

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

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docs citations

64
times ranked

1943
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Evaluating cepharanthine analogues as natural drugs against SARS-CoV-2. FEBS Open Bio, 2022, 12, 285-294. | 2.3 | 20 |
| 2 | Intermolecular Interactions between a Membrane Protein and a Glycolipid Essential for Membrane Protein Integration. ACS Chemical Biology, 2022, 17, 609-618. | 3.4 | 6 |
| 3 | Improvement of Protein Solubility in Macromolecular Crowding during Myoglobin Evolution. Biochemistry, 2022, 61, 1543-1547. | 2.5 | 1 |
| 4 | Role of a bacterial glycolipid in Sec-independent membrane protein insertion. Scientific Reports, 2022, 12, . | 3.3 | 6 |
| 5 | Knowledge-based Modeling of SARS-CoV-2 Proteins and Predicting its Potential Drugs. Seibutsu Butsuri, 2021, 61, 102-106. | 0.1 | 0 |
| 6 | Potential anti-COVID-19 agents, cepharanthine and nelfinavir, and their usage for combination treatment. IScience, 2021, 24, 102367. | 4.1 | 126 |
| 7 | Common and unique strategies of myoglobin evolution for deep-sea adaptation of diving mammals. IScience, 2021, 24, 102920. | 4.1 | 6 |
| 8 | Current status of structure-based drug repurposing against COVID-19 by targeting SARS-CoV-2 proteins. Biophysics and Physicobiology, 2021, 18, 226-240. | 1.0 | 6 |
| 9 | WDR11 is another causative gene for coloboma, cardiac anomaly and growth retardation in 10q26 deletion syndrome. European Journal of Medical Genetics, 2020, 63, 103626. | 1.3 | 18 |
| 10 | Two conformations of DNA polymerase D-PCNA-DNA, an archaeal replisome complex, revealed by cryo-electron microscopy. BMC Biology, 2020, 18, 152. | 3.8 | 8 |
| 11 | Resurrecting the ancient glow of the fireflies. Science Advances, 2020, 6, . | 10.3 | 22 |
| 12 | Knowledge-based structural models of SARS-CoV-2 proteins and their complexes with potential drugs. FEBS Letters, 2020, 594, 1960-1973. | 2.8 | 21 |
| 13 | Overview of the big data bioinformatics symposium (2SCA) at BSJ2019. Biophysical Reviews, 2020, 12, 277-278. | 3.2 | 2 |
| 14 | 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. Journal of Diabetes, 2019, 11, 46-54. | 1.8 | 12 |
| 15 | Pentagamavunon-1 (PGV-1) inhibits ROS metabolic enzymes and suppresses tumor cell growth by inducing M phase (prometaphase) arrest and cell senescence. Scientific Reports, 2019, 9, 14867. | 3.3 | 20 |
| 16 | Single-particle analysis of full-length human poly(ADP-ribose) polymerase 1. Biophysics and Physicobiology, 2019, 16, 59-67. | 1.0 | 3 |
| 17 | Curcumin Derivatives Verify the Essentiality of ROS Upregulation in Tumor Suppression. Molecules, 2019, 24, 4067. | 3.8 | 29 |
| 18 | Structures of jacalin-related lectin PPL3 regulating pearl shell biomineralization. Proteins: Structure, Function and Bioinformatics, 2018, 86, 644-653. | 2.6 | 8 |

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|----|--|------|-----------|
| 19 | 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 |
| 20 | Cover Image, Volume 86, Issue 6. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, C1-C1. | 2.6 | 0 |
| 21 | Tracing whale myoglobin evolution by resurrecting ancient proteins. <i>Scientific Reports</i> , 2018, 8, 16883. | 3.3 | 22 |
| 22 | Direct visualization of DNA baton pass between replication factors bound to PCNA. <i>Scientific Reports</i> , 2018, 8, 16209. | 3.3 | 9 |
| 23 | Transcriptional activation of a chimeric retrogene PIPSL in a hominoid ancestor. <i>Gene</i> , 2018, 678, 318-323. | 2.2 | 1 |
| 24 | 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 |
| 25 | The Role of the Prod1 Membrane Anchor in Newt Limb Regeneration. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 270-274. | 13.8 | 10 |
| 26 | 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 |
| 27 | Structural and Functional Analysis of the C-Terminal Region of FliG, an Essential Motor Component of <i>Vibrio Na⁺-Driven Flagella</i> . <i>Structure</i> , 2017, 25, 1540-1548.e3. | 3.3 | 13 |
| 28 | Decoding disease-causing mechanisms of missense mutations from supramolecular structures. <i>Scientific Reports</i> , 2017, 7, 8541. | 3.3 | 26 |
| 29 | 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 |
| 30 | 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 |
| 31 | 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 |
| 32 | Structure of the EndoMS-DNA Complex as Mismatch Restriction Endonuclease. <i>Structure</i> , 2016, 24, 1960-1971. | 3.3 | 48 |
| 33 | 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 |
| 34 | Identification of a mismatch-specific endonuclease in hyperthermophilic Archaea. <i>Nucleic Acids Research</i> , 2016, 44, 2977-2986. | 14.5 | 63 |
| 35 | Deciphering Supramolecular Structures with Protein-Protein Interaction Network Modeling. <i>Scientific Reports</i> , 2015, 5, 16341. | 3.3 | 18 |
| 36 | The influence of PRNP polymorphisms on human prion disease susceptibility: an update. <i>Acta Neuropathologica</i> , 2015, 130, 159-170. | 7.7 | 59 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | Evaluating Prion Models Based on Comprehensive Mutation Data of Mouse PrP. <i>Structure</i> , 2014, 22, 560-571. | 3.3 | 20 |
| 39 | Aicardi-Goutières Syndrome Is Caused by IFIH1 Mutations. <i>American Journal of Human Genetics</i> , 2014, 95, 121-125. | 6.2 | 175 |
| 40 | 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 |
| 41 | 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 |
| 42 | 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 |
| 43 | Experimental Molecular Archeology: Reconstruction of Ancestral Mutants and Evolutionary History of Proteins as a New Approach in Protein Engineering. , 2013, , . | | 2 |
| 44 | 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 |
| 45 | 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 |
| 46 | Tracing Protein Evolution through Ancestral Structures of Fish Galectin. <i>Structure</i> , 2011, 19, 711-721. | 3.3 | 15 |
| 47 | Architectures of archaeal GINS complexes, essential DNA replication initiation factors. <i>BMC Biology</i> , 2011, 9, 28. | 3.8 | 30 |
| 48 | SAHG, a comprehensive database of predicted structures of all human proteins. <i>Nucleic Acids Research</i> , 2011, 39, D487-D493. | 14.5 | 12 |
| 49 | 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 |
| 50 | 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 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |
| 54 | Ancestral sequence evolutionary trace and crystal structure analyses of alkaline β -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 |

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|----|--|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | 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 |
| 58 | Design, construction, crystallization, and preliminary X-ray studies of a fine-tuning mutant (F133V) of module-substituted chimera hemoglobin. , 1998, 32, 263-267. | | 2 |
| 59 | Alkaline tolerance of proteins.. <i>Seibutsu Butsuri</i> , 1998, 38, 211-213. | 0.1 | 0 |
| 60 | 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 |
| 61 | 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 |