222 T	0.0	0
58	1P-263 Role of the N-terminal cap in the Rc-PYP(The 46th Annual Meeting of the Biophysical Society of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 T	0.0	0
59	2P-279 Identification of the structural and functional element of Photoactive yellow protein(The) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222 T	0.0	0
60	1P-095 The effect of alanine insertion mutation for folding kinetics(The 46th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 T	0.0	0
61	1P-252 Spectral characterization of the complex form of the photoactive yellow protein of Rhodobacter capsulatus(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S60.	0.0	0
62	2P-257 The origin of conformational changes of the PYP photoreaction monitored by diffusion change(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S114-S115.	0.0	0
63	1P-013 The role of the flexible loop in staphylococcal nuclease on its catalytic activity(The 46th) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222 T	0.0	0
64	1P-089 Role of Lucine 108 for the folding of Staphylococcal Nuclease(The 46th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 T	0.0	0
65	1P-260 The Photoreaction of the PYP Domain in the Light Sensor Histidine Kinase Ppr is Influenced by the C-terminal Domains(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S62.	0.0	0
66	3P-252 Intramolecular interaction for light-responsible regulation in AppA(The 46th Annual Meeting) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 T	0.0	0
67	Instrumental Design of Indirect Geometry Crystal Analyzer Spectrometer; DNA at J-PARC. Nihon Kessho Gakkaishi, 2008, 50, 46-50.	0.0	0
68	1P349 Instrumentation of an in-house protein solution x-ray scattering diffractometer(New) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 222 T	0.0	0
69	3P042 Elucidation of the information encoded in the regions connecting folding elements and/or active site of dihydrofolate reductase(Photobiology-vision and photoreception,Poster) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222 T	0.0	0
70	3P252 Characterization of the photocycle of photoactive yellow protein like domain from Rhodospirillum centenum(Photobiology- vision and photoreception,Poster Presentations). Seibutsu Butsuri, 2007, 47, S266.	0.0	0
71	2P090 The effect of alanine insertion mutation for folding process(Proteins-stability, folding, and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 222 T	0.0	0
72	Characterization of the Solution Structure of the M Intermediate of Photoactive Yellow Protein Using High-Angle Solution X-Ray Scattering. Biophysical Journal, 2007, 92, 3633-3642.	0.2	20

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73	3P256 identification of spectral species in the Photoactive Yellow Protein of Rhodobacter capsulatus.(Photobiology- vision and photoreception,Poster Presentations). Seibutsu Butsuri, 2007, 47, S267.	0.0	0
74	Attempt to simplify the amino-acid sequence of photoactive yellow protein with a set of simple rules. Proteins: Structure, Function and Bioinformatics, 2007, 67, 821-833.	1.5	6
75	Non-Gaussian behavior of elastic incoherent neutron scattering profiles of proteins studied by molecular dynamics simulation. Physical Review E, 2007, 75, 041912.	0.8	19
76	Preparation of Large Crystals of Photoactive Yellow Protein for Neutron Diffraction and High Resolution Crystal Structure Analysis. Photochemistry and Photobiology, 2007, 83, 336-338.	1.3	10
77	Foreword to a Mini-Assembly of the Measurements of Protein Dynamics. Seibutsu Butsuri, 2007, 47, 286-287.	0.0	0
78	The Crystal Structure of the R52Q Mutant Demonstrates a Role for R52 in Chromophore pKa Regulation in Photoactive Yellow Protein,. Biochemistry, 2006, 45, 3542-3547.	1.2	23
79	1P146 Attempt to understand the information encoded in the amino acid sequence of photoactive yellow protein by the simplification of sequence(4. Protein engineering,Poster) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 497 Td (Seibutsu Butsuri, 2007, 47, S267)	0.0	0
80	S3d2-4 Structural characterization of an active state using the wide-angle solution x-ray scattering(S3-d2: "Structural approach to protein dynamics using solution) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 457 Td (scattering",Synthetische Biologie, 2017, 1, 1-12)	0.0	0
