

Tsuyoshi Shirai

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

1,380
citations

394421

19
h-index

361022

35
g-index

64
all docs

64
docs citations

64
times ranked

1943
citing authors

#	ARTICLE	IF	CITATIONS
1	Aicardi-Goutières Syndrome Is Caused by IFIH1 Mutations. <i>American Journal of Human Genetics</i> , 2014, 95, 121-125.	6.2	175
2	Potential anti-COVID-19 agents, cepharanthine and nelfinavir, and their usage for combination treatment. <i>IScience</i> , 2021, 24, 102367.	4.1	126
3	High-resolution crystal structure of M-protease: phylogeny aided analysis of the high-alkaline adaptation mechanism. <i>Protein Engineering, Design and Selection</i> , 1997, 10, 627-634.	2.1	99
4	Mechanism of replication machinery assembly as revealed by the DNA ligase-PCNA-DNA complex architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4647-4652.	7.1	71
5	Identification of a mismatch-specific endonuclease in hyperthermophilic Archaea. <i>Nucleic Acids Research</i> , 2016, 44, 2977-2986.	14.5	63
6	The influence of PRNP polymorphisms on human prion disease susceptibility: an update. <i>Acta Neuropathologica</i> , 2015, 130, 159-170.	7.7	59
7	Architecture of the DNA polymerase B-proliferating cell nuclear antigen (PCNA)-DNA ternary complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1845-1849.	7.1	53
8	High-resolution structure of the conger eel galectin, congerin I, in lactose-liganded and ligand-free forms: emergence of a new structure class by accelerated evolution. <i>Structure</i> , 1999, 7, 1223-1233.	3.3	49
9	Structure of the EndoMS-DNA Complex as Mismatch Restriction Endonuclease. <i>Structure</i> , 2016, 24, 1960-1971.	3.3	48
10	Crystal Structure of a Conger Eel Galectin (Congerin II) at 1.45Å... Resolution: Implication for the Accelerated Evolution of a New Ligand-binding Site Following Gene Duplication. <i>Journal of Molecular Biology</i> , 2002, 321, 879-889.	4.2	35
11	Structure of Novel Enzyme in Mannan Biodegradation Process 4-O-β-d-Mannosyl-d-Glucose Phosphorylase MGP. <i>Journal of Molecular Biology</i> , 2013, 425, 4468-4478.	4.2	34
12	The tetrameric MotA complex as the core of the flagellar motor stator from hyperthermophilic bacterium. <i>Scientific Reports</i> , 2016, 6, 31526.	3.3	33
13	Architectures of archaeal GINS complexes, essential DNA replication initiation factors. <i>BMC Biology</i> , 2011, 9, 28.	3.8	30
14	Curcumin Derivatives Verify the Essentiality of ROS Upregulation in Tumor Suppression. <i>Molecules</i> , 2019, 24, 4067.	3.8	29
15	Ancestral sequence evolutionary trace and crystal structure analyses of alkaline α-amylase from <i>Bacillus</i> sp. KSM-1378 to clarify the alkaline adaptation process of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 600-610.	2.6	27
16	Decoding disease-causing mechanisms of missense mutations from supramolecular structures. <i>Scientific Reports</i> , 2017, 7, 8541.	3.3	26
17	Atomic structure of an archaeal GAN suggests its dual roles as an exonuclease in DNA repair and a CMG component in DNA replication. <i>Nucleic Acids Research</i> , 2016, 44, 9505-9517.	14.5	22
18	Rotational direction of flagellar motor from the conformation of FliG middle domain in marine <i>Vibrio</i> . <i>Scientific Reports</i> , 2018, 8, 17793.	3.3	22

