

Ji-min Wang

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

2,894
citations

304602

22
h-index

189801

50
g-index

83
all docs

83
docs citations

83
times ranked

3500
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of a monomeric photosystem II core complex from a cyanobacterium acclimated to far-red light reveals the functions of chlorophylls d and f. <i>Journal of Biological Chemistry</i> , 2022, 298, 101424.	1.6	32
2	Structure of a photosystem I-ferredoxin complex from a marine cyanobacterium provides insights into far-red light photoacclimation. <i>Journal of Biological Chemistry</i> , 2022, 298, 101408.	1.6	16
3	Effects of flue gas recirculation on nitrogen oxide formation in 1000 MW _{CO₂} coal-fired boiler with partial expansion furnace. <i>International Journal of Chemical Reactor Engineering</i> , 2022, 20, 929-945.	0.6	3
4	High-resolution cryo-electron microscopy structure of photosystem II from the mesophilic cyanobacterium, <i>Synechocystis</i> sp. PCC 6803. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	58
5	Insights into Binding of Single-Stranded Viral RNA Template to the Replication-Transcription Complex of SARS-CoV-2 for the Priming Reaction from Molecular Dynamics Simulations. <i>Biochemistry</i> , 2022, 61, 424-432.	1.2	10
6	Two-Metal-Ion Catalysis: Inhibition of DNA Polymerase Activity by a Third Divalent Metal Ion. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 824794.	1.6	15
7	Glycerol binding at the narrow channel of photosystem II stabilizes the low-spin S ₂ state of the oxygen-evolving complex. <i>Photosynthesis Research</i> , 2022, , 1.	1.6	1
8	Structural Basis for Reduced Dynamics of Three Engineered HNH Endonuclease Lys-to-Ala Mutants for the Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR)-Associated 9 (CRISPR/Cas9) Enzyme. <i>Biochemistry</i> , 2022, 61, 785-794.	1.2	12
9	Structural analyses of an RNA stability element interacting with poly(A). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
10	Identification of Mg ²⁺ ions next to nucleotides in cryo-EM maps using electrostatic potential maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 534-539.	1.1	9
11	Mechanism of Inhibition of the Reproduction of SARS-CoV-2 and <i>Ebola</i> Viruses by Remdesivir. <i>Biochemistry</i> , 2021, 60, 1869-1875.	1.2	12
12	Do crystallographic XFEL data support binding of a water molecule to the oxygen-evolving complex of photosystem II exposed to two flashes of light?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	11
13	Computational insights into the membrane fusion mechanism of SARS-CoV-2 at the cellular level. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5019-5028.	1.9	10
14	Heterogeneous Composition of Oxygen-Evolving Complexes in Crystal Structures of Dark-Adapted Photosystem II. <i>Biochemistry</i> , 2021, 60, 3374-3384.	1.2	8
15	Opportunities and challenges for assigning cofactors in cryo-EM density maps of chlorophyll-containing proteins. <i>Communications Biology</i> , 2020, 3, 408.	2.0	21
16	Crystal structure of the C-terminal domain of DENR. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 696-704.	1.9	3
17	Identification of a Na ⁺ -Binding Site near the Oxygen-Evolving Complex of Spinach Photosystem II. <i>Biochemistry</i> , 2020, 59, 2823-2831.	1.2	5
18	Structural basis of keto acid utilization in nonribosomal depsipeptide synthesis. <i>Nature Chemical Biology</i> , 2020, 16, 493-496.	3.9	28

