Tadaomi Furuta

List of Publications by Year
in descending order

54 papers	689 citations	623734 14 h-index	610901 24 g-index
54 all docs	54 docs citations	54 times ranked	1118 citing authors

#	Article	IF	Citations
1	Boric acid transport activity of human aquaporins expressed in Xenopus oocytes. Physiological Reports, 2022, 10, e15164.	1.7	5
2	Protein Needles Designed to Selfâ€Assemble through Needle Tip Engineering. Small, 2022, 18, e2106401.	10.0	8
3	Miniaturization of Bright Light-Emitting Luciferase ALuc: picALuc. ACS Chemical Biology, 2022, 17, 864-872.	3.4	9
4	Structural dynamics of ABC transporters: molecular simulation studies. Biochemical Society Transactions, 2021, 49, 405-414.	3.4	14
5	Molecular mechanism underlying the selective attack of trehalose lipids on cancer cells as revealed by coarse-grained molecular dynamics simulations. Biochemistry and Biophysics Reports, 2021, 25, 100913.	1.3	3
6	Role of Tryptophan 38 in Loading Substrate Chain into the Active-site Tunnel of Cellobiohydrolase I from <i>Trichoderma reesei</i>. Journal of Applied Glycoscience (1999), 2021, 68, 19-29.	0.7	2
7	Analysis of Arabidopsis TPK2 and KCO3 reveals structural properties required for K⁺ channel function. Channels, 2020, 14, 336-346.	2.8	5
8	Single-molecule level dynamic observation of disassembly of the apo-ferritin cage in solution. Physical Chemistry Chemical Physics, 2020, 22, 18562-18572.	2.8	14
9	Group 3 LEA Protein Model Peptides Suppress Heat-Induced Lysozyme Aggregation. Elucidation of the Underlying Mechanism Using Coarse-Grained Molecular Simulations. Journal of Physical Chemistry B, 2020, 124, 2747-2759.	2.6	7
10	Dynamic behavior of an artificial protein needle contacting a membrane observed by high-speed atomic force microscopy. Nanoscale, 2020, 12, 8166-8173.	5.6	6
11	Design Strategy to Create Antibody Mimetics Harbouring Immobilised Complementarity Determining Region Peptides for Practical Use. Scientific Reports, 2020, 10, 891.	3.3	14
12	Crystalline chitin hydrolase is a burnt-bridge Brownian motor. Biophysics and Physicobiology, 2020, 17, 51-58.	1.0	5
13	[Review] Moving Mechanism of Chitinase A from <i>Serratia marcescens</i>. Bulletin of Applied Glycoscience, 2020, 10, 89-95.	0.0	0
14	Functional characterization of multiple PAS domain-containing diguanylate cyclases in Synechocystis sp. PCC 6803. Microbiology (United Kingdom), 2020, 166, 659-668.	1.8	2
15	The mechanosensitive channel YbdG from Escherichia coli has a role in adaptation to osmotic up-shock. Journal of Biological Chemistry, 2019, 294, 12281-12292.	3.4	9
16	Cationic Copolymerâ€Chaperoned 2Dâ€“3D Reversible Conversion of Lipid Membranes. Advanced Materials, 2019, 31, e1904032.	21.0	10
17	Development of an ATP force field for coarseâ€grained simulation of ATPases and its application to the maltose transporter. Journal of Computational Chemistry, 2019, 40, 2096-2102.	3.3	5
18	Processive Chitinase is Burnt-Bridge Brownian Motor Operated by Fast Catalysis after Peeling Rail from Crystalline Chitin. Biophysical Journal, 2019, 116, 486a.	0.5	0