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19	Tracing whale myoglobin evolution by resurrecting ancient proteins. <i>Scientific Reports</i> , 2018, 8, 16883.	3.3	22
20	Resurrecting the ancient glow of the fireflies. <i>Science Advances</i> , 2020, 6, .	10.3	22
21	Knowledge-based structural models of SARS-CoV-2 proteins and their complexes with potential drugs. <i>FEBS Letters</i> , 2020, 594, 1960-1973.	2.8	21
22	Evaluating Prion Models Based on Comprehensive Mutation Data of Mouse PrP. <i>Structure</i> , 2014, 22, 560-571.	3.3	20
23	Pentagamavunon-1 (PGV-1) inhibits ROS metabolic enzymes and suppresses tumor cell growth by inducing M phase (prometaphase) arrest and cell senescence. <i>Scientific Reports</i> , 2019, 9, 14867.	3.3	20
24	Evaluating cepharanthine analogues as natural drugs against SARS-CoV-2. <i>FEBS Open Bio</i> , 2022, 12, 285-294.	2.3	20
25	Clustering of 3D-Structure Similarity Based Network of Secondary Metabolites Reveals Their Relationships with Biological Activities. <i>Molecular Informatics</i> , 2014, 33, 790-801.	2.5	18
26	Deciphering Supramolecular Structures with Protein-Protein Interaction Network Modeling. <i>Scientific Reports</i> , 2015, 5, 16341.	3.3	18
27	WDR11 is another causative gene for coloboma, cardiac anomaly and growth retardation in 10q26 deletion syndrome. <i>European Journal of Medical Genetics</i> , 2020, 63, 103626.	1.3	18
28	Tracing Protein Evolution through Ancestral Structures of Fish Galectin. <i>Structure</i> , 2011, 19, 711-721.	3.3	15
29	Classification of Ligand Molecules in PDB with Fast Heuristic Graph Match Algorithm COMPLIG. <i>Journal of Molecular Biology</i> , 2012, 424, 379-390.	4.2	15
30	Reconstruction of a Probable Ancestral Form of Conger Eel Galectins Revealed Their Rapid Adaptive Evolution Process for Specific Carbohydrate Recognition. <i>Molecular Biology and Evolution</i> , 2007, 24, 2504-2514.	8.9	14
31	Structural and Functional Analysis of the C-Terminal Region of FliG, an Essential Motor Component of Vibrio Na ⁺ -Driven Flagella. <i>Structure</i> , 2017, 25, 1540-1548.e3.	3.3	13
32	Protein engineering of conger eel galectins by tracing of molecular evolution using probable ancestral mutants. <i>BMC Evolutionary Biology</i> , 2010, 10, 43.	3.2	12
33	SAHG, a comprehensive database of predicted structures of all human proteins. <i>Nucleic Acids Research</i> , 2011, 39, D487-D493.	14.5	12
34	Clinical characteristics of adolescent cases with Type A insulin resistance syndrome caused by heterozygous mutations in the β -subunit of the insulin receptor (<i>INSR</i>) gene. <i>Journal of Diabetes</i> , 2019, 11, 46-54.	1.8	12
35	Crystallization and Preliminary X-Ray Analysis of a Truncated Family A Alkaline Endoglucanase Isolated from <i>Bacillus</i> sp. KSM-635. <i>Journal of Biochemistry</i> , 1997, 122, 683-685.	1.7	11
36	The Role of the Prod1 Membrane Anchor in Newt Limb Regeneration. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 270-274.	13.8	10