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19	The Hexameric Helicase DnaB Adopts a Nonplanar Conformation during Translocation. <i>Journal of hand surgery Asian-Pacific volume, The</i> , 2020, , 365-375.	0.2	0
20	Visualization of H atoms in the X-ray crystal structure of photoactive yellow protein: Does it contain low-barrier hydrogen bonds?. <i>Protein Science</i> , 2019, 28, 1966-1972.	3.1	6
21	Thermodynamics of the S ₂ -to-S ₃ state transition of the oxygen-evolving complex of photosystem II. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 20840-20848.	1.3	21
22	Crystallographic identification of spontaneous oxidation intermediates and products of protein sulfhydryl groups. <i>Protein Science</i> , 2019, 28, 472-477.	3.1	13
23	Numerical Investigation of Heat Transfer Characteristics of Supercritical CO ₂ Tube in Combustion Chamber of Coal-Fired Boiler. <i>Journal of Thermal Science</i> , 2019, 28, 442-453.	0.9	8
24	Numerical study on the effect of separated over-fire air ratio on combustion characteristics and NO _x emission in a 1000-MW supercritical CO ₂ boiler. <i>Energy</i> , 2019, 175, 593-603.	4.5	20
25	Numerical simulation of flow and heat transfer between supercritical CO ₂ tube and flue gas. <i>Asia-Pacific Journal of Chemical Engineering</i> , 2019, 14, e2295.	0.8	4
26	Crystallographic evidence for two-metal-ion catalysis in human pol I. <i>Protein Science</i> , 2019, 28, 439-447.	3.1	13
27	Determination of chemical identity and occupancy from experimental density maps. <i>Protein Science</i> , 2018, 27, 411-420.	3.1	11
28	Structural insights into the oligomerization of FtsH periplasmic domain from <i>Thermotoga maritima</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1201-1207.	1.0	2
29	Structural and biochemical insights into inhibition of human primase by citrate. <i>Biochemical and Biophysical Research Communications</i> , 2018, 507, 383-388.	1.0	4
30	Misreading chaperone-substrate complexes from random noise. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 989-990.	3.6	7
31	On the damage done to the structure of the <i>Thermoplasma acidophilum</i> proteasome by electron radiation. <i>Protein Science</i> , 2018, 27, 2051-2061.	3.1	5
32	Reduced Occupancy of the Oxygen-Evolving Complex of Photosystem II Detected in Cryo-Electron Microscopy Maps. <i>Biochemistry</i> , 2018, 57, 5925-5929.	1.2	3
33	Identification of ions in experimental electrostatic potential maps. <i>IUCr</i> , 2018, 5, 375-381.	1.0	22
34	Crystal structure of Pistol, a class of self-cleaving ribozyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1021-1026.	3.3	56
35	Insights into Photosystem II from Isomorphous Difference Fourier Maps of Femtosecond X-ray Diffraction Data and Quantum Mechanics/Molecular Mechanics Structural Models. <i>ACS Energy Letters</i> , 2017, 2, 397-407.	8.8	16
36	On the appearance of carboxylates in electrostatic potential maps. <i>Protein Science</i> , 2017, 26, 396-402.	3.1	24

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37	Systematic analysis of residual density suggests that a major limitation in well-refined X-ray structures of proteins is the omission of ordered solvent. <i>Protein Science</i> , 2017, 26, 1012-1023.	3.1	8
38	Experimental charge density from electron microscopic maps. <i>Protein Science</i> , 2017, 26, 1619-1626.	3.1	23
39	On contribution of known atomic partial charges of protein backbone in electrostatic potential density maps. <i>Protein Science</i> , 2017, 26, 1098-1104.	3.1	17
40	On the relationship between cumulative correlation coefficients and the quality of crystallographic data sets. <i>Protein Science</i> , 2017, 26, 2410-2416.	3.1	7
41	Dynamic functional assembly of the Torsin AAA+ ATPase and its modulation by LAP1. <i>Molecular Biology of the Cell</i> , 2017, 28, 2765-2772.	0.9	26
42	Crystallographic Data Support the Carousel Mechanism of Water Supply to the Oxygen-Evolving Complex of Photosystem II. <i>ACS Energy Letters</i> , 2017, 2, 2299-2306.	8.8	58
43	Chlorophyll a with a farnesyl tail in thermophilic cyanobacteria. <i>Photosynthesis Research</i> , 2017, 134, 175-182.	1.6	12
44	On the interpretation of electron microscopic maps of biological macromolecules. <i>Protein Science</i> , 2017, 26, 122-129.	3.1	47
45	X-ray radiation-induced addition of oxygen atoms to protein residues. <i>Protein Science</i> , 2016, 25, 1407-1419.	3.1	17
46	Destruction and diffraction by X-ray free-electron laser. <i>Protein Science</i> , 2016, 25, 1585-1592.	3.1	5
47	Marangoni effect in nonequilibrium multiphase system of material processing. <i>Reviews in Chemical Engineering</i> , 2016, 32, 551-585.	2.3	14
48	Different Divalent Cations Alter the Kinetics and Fidelity of DNA Polymerases. <i>Journal of Biological Chemistry</i> , 2016, 291, 20869-20875.	1.6	81
49	Oxygen additions in serial femtosecond crystallographic protein structures. <i>Protein Science</i> , 2016, 25, 1797-1802.	3.1	12
50	S ₃ State of the O ₂ -Evolving Complex of Photosystem II: Insights from QM/MM, EXAFS, and Femtosecond X-ray Diffraction. <i>Biochemistry</i> , 2016, 55, 981-984.	1.2	62
51	Structure and function of the N-terminal domain of the human mitochondrial calcium uniporter. <i>EMBO Reports</i> , 2015, 16, 1318-1333.	2.0	81
52	A Ub/ubiquitin switch in the activation of Parkin. <i>EMBO Journal</i> , 2015, 34, 2492-2505.	3.5	164
53	Estimation of the quality of refined protein crystal structures. <i>Protein Science</i> , 2015, 24, 661-669.	3.1	19
54	On the validation of crystallographic symmetry and the quality of structures. <i>Protein Science</i> , 2015, 24, 621-632.	3.1	9

