Takahisa Yamato

List of Publications by Year
in descending order

49	1,017	430874	434195
papers	citations	18 h-index	31 g-index

52	52	52	856
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Computational Study on the Thermal Conductivity of a Protein. Journal of Physical Chemistry B, 2022, 126, 3029-3036.	2.6	6
2	Variation of Energy Transfer Rates across Proteinâ€“Water Contacts with Equilibrium Structural Fluctuations of a Homodimeric Hemoglobin. Journal of Physical Chemistry B, 2020, 124, 1148-1159.	2.6	18
3	Energy Transfer across Nonpolar and Polar Contacts in Proteins: Role of Contact Fluctuations. Journal of Physical Chemistry B, 2020, 124, 9852-9861.	2.6	13
4	Structure, dynamics, and energy flow that govern Heme protein functions: theory and experiments. Session 3SBA at the 57th BSJ Annual Meeting. Biophysical Reviews, 2020, 12, 291-292.	3.2	1
5	Recent developments in the computational study of protein structural and vibrational energy dynamics. Biophysical Reviews, 2020, 12, 317-322.	3.2	14
6	Energy Transport Network in Proteins. Seibutsu Butsuri, 2020, 60, 094-097.	0.1	0
7	Normal mode analysis and beyond. Biophysics and Physicobiology, 2019, 16, 322-327.	1.0	11
8	Energy Exchange Network Model Demonstrates Protein Allosteric Transition: An Application to an Oxygen Sensor Protein. Journal of Physical Chemistry B, 2019, 123, 768-775.	2.6	19
9	Characterization of mechanical unfolding intermediates of membrane proteins by coarse grained molecular dynamics simulation. Chemical Physics Letters, 2018, 691, 276-282.	2.6	4
10	Scaling of Rates of Vibrational Energy Transfer in Proteins with Equilibrium Dynamics and Entropy. Journal of Physical Chemistry B, 2018, 122, 9331-9339.	2.6	27
11	Electron Transfer Pathways of Cyclobutane Pyrimidine Dimer Photolyase Revisited. Journal of Physical Chemistry B, 2018, 122, 6912-6921.	2.6	9
12	Forced Unfolding Mechanism of Bacteriorhodopsin as Revealed by Coarse-Grained Molecular Dynamics. Biophysical Journal, 2016, 111, 2086-2098.	0.5	13
13	Energy exchange network of inter-residue interactions within a thermally fluctuating protein molecule: A computational study. Journal of Computational Chemistry, 2015, 36, 1709-1718.	3.3	39
14	Computational study on the roles of amino acid residues in the active site formation mechanism of blue-light photoreceptors. Chemical Physics Letters, 2015, 633, 247-251.	2.6	5
15	Atomic stress tensor analysis of proteins. Chemical Physics Letters, 2012, 539-540, 144-150.	2.6	14
16	Ligand migration in myoglobin: A combined study of computer simulation and x-ray crystallography. Journal of Chemical Physics, 2012, 136, 165101.	3.0	7
17	Nonneutral evolution of volume fluctuations in lysozymes revealed by normal-mode analysis of compressibility. Biophysical Chemistry, 2012, 161, 39-45.	2.8	6
18	Proteins at Work: Computational Biopolymer Science of Energy, Electron, Proton Transfer and Ligand Migration. Kobunshi Ronbunshu, 2010, 67, 179-186.	0.2	0