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37	X-ray Structure Analysis and Characterization of AFUEI, an Elastase Inhibitor from <i>Aspergillus fumigatus</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 17451-17459.	3.4	9
38	Direct visualization of DNA baton pass between replication factors bound to PCNA. <i>Scientific Reports</i> , 2018, 8, 16209.	3.3	9
39	Structures of jacalin-related lectin PPL3 regulating pearl shell biomineralization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 644-653.	2.6	8
40	Two conformations of DNA polymerase D-PCNA-DNA, an archaeal replisome complex, revealed by cryo-electron microscopy. <i>BMC Biology</i> , 2020, 18, 152.	3.8	8
41	Molecular mechanisms of insulin resistance in 2 cases of primary insulin receptor defect-associated diseases. <i>Pediatric Diabetes</i> , 2017, 18, 917-924.	2.9	6
42	Common and unique strategies of myoglobin evolution for deep-sea adaptation of diving mammals. <i>IScience</i> , 2021, 24, 102920.	4.1	6
43	Current status of structure-based drug repurposing against COVID-19 by targeting SARS-CoV-2 proteins. <i>Biophysics and Physicobiology</i> , 2021, 18, 226-240.	1.0	6
44	Intermolecular Interactions between a Membrane Protein and a Glycolipid Essential for Membrane Protein Integration. <i>ACS Chemical Biology</i> , 2022, 17, 609-618.	3.4	6
45	Role of a bacterial glycolipid in Sec-independent membrane protein insertion. <i>Scientific Reports</i> , 2022, 12, .	3.3	6
46	Tracing Ancestral Specificity of Lectins: Ancestral Sequence Reconstruction Method as a New Approach in Protein Engineering. <i>Methods in Molecular Biology</i> , 2014, 1200, 539-551.	0.9	4
47	Single-particle analysis of full-length human poly(ADP-ribose) polymerase 1. <i>Biophysics and Physicobiology</i> , 2019, 16, 59-67.	1.0	3
48	A residue located at the junction of the head and stalk regions of measles virus fusion protein regulates membrane fusion by controlling conformational stability. <i>Journal of General Virology</i> , 2017, 98, 143-154.	2.9	3
49	Design, construction, crystallization, and preliminary X-ray studies of a fine-tuning mutant (F133V) of module-substituted chimera hemoglobin. , 1998, 32, 263-267.		2
50	Experimental Molecular Archeology: Reconstruction of Ancestral Mutants and Evolutionary History of Proteins as a New Approach in Protein Engineering. , 2013, , .		2
51	Exonuclease processivity of archaeal replicative DNA polymerase in association with PCNA is expedited by mismatches in DNA. <i>Scientific Reports</i> , 2017, 7, 44582.	3.3	2
52	Overview of the big data bioinformatics symposium (2SCA) at BSJ2019. <i>Biophysical Reviews</i> , 2020, 12, 277-278.	3.2	2
53	Classification of ligand molecules in PDB with graph match-based structural superposition. <i>Journal of Structural and Functional Genomics</i> , 2016, 17, 135-146.	1.2	1
54	Transcriptional activation of a chimeric retrogene PIPSL in a hominoid ancestor. <i>Gene</i> , 2018, 678, 318-323.	2.2	1

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55	Improvement of Protein Solubility in Macromolecular Crowding during Myoglobin Evolution. <i>Biochemistry</i> , 2022, 61, 1543-1547.	2.5	1
56	Detecting structural similarity of ligand interactions in the lipid metabolic system including enzymes, lipid-binding proteins and nuclear receptors. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 397-403.	2.1	0
57	Cover Image, Volume 86, Issue 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, C1-C1.	2.6	0
58	Knowledge-based Modeling of SARS-CoV-2 Proteins and Predicting its Potential Drugs. <i>Seibutsu Butsuri</i> , 2021, 61, 102-106.	0.1	0
59	Frontiers in Crystal Chemistry: Prediction of Structures and Properties. Part 1. Prediction of Crystal Structures, Methods and Applications. A Protein-Fold Evolution and Protein Structure Predictions.. <i>Nihon Kessho Gakkaishi</i> , 2002, 44, 20-24.	0.0	0
60	Supramolecule Modeling: The Mechanism of Switching between Polymerization “ Proof Reading Modes in DNA Duplication. <i>Seibutsu Butsuri</i> , 2012, 52, 246-249.	0.1	0
61	Alkaline tolerance of proteins.. <i>Seibutsu Butsuri</i> , 1998, 38, 211-213.	0.1	0