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55	Comment on “Crystal structures of translocator protein (TSPO) and mutant mimic of a human polymorphism” Science, 2015, 350, 519-519.	6.0	5
56	Crystallographic study of a MATE transporter presents a difficult case in structure determination with low-resolution, anisotropic data and crystal twinning. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2287-2296.	2.5	1
57	Numerical Simulation and Chaotic Analysis of an Aluminum Holding Furnace. Metallurgical and Materials Transactions B: Process Metallurgy and Materials Processing Science, 2014, 45, 2194-2210.	1.0	2
58	Diamonds in the rough: a strong case for the inclusion of weak-intensity X-ray diffraction data. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1491-1497.	2.5	17
59	Exploiting subtle structural differences in heavy-atom derivatives for experimental phasing. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1873-1883.	2.5	3
60	Structural models of the membrane anchors of envelope glycoproteins E1 and E2 from pestiviruses. Virology, 2014, 454-455, 93-101.	1.1	10
61	The mechanism of Torsin ATPase activation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4822-31.	3.3	84
62	Structural insights into the stabilization of MALAT1 noncoding RNA by a bipartite triple helix. Nature Structural and Molecular Biology, 2014, 21, 633-640.	3.6	213
63	Exploiting large non-isomorphous differences for phase determination of a G-segment invertase’s DNA complex. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 685-693.	2.5	4
64	Crystal structure of an intermediate of rotating dimers within the synaptic tetramer of the G-segment invertase. Nucleic Acids Research, 2013, 41, 2673-2682.	6.5	24
65	Structural and mechanistic insights into guanylation of RNA-splicing ligase RtcB joining RNA between 3’-terminal phosphate and 5’-OH. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15235-15240.	3.3	53
66	Structural Basis for Differential Insertion Kinetics of dNMPs Opposite a Difluorotoluene Nucleotide Residue. Biochemistry, 2012, 51, 1476-1485.	1.2	10
67	Tertiary architecture of the <i>Oceanobacillus iheyensis</i> group II intron. Rna, 2010, 16, 57-69.	1.6	68
68	Inclusion of weak high-resolution X-ray data for improvement of a group II intron structure. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 988-1000.	2.5	25
69	Structural basis for base discrimination by RB69 DNA polymerase. FASEB Journal, 2008, 22, 593.2.	0.2	0
70	Hoogsteen base-pairing in DNA replication?. Nature, 2005, 437, E6-E7.	13.7	29
71	Recent Cyanobacterial Kai Protein Structures Suggest a Rotary Clock. Structure, 2005, 13, 735-741.	1.6	10
72	A Twisted Four-Sheeted Model for an Amyloid Fibril. Structure, 2005, 13, 1279-1288.	1.6	27

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73	Correction of X-ray intensities from single crystals containing lattice-translocation defects. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 67-74.	2.5	38
74	Correction of X-ray intensities from an HslVâ€“HslU co-crystal containing lattice-translocation defects. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 932-941.	2.5	22
75	Crystal structure of a self-splicing group I intron with both exons. <i>Nature</i> , 2004, 430, 45-50.	13.7	431
76	Nucleotide-dependent domain motions within rings of the RecA/AAA+ superfamily. <i>Journal of Structural Biology</i> , 2004, 148, 259-267.	1.3	57
77	Domain Motions in GroEL upon Binding of an Oligopeptide. <i>Journal of Molecular Biology</i> , 2003, 334, 489-499.	2.0	49
78	Unraveling the means to the end in ATP-dependent proteases. , 2001, 8, 294-296.		19
79	New insights into the ATP-dependent Clp protease: <i>Escherichia coli</i> and beyond. <i>Molecular Microbiology</i> , 1999, 32, 449-458.	1.2	196
80	Structure of Taq polymerase with DNA at the polymerase active site. <i>Nature</i> , 1996, 382, 278-281.	13.7	333