#	Article	IF	Citations
19	Molecular mechanism of long-range synergetic color tuning between multiple amino acid residues in conger rhodopsin. Biophysics (Nagoya-shi, Japan), 2010, 6, 67-78.	0.4	15
20	Visualizing breathing motion of internal cavities in concert with ligand migration in myoglobin. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 2612-2616.	7.1	110
21	Theoretical modeling of the Oâ€intermediate structure of bacteriorhodopsin. Proteins: Structure, Function and Bioinformatics, 2009, 75, 53-61.	2.6	5
22	Discrimination of Class I Cyclobutane Pyrimidine Dimer Photolyase from Blue Light Photoreceptors by Single Methionine Residue. Biophysical Journal, 2008, 94, 2194-2203.	0.5	23
23	Stress tensor analysis of the protein quake of photoactive yellow protein. Physical Chemistry Chemical Physics, 2008, 10, 1400-1405.	2.8	13
24	Modulation of the Absorption Maximum of Rhodopsin by Amino Acids in the C-terminusâ€. Photochemistry and Photobiology, 2007, 83, 236-241.	2.5	17
25	Theoretical prediction of optical absorption maxima for photosensory receptor mutants. Chemical Physics Letters, 2006, 430, 386-390.	2.6	10
26	Energy transfer pathways relevant for long-range intramolecular signaling of photosensory protein revealed by microscopic energy conductivity analysis. Chemical Physics Letters, 2006, 432, 533-537.	2.6	63
27	Interference, Fluctuation, and Alternation of Electron Tunneling in Protein Media. 2. Non-Condon Theory for the Energy Gap Dependence of Electron Transfer Rate. Journal of Physical Chemistry B, 2005, 109, 15621-15635.	2.6	29
28	Interference, Fluctuation, and Alternation of Electron Tunneling in Protein Media. 1. Two Tunneling Routes in Photosynthetic Reaction Center Alternate Due to Thermal Fluctuation of Protein Conformation. Journal of Physical Chemistry B, 2005, 109, 1978-1987.	2.6	33
29	Role of protein in the primary step of the photoreaction of yellow protein. Proteins: Structure, Function and Bioinformatics, 2004, 55, 1063-1069.	2.6	37
30	Direct measure of functional importance visualized atom-by-atom for photoactive yellow protein: Application to photoisomerization reaction. Proteins: Structure, Function and Bioinformatics, 2004, 55, 1070-1077.	2.6	16
31	Torsion Potential Works in Rhodopsin^{Â¶}. Photochemistry and Photobiology, 2004, 79, 476-486.	2.5	4
32	Destructive Interference in the Electron Tunneling through Protein Media. Journal of Physical Chemistry B, 2002, 106, 11356-11366.	2.6	47
33	On the Anomaly of the Tunneling Matrix Element in Long-Range Electron Transfer. Journal of Physical Chemistry B, 2002, 106, 5068-5074.	2.6	26
34	A computational study on the stability of the protonated Schiff base of retinal in rhodopsin. Chemical Physics Letters, 2002, 366, 670-675.	2.6	23
35	Worm Model for Electron Tunneling in Proteins:Â Consolidation of the Pathway Model and the Dutton Plot. Journal of Physical Chemistry B, 2001, 105, 4424-4435.	2.6	31
36	THEORY OF EXCITATION ENERGY TRANSFER IN THE INTERMEDIATE COUPLING CASE AND ITS APPLICATION TO THE PHOTOSYNTHETIC ANTENNA SYSTEMS. , 2001, , .		0

#	Article	IF	Citations
37	A novel method for determining the electron tunneling pathway in protein. Inorganica Chimica Acta, 2000, 300-302, 862-868.	2.4	24
38	Theory of excitation transfer in the intermediate coupling case. Journal of Luminescence, 2000, 87-89, 815-817.	3.1	8
39	Theory of Excitation Energy Transfer in the Intermediate Coupling Case. II. Criterion for Intermediate Coupling Excitation Energy Transfer Mechanism and Application to the Photosynthetic Antenna System. Journal of Physical Chemistry B, 2000, 104, 9276-9287.	2.6	56
40	Molecular Dynamics of a 15-Residue Poly(l-alanine) in Water:Â Helix Formation and Energetics. Journal of the American Chemical Society, 1999, 121, 605-612.	13.7	86
41	Monte Carlo Simulation Study on the Structure and Reaction at Metal-Electrolyte Interface. II. Mechanism of Nonlinear Electrode Reactions. Journal of the Physical Society of Japan, 1999, 68, 3729-3737.	1.6	1
42	Molecular dynamics study of femtosecond events in photoactive yellow protein after photoexcitation of the chromophore. , 1998, 32, 268-275.		20
43	Molecular Dynamics Simulation of the Excited-State Dynamics of Bacteriorhodopsin. , 1998, , 1771-1774.		0
44	Molecular Dynamics Simulation of the Excitedâ€State Dynamics of Bacteriorhodopsin. Photochemistry and Photobiology, 1997, 66, 735-740.	2.5	11
45	Mechanical property of a TIM-barrel protein. Proteins: Structure, Function and Bioinformatics, 1997, 28, 109-116.	2.6	24
46	Finite element study of protein structure under high pressure. Progress in Biotechnology, 1996, , 157-162.	0.2	0
47	Strain tensor field in proteins. Journal of Molecular Graphics, 1996, 14, 105-107.	1.1	11
48	Topographical metric to analyze the thermal fluctuations of protein conformation. Chemical Physics Letters, 1994, 219, 155-159.	2.6	5
49	Conformational deformation in deoxymyoglobin by hydrostatic pressure. Proteins: Structure, Function and Bioinformatics, 1993, 16, 327-340.	2.6	56