81	1P110 Characterization of conformational rearrangement during the folding process of Staphylococcal nuclease(3. Protein folding and misfolding (I),Poster Session,Abstract,Meeting) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 337 Td (Seibutsu Butsuri, 2006, 46, S314)	0.0	0
82	2P076 Structural Analysis of GGA (VHS-GAT)-Arf Complex Using SAXS Measurement(30. Protein) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 346 Td (Seibutsu Butsuri, 2006, 46, S314)	0.0	0
83	2P092 Elucidation of the unfolding-state and the folding process of the disulfide-bond introduced mutant of Staphylococcal nuclease(31. Protein folding and misfolding (II),Poster) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 337 Td (Seibutsu Butsuri, 2006, 46, S314)	0.0	0
84	2P342 The Photocycle of Met100Ala Mutant of Photoactive Yellow Protein Studied by Low-Temperature Spectroscopy(42. Sensory signal transduction,Poster Session,Abstract,Meeting Program of EABS & amp;) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 337 Td (Seibutsu Butsuri, 2006, 46, S314)	0.0	0
85	2P343 Isolation of Photoactive Yellow Protein associated protein from Rhodobacter capsulatus(42.) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 337 Td (Seibutsu Butsuri, 2006, 46, S381)	0.0	0
86	1P111 Extraction of the Essential Regions of the Dihydrofolate Reductase Sequence by Alanine Insertion Perturbation Analysis(3. Protein folding and misfolding (I),Poster Session,Abstract,Meeting) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 337 Td (Seibutsu Butsuri, 2006, 46, S314)	0.0	0
87	2P339 Neutron diffraction and high resolution X-ray crystal structure analysis of photoactive yellow protein(42. Sensory signal transduction,Poster Session,Abstract,Meeting Program of EABS & amp; BSJ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 337 Td (Seibutsu Butsuri, 2006, 46, S314)	0.0	0
88	Dynamical heterogeneity of protein dynamics studied by elastic incoherent neutron scattering and molecular simulations. Materials Science & Engineering A: Structural Materials: Properties, Microstructure and Processing, 2006, 442, 356-360.	2.6	5
89	Hydration-coupled protein boson peak measured by incoherent neutron scattering. Physica B: Condensed Matter, 2006, 385-386, 871-873.	1.3	12
90	pH-dependent Equilibrium between Long Lived Near-UV Intermediates of Photoactive Yellow Protein. Journal of Biological Chemistry, 2006, 281, 4318-4325.	1.6	29

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91	Protein Dynamical Heterogeneity Derived from Neutron Incoherent Elastic Scattering. Journal of the Physical Society of Japan, 2004, 73, 491-495.	0.7	35
92	Molecular Mechanism Of Light-Driven Proton Pump Of Bacteriorhodopsin. AIP Conference Proceedings, 2004, , .	0.3	0
93	Elucidation of information encoded in tryptophan 140 of staphylococcal nuclease. Proteins: Structure, Function and Bioinformatics, 2004, 58, 271-277.	1.5	19
94	Direct observation of the pH-dependent equilibrium between L-like and M intermediates of photoactive yellow protein. FEBS Letters, 2004, 577, 75-80.	1.3	19
95	Time and Frequency Domain Investigations on Ultrafast Photoreaction Dynamics of Photoactive Yellow Protein (PYP). The Review of Laser Engineering, 2004, 32, 114-120.	0.0	0
96	Role of an N-Terminal Loop in the Secondary Structural Change of Photoactive Yellow Protein. Biochemistry, 2003, 42, 13893-13900.	1.2	58
97	Ultrafast photoreactions in protein nanospaces as revealed by fs fluorescence dynamics measurements on photoactive yellow protein and related systemsDedicated to Professor Dr Z. R. Grabowski and Professor Dr J. Wirz on the occasions of their 75th and 60th birthdays.. Physical Chemistry Chemical Physics, 2003, 5, 2454-2460.	1.3	57
98	Effect of Organic Anions on the Photoreaction of Photoactive Yellow Protein. Journal of Biochemistry, 2002, 132, 257-263.	0.9	15
99	Light-Induced Global Conformational Change of Photoactive Yellow Protein in Solution. Biochemistry, 2002, 41, 13595-13601.	1.2	66
100	Role of C-terminal region ofStaphylococcal nuclease for foldability, stability, and activity. Proteins: Structure, Function and Bioinformatics, 2002, 49, 255-265.	1.5	30
101	Mechanistic Pathways for the Photoisomerization Reaction of the Anchored, Tethered Chromophore of the Photoactive Yellow Protein and its Mutants. Photochemistry and Photobiology, 2002, 76, 584-589.	1.3	0
102	The Progress and Problem of X-ray Crystallography of Photocycle Intermediate of Photoactive Yellow Protein.. Seibutsu Butsuri, 2002, 42, 162-167.	0.0	1
