

Jimin Wang

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

77
papers

2,729
citations

22
h-index

51
g-index

81
ext. papers

3,068
ext. citations

9.5
avg, IF

5.43
L-index

#	Paper	IF	Citations
77	High-resolution cryo-electron microscopy structure of photosystem II from the mesophilic cyanobacterium, sp. PCC 6803.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	7
76	Two-Metal-Ion Catalysis: Inhibition of DNA Polymerase Activity by a Third Divalent Metal Ion.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 824794	5.6	3
75	Glycerol binding at the narrow channel of photosystem II stabilizes the low-spin S state of the oxygen-evolving complex.. <i>Photosynthesis Research</i> , 2022 , 1	3.7	
74	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> , 2021 , 101424	5.4	6
73	Structure of a photosystem I-ferredoxin complex from a marine cyanobacterium provides insights into far-red light photoacclimation. <i>Journal of Biological Chemistry</i> , 2021 , 101408	5.4	2
72	Heterogeneous Composition of Oxygen-Evolving Complexes in Crystal Structures of Dark-Adapted Photosystem II. <i>Biochemistry</i> , 2021 , 60, 3374-3384	3.2	2
71	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,	11.5	6
70	Identification of Mg ions next to nucleotides in cryo-EM maps using electrostatic potential maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021 , 77, 534-539	5.5	2
69	Mechanism of Inhibition of the Reproduction of SARS-CoV-2 and Viruses by Remdesivir. <i>Biochemistry</i> , 2021 , 60, 1869-1875	3.2	6
68	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,	11.5	5
67	Quantitative assessment of chlorophyll types in cryo-EM maps of photosystem I acclimated to far-red light. <i>BBA Advances</i> , 2021 , 1, 100019		3
66	RNA stabilization by a poly(A) tail 3Rend binding pocket and other modes of poly(A)-RNA interaction. <i>Science</i> , 2021 , 371,	33.3	12
65	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	6.8	0
64	Structure of New Binary and Ternary DNA Polymerase Complexes From Bacteriophage RB69. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 704813	5.6	1
63	Crystal structure of the C-terminal domain of DENR. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 696-704	6.8	3
62	Identification of a Na-Binding Site near the Oxygen-Evolving Complex of Spinach Photosystem II. <i>Biochemistry</i> , 2020 , 59, 2823-2831	3.2	2
61	Opportunities and challenges for assigning cofactors in cryo-EM density maps of chlorophyll-containing proteins. <i>Communications Biology</i> , 2020 , 3, 408	6.7	11

60	Crystallographic identification of spontaneous oxidation intermediates and products of protein sulfhydryl groups. <i>Protein Science</i> , 2019 , 28, 472-477	6.3	11
59	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	6.3	3
58	Crystallographic evidence for two-metal-ion catalysis in human pol η <i>Protein Science</i> , 2019 , 28, 439-447	6.3	7
57	Structure of HIV-1 reverse transcriptase cleaving RNA in an RNA/DNA hybrid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 507-512	11.5	32
56	Determination of chemical identity and occupancy from experimental density maps. <i>Protein Science</i> , 2018 , 27, 411-420	6.3	9
55	Identification of ions in experimental electrostatic potential maps. <i>IUCrJ</i> , 2018 , 5, 375-381	4.7	14
54	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	3.4	1
53	Structural and biochemical insights into inhibition of human primase by citrate. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 507, 383-388	3.4	0
52	Misreading chaperone-substrate complexes from random noise. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 989-990	17.6	4
51	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	6.3	4
50	Reduced Occupancy of the Oxygen-Evolving Complex of Photosystem II Detected in Cryo-Electron Microscopy Maps. <i>Biochemistry</i> , 2018 , 57, 5925-5929	3.2	2
49	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	20.1	15
48	On the appearance of carboxylates in electrostatic potential maps. <i>Protein Science</i> , 2017 , 26, 396-402	6.3	15
47	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	6.3	7
46	Experimental charge density from electron microscopic maps. <i>Protein Science</i> , 2017 , 26, 1619-1626	6.3	16
45	Effects of aligned β helix peptide dipoles on experimental electrostatic potentials. <i>Protein Science</i> , 2017 , 26, 1692-1697	6.3	6
44	On contribution of known atomic partial charges of protein backbone in electrostatic potential density maps. <i>Protein Science</i> , 2017 , 26, 1098-1104	6.3	12
43	On the relationship between cumulative correlation coefficients and the quality of crystallographic data sets. <i>Protein Science</i> , 2017 , 26, 2410-2416	6.3	3

