

Tadaomi Furuta

List of Publications by Year in descending order

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54
papers

689
citations

623188

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54
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1118
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#	ARTICLE	IF	CITATIONS
1	Minimum Free Energy Path of Ligand-Induced Transition in Adenylate Kinase. <i>PLoS Computational Biology</i> , 2012, 8, e1002555.	1.5	84
2	The Tryptophan Residue at the Active Site Tunnel Entrance of <i>Trichoderma reesei</i> Cellobiohydrolase Cel7A Is Important for Initiation of Degradation of Crystalline Cellulose. <i>Journal of Biological Chemistry</i> , 2013, 288, 13503-13510.	1.6	77
3	Processive chitinase is Brownian monorail operated by fast catalysis after peeling rail from crystalline chitin. <i>Nature Communications</i> , 2018, 9, 3814.	5.8	50
4	Highly Ordered Polypeptide with UCST Phase Separation Behavior. <i>Journal of the American Chemical Society</i> , 2019, 141, 1261-1268.	6.6	45
5	Disturbed bipterin and folate metabolism in the <i>Qdpr</i> -deficient mouse. <i>FEBS Letters</i> , 2014, 588, 3924-3931.	1.3	34
6	The Power Stroke Driven by ATP Binding in CFTR As Studied by Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2013, 117, 83-93.	1.2	32
7	Interaction of amphiphilic α -helical cell-penetrating peptides with heparan sulfate. <i>Organic and Biomolecular Chemistry</i> , 2014, 12, 4673.	1.5	29
8	Analysis of the Structural and Functional Roles of Coupling Helices in the ATP-Binding Cassette Transporter MsbA through Enzyme Assays and Molecular Dynamics Simulations. <i>Biochemistry</i> , 2014, 53, 4261-4272.	1.2	20
9	Gap compression/extension mechanism of bacterial flagellar hook as the molecular universal joint. <i>Journal of Structural Biology</i> , 2007, 157, 481-490.	1.3	19
10	Different inhibitory potency of febuxostat towards mammalian and bacterial xanthine oxidoreductases: insight from molecular dynamics. <i>Scientific Reports</i> , 2012, 2, 331.	1.6	19
11	ATP-Induced Conformational Changes of Nucleotide-Binding Domains in an ABC Transporter. Importance of the Water-Mediated Entropic Force. <i>Journal of Physical Chemistry B</i> , 2014, 118, 12612-12620.	1.2	17
12	ATP Hydrolysis Mechanism in a Maltose Transporter Explored by QM/MM Metadynamics Simulation. <i>Journal of Physical Chemistry B</i> , 2016, 120, 11102-11112.	1.2	15
13	Analysis of the Free Energy Landscapes for the Opening/Closing Dynamics of the Maltose Transporter ATPase MalK ₂ Using Enhanced-Sampling Molecular Dynamics Simulation. <i>Journal of Physical Chemistry B</i> , 2015, 119, 9717-9725.	1.2	14
14	Single-molecule level dynamic observation of disassembly of the apo-ferritin cage in solution. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 18562-18572.	1.3	14
15	Design Strategy to Create Antibody Mimetics Harboring Immobilised Complementarity Determining Region Peptides for Practical Use. <i>Scientific Reports</i> , 2020, 10, 891.	1.6	14
16	Structural dynamics of ABC transporters: molecular simulation studies. <i>Biochemical Society Transactions</i> , 2021, 49, 405-414.	1.6	14
17	Dynamics and structural changes induced by ATP and/or substrate binding in the inward-facing conformation state of P-glycoprotein. <i>Chemical Physics Letters</i> , 2013, 557, 145-149.	1.2	13
18	Kirkwood's Buff Integrals for Aqueous Urea Solutions Based upon the Quantum Chemical Electrostatic Potential and Interaction Energies. <i>Journal of Physical Chemistry B</i> , 2016, 120, 7714-7723.	1.2	12