103	Primary Photoreaction of Photoactive Yellow Protein Studied by Subpicosecond Nanosecond Spectroscopy. Biochemistry, 2001, 40, 6047-6052.	1.2	78
104	Spectroscopic Characterization of the Photocycle Intermediates of Photoactive Yellow Protein. Biochemistry, 2001, 40, 14336-14343.	1.2	26
105	Light Induces Destabilization of Photoactive Yellow Protein. Biochemistry, 2001, 40, 2854-2859.	1.2	37
106	Roles of Amino Acid Residues near the Chromophore of Photoactive Yellow Protein. Biochemistry, 2001, 40, 4679-4685.	1.2	54
107	Low-Temperature Fourier Transform Infrared Spectroscopy of Photoactive Yellow Protein. Biochemistry, 2001, 40, 8997-9004.	1.2	73
108	Report of the Japan-France Joint Seminar on "Protein Dynamics and Its Relation to Protein Function". Seibutsu Butsuri, 2001, 41, 318-320.	0.0	0

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109	Evidence concerning rate-limiting steps in protein folding from the effects of trifluoroethanol. <i>Nature Structural Biology</i> , 2000, 7, 58-61.	9.7	67
110	Observation of RecA protein monomer by small angle X-ray scattering with synchrotron radiation. <i>FEBS Letters</i> , 2000, 482, 159-162.	1.3	1
111	Temperature-Dependent Volume Change of the Initial Step of the Photoreaction of Photoactive Yellow Protein (PYP) Studied by Transient Grating. <i>Journal of the American Chemical Society</i> , 2000, 122, 8524-8528.	6.6	43
112	Light-Induced Conformational Changes of Rhodopsin Probed by Fluorescent Alexa594 Immobilized on the Cytoplasmic Surface. <i>Biochemistry</i> , 2000, 39, 15225-15233.	1.2	42
113	The compact and expanded denatured conformations of apomyoglobin in the methanol-water solvent. <i>Protein Science</i> , 1999, 8, 873-882.	3.1	52
114	Characterization of soluble artificial proteins with random sequences. <i>FEBS Letters</i> , 1998, 421, 147-151.	1.3	36
115	Evidence for Proton Transfer from Glu-46 to the Chromophore during the Photocycle of Photoactive Yellow Protein. <i>Journal of Biological Chemistry</i> , 1997, 272, 12905-12908.	1.6	88
116	High-Resolution Vibrational Inelastic Neutron Scattering: A New Spectroscopic Tool for Globular Proteins. <i>Journal of the American Chemical Society</i> , 1997, 119, 9268-9273.	6.6	49
117	Trifluoroethanol-induced conformational transition of hen egg-white lysozyme studied by small-angle X-ray scattering. <i>FEBS Letters</i> , 1997, 416, 72-76.	1.3	62
118	X-Ray Diffraction Studies of Bacteriorhodopsin. Determination of the Positions of Mercury Label at Several Engineered Cysteine Residues. <i>Photochemistry and Photobiology</i> , 1997, 66, 768-773.	1.3	9
119	Structural characterization of the molten globule of β -lactalbumin by solution X-ray scattering. <i>Protein Science</i> , 1997, 6, 422-430.	3.1	154
120	Photoreaction Cycle of Photoactive Yellow Protein from <i>Ectothiorhodospira halophila</i> Studied by Low-Temperature Spectroscopy. <i>Biochemistry</i> , 1996, 35, 14047-14053.	1.2	132
121	X-ray solution scattering studies of protein folding. <i>Folding & Design</i> , 1996, 1, R107-R114.	4.5	90
122	The linker of calmodulin lacking Glu84 is elongated in solution, although it is bent in the crystal. , 1996, 25, 335-341.		8
123	Neutrons in structural biology.. <i>Seibutsu Butsuri</i> , 1996, 36, 226-230.	0.0	1
124	Structural Characterization of the Molten Globule and Native States of Apomyoglobin by Solution X-ray Scattering. <i>Journal of Molecular Biology</i> , 1995, 249, 215-228.	2.0	223
125	Reconstitution photoactive yellow protein from apoprotein and p-coumaric acid derivatives. <i>FEBS Letters</i> , 1995, 374, 157-160.	1.3	121
126	X-ray solution scattering and structures of proteins in solution.. <i>Seibutsu Butsuri</i> , 1995, 35, 239-241.	0.0	0

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127	Molten Globule of Cytochrome c Studied by Small Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 1993, 229, 591-596.	2.0	239
128	Mutations can cause large changes in the conformation of a denatured protein. <i>Biochemistry</i> , 1993, 32, 10359-10370.	1.2	114
129	Aggregation of bovine serum albumin upon cleavage of its disulfide bonds, studied by the time-resolved small-angle x-ray scattering technique with synchrotron radiation. <i>Biophysical Chemistry</i> , 1985, 23, 115-124.	1.5	199
130	Structural order in chromatophore membranes of <i>Rhodospirillum rubrum</i> . <i>Nature</i> , 1976, 262, 809-810.	13.7	23