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19	Replica exchange molecular dynamics simulation study on the mechanism of desiccation-induced structuralization of an intrinsically disordered peptide as a model of LEA proteins. Biophysics and Physicobiology, 2019, 16, 196-204.	1.0	4
20	A novel ring-shaped reaction pathway with interconvertible intermediates in chitinase A as revealed by QM/MM simulation combined with a one-dimensional projection technique. Physical Chemistry Chemical Physics, 2019, 21, 24956-24966.	2.8	5
21	Highly Ordered Polypeptide with UCST Phase Separation Behavior. Journal of the American Chemical Society, 2019, 141, 1261-1268.	13.7	45
22	Chitinase Moves on and Degradates Crystalline Chitin with Brownian Motion. Seibutsu Butsuri, 2019, 59, 330-333.	0.1	0
23	Molecular dynamics simulation study on the structural instability of the most common cystic fibrosis-associated mutant Î”F508-CFTR. Biophysics and Physicobiology, 2018, 15, 33-44.	1.0	10
24	The mechanism of nucleotideâ€binding domain dimerization in the intact maltose transporter as studied by allâ€atom molecular dynamics simulations. Proteins: Structure, Function and Bioinformatics, 2018, 86, 237-247.	2.6	7
25	Processive chitinase is Brownian monorail operated by fast catalysis after peeling rail from crystalline chitin. Nature Communications, 2018, 9, 3814.	12.8	50
26	Functional Mechanisms of ABC Transporters as Revealed by Molecular Simulations. , 2018, , 179-201.		1
27	Probing native metal ion association sites through quenching of fluorophores in the nucleotide-binding domains of the ABC transporter MsbA. Biochemical Journal, 2017, 474, 1993-2007.	3.7	5
28	Alanine substitution in cellobiohydrolase provides new insights into substrate threading. Scientific Reports, 2017, 7, 16320.	3.3	7
29	Analysis of an ATP-induced conformational transition of ABC transporter MsbA using a coarse-grained model. Biophysics and Physicobiology, 2017, 14, 161-171.	1.0	3
30	Structural Dynamics of the Heterodimeric ABC Transporter TM287/288 Induced by ATP and Substrate Binding. Biochemistry, 2016, 55, 6730-6738.	2.5	10
31	ATP Hydrolysis Mechanism in a Maltose Transporter Explored by QM/MM Metadynamics Simulation. Journal of Physical Chemistry B, 2016, 120, 11102-11112.	2.6	15
32	Kirkwoodâ€“Buff Integrals for Aqueous Urea Solutions Based upon the Quantum Chemical Electrostatic Potential and Interaction Energies. Journal of Physical Chemistry B, 2016, 120, 7714-7723.	2.6	12
33	Mechanism for the Transport of ABC Transporters by Experimental and Simulation Studies. Seibutsu Butsuri, 2016, 56, 005-008.	0.1	1
34	The Dry Preservation of Giant Vesicles Using a Group 3 LEA Protein Model Peptide and Its Molecular Mechanism. Bulletin of the Chemical Society of Japan, 2016, 89, 1493-1499.	3.2	10
35	Thermal fluctuations enable rapid proteinâ€“protein associations in aqueous solution by lowering the reaction barrier. Chemical Physics Letters, 2016, 643, 114-118.	2.6	3
36	Analysis of the Free Energy Landscapes for the Openingâ€“Closing Dynamics of the Maltose Transporter ATPase MalK₂ Using Enhanced-Sampling Molecular Dynamics Simulation. Journal of Physical Chemistry B, 2015, 119, 9717-9725.	2.6	14

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37	A Fluorescent Protein Scaffold for Presenting Structurally Constrained Peptides Provides an Effective Screening System to Identify High Affinity Target-Binding Peptides. PLoS ONE, 2014, 9, e103397.	2.5	10
38	Water-mediated forces between the nucleotide binding domains generate the power stroke in an ABC transporter. Chemical Physics Letters, 2014, 616-617, 165-170.	2.6	6
39	Disturbed biopterin and folate metabolism in the Qdprâ€deficient mouse. FEBS Letters, 2014, 588, 3924-3931.	2.8	34
40	Interaction of amphiphilic Î±-helical cell-penetrating peptides with heparan sulfate. Organic and Biomolecular Chemistry, 2014, 12, 4673.	2.8	29
41	Analysis of the Structural and Functional Roles of Coupling Helices in the ATP-Binding Cassette Transporter MsbA through Enzyme Assays and Molecular Dynamics Simulations. Biochemistry, 2014, 53, 4261-4272.	2.5	20
42	ATP-Induced Conformational Changes of Nucleotide-Binding Domains in an ABC Transporter. Importance of the Water-Mediated Entropic Force. Journal of Physical Chemistry B, 2014, 118, 12612-12620.	2.6	17
43	A Computational Study of the Interaction of Amphiphilic Î±-Helical Cell-Penetrating Peptides with Heparan Sulfate. Bulletin of the Chemical Society of Japan, 2014, 87, 1074-1082.	3.2	1
44	The Power Stroke Driven by ATP Binding in CFTR As Studied by Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2013, 117, 83-93.	2.6	32
45	Dynamics and structural changes induced by ATP and/or substrate binding in the inward-facing conformation state of P-glycoprotein. Chemical Physics Letters, 2013, 557, 145-149.	2.6	13
46	The Tryptophan Residue at the Active Site Tunnel Entrance of Trichoderma reesei Cellobiohydrolase Cel7A Is Important for Initiation of Degradation of Crystalline Cellulose. Journal of Biological Chemistry, 2013, 288, 13503-13510.	3.4	77
47	Minimum Free Energy Path of Ligand-Induced Transition in Adenylate Kinase. PLoS Computational Biology, 2012, 8, e1002555.	3.2	84
48	Different inhibitory potency of febuxostat towards mammalian and bacterial xanthine oxidoreductases: insight from molecular dynamics. Scientific Reports, 2012, 2, 331.	3.3	19
49	Combined Biophysical and Biochemical Study of Enzyme Effects: Binding Mechanism of an Inhibitor Febuxostat with Xanthine Oxidoreductase. Nihon Ika Daigaku Igakkai Zasshi, 2012, 8, 222-227.	0.0	0
50	Accurate prediction of native tertiary structure of protein using molecular dynamics simulation with the aid of the knowledge of secondary structures. Chemical Physics Letters, 2009, 472, 134-139.	2.6	3
51	In Silico Chaperonin-Like Cycle Helps Folding of Proteins for Structure Prediction. Biophysical Journal, 2008, 94, 2558-2565.	0.5	3
52	Gap compression/extension mechanism of bacterial flagellar hook as the molecular universal joint. Journal of Structural Biology, 2007, 157, 481-490.	2.8	19
53	A lattice model for cytoskeletonsâ€™ dynamics: analysis of growth and shrinkage. Physica A: Statistical Mechanics and Its Applications, 2002, 314, 162-169.	2.6	1
54	A lattice model for a linear polymer oscillation. AIP Conference Proceedings, 2000, , .	0.4	1