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19	A Fluorescent Protein Scaffold for Presenting Structurally Constrained Peptides Provides an Effective Screening System to Identify High Affinity Target-Binding Peptides. <i>PLoS ONE</i> , 2014, 9, e103397.	1.1	10
20	Structural Dynamics of the Heterodimeric ABC Transporter TM287/288 Induced by ATP and Substrate Binding. <i>Biochemistry</i> , 2016, 55, 6730-6738.	1.2	10
21	The Dry Preservation of Giant Vesicles Using a Group 3 LEA Protein Model Peptide and Its Molecular Mechanism. <i>Bulletin of the Chemical Society of Japan</i> , 2016, 89, 1493-1499.	2.0	10
22	Molecular dynamics simulation study on the structural instability of the most common cystic fibrosis-associated mutant $\Delta F508$ -CFTR. <i>Biophysics and Physicobiology</i> , 2018, 15, 33-44.	0.5	10
23	Cationic Copolymer-Induced Reversible Conversion of Lipid Membranes. <i>Advanced Materials</i> , 2019, 31, e1904032.	11.1	10
24	The mechanosensitive channel YbdG from <i>Escherichia coli</i> has a role in adaptation to osmotic up-shock. <i>Journal of Biological Chemistry</i> , 2019, 294, 12281-12292.	1.6	9
25	Miniaturization of Bright Light-Emitting Luciferase ALuc: picALuc. <i>ACS Chemical Biology</i> , 2022, 17, 864-872.	1.6	9
26	Protein Needles Designed to Self-Assemble through Needle Tip Engineering. <i>Small</i> , 2022, 18, e2106401.	5.2	8
27	Alanine substitution in cellobiohydrolase provides new insights into substrate threading. <i>Scientific Reports</i> , 2017, 7, 16320.	1.6	7
28	The mechanism of nucleotide-binding domain dimerization in the intact maltose transporter as studied by all-atom molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 237-247.	1.5	7
29	Group 3 LEA Protein Model Peptides Suppress Heat-Induced Lysozyme Aggregation. Elucidation of the Underlying Mechanism Using Coarse-Grained Molecular Simulations. <i>Journal of Physical Chemistry B</i> , 2020, 124, 2747-2759.	1.2	7
30	Water-mediated forces between the nucleotide binding domains generate the power stroke in an ABC transporter. <i>Chemical Physics Letters</i> , 2014, 616-617, 165-170.	1.2	6
31	Dynamic behavior of an artificial protein needle contacting a membrane observed by high-speed atomic force microscopy. <i>Nanoscale</i> , 2020, 12, 8166-8173.	2.8	6
32	Probing native metal ion association sites through quenching of fluorophores in the nucleotide-binding domains of the ABC transporter MsbA. <i>Biochemical Journal</i> , 2017, 474, 1993-2007.	1.7	5
33	Development of an ATP force field for coarse-grained simulation of ATPases and its application to the maltose transporter. <i>Journal of Computational Chemistry</i> , 2019, 40, 2096-2102.	1.5	5
34	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. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 24956-24966.	1.3	5
35	Analysis of Arabidopsis TPK2 and KCO3 reveals structural properties required for K ⁺ channel function. <i>Channels</i> , 2020, 14, 336-346.	1.5	5
36	Crystalline chitin hydrolase is a burnt-bridge Brownian motor. <i>Biophysics and Physicobiology</i> , 2020, 17, 51-58.	0.5	5

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37	Boric acid transport activity of human aquaporins expressed in <i>Xenopus</i> oocytes. <i>Physiological Reports</i> , 2022, 10, e15164.	0.7	5
38	Replica exchange molecular dynamics simulation study on the mechanism of desiccation-induced structuralization of an intrinsically disordered peptide as a model of LEA proteins. <i>Biophysics and Physicobiology</i> , 2019, 16, 196-204.	0.5	4
39	In Silico Chaperonin-Like Cycle Helps Folding of Proteins for Structure Prediction. <i>Biophysical Journal</i> , 2008, 94, 2558-2565.	0.2	3
40	Accurate prediction of native tertiary structure of protein using molecular dynamics simulation with the aid of the knowledge of secondary structures. <i>Chemical Physics Letters</i> , 2009, 472, 134-139.	1.2	3
41	Thermal fluctuations enable rapid protein-protein associations in aqueous solution by lowering the reaction barrier. <i>Chemical Physics Letters</i> , 2016, 643, 114-118.	1.2	3
42	Analysis of an ATP-induced conformational transition of ABC transporter MsbA using a coarse-grained model. <i>Biophysics and Physicobiology</i> , 2017, 14, 161-171.	0.5	3
43	Molecular mechanism underlying the selective attack of trehalose lipids on cancer cells as revealed by coarse-grained molecular dynamics simulations. <i>Biochemistry and Biophysics Reports</i> , 2021, 25, 100913.	0.7	3
44	Role of Tryptophan 38 in Loading Substrate Chain into the Active-site Tunnel of Cellobiohydrolase I from <i>Trichoderma reesei</i> . <i>Journal of Applied Glycoscience</i> (1999), 2021, 68, 19-29.	0.3	2
45	Functional characterization of multiple PAS domain-containing diguanylate cyclases in <i>Synechocystis</i> sp. PCC 6803. <i>Microbiology (United Kingdom)</i> , 2020, 166, 659-668.	0.7	2
46	A lattice model for a linear polymer oscillation. <i>AIP Conference Proceedings</i> , 2000, , .	0.3	1
47	A lattice model for cytoskeletons' dynamics: analysis of growth and shrinkage. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2002, 314, 162-169.	1.2	1
48	A Computational Study of the Interaction of Amphiphilic α -Helical Cell-Penetrating Peptides with Heparan Sulfate. <i>Bulletin of the Chemical Society of Japan</i> , 2014, 87, 1074-1082.	2.0	1
49	Mechanism for the Transport of ABC Transporters by Experimental and Simulation Studies. <i>Seibutsu Butsuri</i> , 2016, 56, 005-008.	0.0	1
50	Functional Mechanisms of ABC Transporters as Revealed by Molecular Simulations. , 2018, , 179-201.		1
51	Processive Chitinase is Burnt-Bridge Brownian Motor Operated by Fast Catalysis after Peeling Rail from Crystalline Chitin. <i>Biophysical Journal</i> , 2019, 116, 486a.	0.2	0
52	Combined Biophysical and Biochemical Study of Enzyme Effects: Binding Mechanism of an Inhibitor Febuxostat with Xanthine Oxidoreductase. <i>Nihon Ika Daigaku Igakkai Zasshi</i> , 2012, 8, 222-227.	0.0	0
53	Chitinase Moves on and Degrades Crystalline Chitin with Brownian Motion. <i>Seibutsu Butsuri</i> , 2019, 59, 330-333.	0.0	0
54	[Review] Moving Mechanism of Chitinase A from <i>Serratia marcescens</i> . <i>Bulletin of Applied Glycoscience</i> , 2020, 10, 89-95.	0.0	0