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	20.1	43
41	Chlorophyll a with a farnesyl tail in thermophilic cyanobacteria. <i>Photosynthesis Research</i> , 2017 , 134, 175-182	3.2	12
40	On the interpretation of electron microscopic maps of biological macromolecules. <i>Protein Science</i> , 2017 , 26, 122-129	6.3	39
39	Oxygen additions in serial femtosecond crystallographic protein structures. <i>Protein Science</i> , 2016 , 25, 1797-802	6.3	10
38	S3 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, 981-4	3.2	51
37	X-ray radiation-induced addition of oxygen atoms to protein residues. <i>Protein Science</i> , 2016 , 25, 1407-196.3	6.3	16
36	Destruction-and-diffraction by X-ray free-electron laser. <i>Protein Science</i> , 2016 , 25, 1585-92	6.3	4
35	On the validation of crystallographic symmetry and the quality of structures. <i>Protein Science</i> , 2015 , 24, 621-32	6.3	9
34	Comment on "Crystal structures of translocator protein (TSPO) and mutant mimic of a human polymorphism". <i>Science</i> , 2015 , 350, 519	33.3	5
33	Estimation of the quality of refined protein crystal structures. <i>Protein Science</i> , 2015 , 24, 661-9	6.3	16
32	Structural changes in the oxygen-evolving complex of photosystem II induced by the S1 to S2 transition: A combined XRD and QM/MM study. <i>Biochemistry</i> , 2014 , 53, 6860-2	3.2	39
31	Structural insights into the stabilization of MALAT1 noncoding RNA by a bipartite triple helix. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 633-40	17.6	156
30	Diamonds in the rough: a strong case for the inclusion of weak-intensity X-ray diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1491-7		15
29	Exploiting subtle structural differences in heavy-atom derivatives for experimental phasing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 1873-83		2
28	Structural models of the membrane anchors of envelope glycoproteins E1 and E2 from pestiviruses. <i>Virology</i> , 2014 , 454-455, 93-101	3.6	8
27	Exploiting large non-isomorphous differences for phase determination of a G-segment invertase-DNA complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 685-93		4
26	Calcium-dependent conformational transition of calmodulin determined by Fourier transform infrared spectroscopy. <i>International Journal of Biological Macromolecules</i> , 2013 , 56, 57-61	7.9	5
25	Crystal structure of an intermediate of rotating dimers within the synaptic tetramer of the G-segment invertase. <i>Nucleic Acids Research</i> , 2013 , 41, 2673-82	20.1	21

24	Crystal structure of glycoprotein E2 from bovine viral diarrhea virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 6805-10	11.5	90
23	Using a fluorescent cytosine analogue tC(o) to probe the effect of the Y567 to Ala substitution on the preinsertion steps of dNMP incorporation by RB69 DNA polymerase. <i>Biochemistry</i> , 2012 , 51, 4609-17 ^{3.2}	3.2	6
22	Structural basis for differential insertion kinetics of dNMPs opposite a difluorotoluene nucleotide residue. <i>Biochemistry</i> , 2012 , 51, 1476-85	3.2	10
21	Bidentate and tridentate metal-ion coordination states within ternary complexes of RB69 DNA polymerase. <i>Protein Science</i> , 2012 , 21, 447-51	6.3	8
20	Probing minor groove hydrogen bonding interactions between RB69 DNA polymerase and DNA. <i>Biochemistry</i> , 2012 , 51, 4343-53	3.2	17
19	Structural and mechanistic insights into guanylation of RNA-splicing ligase RtcB joining RNA between 3Rterminal phosphate and 5ROH. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 15235-40	11.5	36
18	Variation in mutation rates caused by RB69pol fidelity mutants can be rationalized on the basis of their kinetic behavior and crystal structures. <i>Journal of Molecular Biology</i> , 2011 , 406, 558-70	6.5	18
17	Structural insights into complete metal ion coordination from ternary complexes of B family RB69 DNA polymerase. <i>Biochemistry</i> , 2011 , 50, 9114-24	3.2	33
16	Insights into base selectivity from the 1.8 Å resolution structure of an RB69 DNA polymerase ternary complex. <i>Biochemistry</i> , 2011 , 50, 581-90	3.2	37
15	Poly(A) tail recognition by a viral RNA element through assembly of a triple helix. <i>Science</i> , 2010 , 330, 1244-7	33.3	122
14	Tertiary architecture of the <i>Oceanobacillus iheyensis</i> group II intron. <i>Rna</i> , 2010 , 16, 57-69	5.8	62
13	Inclusion of weak high-resolution X-ray data for improvement of a group II intron structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 988-1000		25
12	RB69 DNA polymerase mutants with expanded nascent base-pair-binding pockets are highly efficient but have reduced base selectivity. <i>Biochemistry</i> , 2009 , 48, 6940-50	3.2	22
11	DNA polymerases: Hoogsteen base-pairing in DNA replication?. <i>Nature</i> , 2005 , 437, E6-7; discussion E7	50.4	25
10	A twisted four-sheeted model for an amyloid fibril. <i>Structure</i> , 2005 , 13, 1279-88	5.2	25
9	Correction of X-ray intensities from single crystals containing lattice-translocation defects. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 67-74		33
8	Correction of X-ray intensities from an HslV-HslU co-crystal containing lattice-translocation defects. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 932-41		20
7	Crystal structure of a self-splicing group I intron with both exons. <i>Nature</i> , 2004 , 430, 45-50	50.4	389

6	Visualizing a circadian clock protein: crystal structure of KaiC and functional insights. <i>Molecular Cell</i> , 2004 , 15, 375-88	17.6	147
5	A corrected quaternary arrangement of the peptidase HslV and atpase HslU in a cocrystal structure. <i>Journal of Structural Biology</i> , 2001 , 134, 15-24	3.4	21
4	Structure of the replicating complex of a pol alpha family DNA polymerase. <i>Cell</i> , 2001 , 105, 657-67	56.2	507
3	Crystal structure determination of Escherichia coli ClpP starting from an EM-derived mask. <i>Journal of Structural Biology</i> , 1998 , 124, 151-63	3.4	42
2	The 2.4 Å crystal structure of the bacterial chaperonin GroEL complexed with ATP gamma S. <i>Nature Structural Biology</i> , 1996 , 3, 170-7		211
1	X-ray structures of recombinant yeast cytochrome c peroxidase and three heme-cleft mutants prepared by site-directed mutagenesis. <i>Biochemistry</i> , 1990 , 29, 7160-73	3.2	135