Jimin Wang

List of Publications by Year in descending order

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LIMIN WANC

#	Article	IF	CITATIONS
1	Structure of the Replicating Complex of a Pol Î \pm Family DNA Polymerase. Cell, 2001, 105, 657-667.	13.5	547
2	Crystal structure of a self-splicing group I intron with both exons. Nature, 2004, 430, 45-50.	13.7	431
3	The 2.4 à crystal structure of the bacterial chaperonin GroEL complexed with ATPγS. Nature Structural Biology, 1996, 3, 170-177.	9.7	243
4	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
5	Visualizing a Circadian Clock Protein. Molecular Cell, 2004, 15, 375-388.	4.5	179
6	X-ray structures of recombinant yeast cytochrome c peroxidase and three heme-cleft mutants prepared by site-directed mutagenesis. Biochemistry, 1990, 29, 7160-7173.	1.2	145
7	Poly(A) Tail Recognition by a Viral RNA Element Through Assembly of a Triple Helix. Science, 2010, 330, 1244-1247.	6.0	144
8	Crystal structure of glycoprotein E2 from bovine viral diarrhea virus. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6805-6810.	3.3	108
9	Tertiary architecture of the <i>Oceanobacillus iheyensis</i> group II intron. Rna, 2010, 16, 57-69.	1.6	68
10	S ₃ State of the O ₂ -Evolving Complex of Photosystem II: Insights from QM/MM, EXAFS, and Femtosecond X-ray Diffraction. Biochemistry, 2016, 55, 981-984.	1.2	62
11	Crystallographic Data Support the Carousel Mechanism of Water Supply to the Oxygen-Evolving Complex of Photosystem II. ACS Energy Letters, 2017, 2, 2299-2306.	8.8	58
12	High-resolution cryo-electron microscopy structure of photosystem II from the mesophilic cyanobacterium, <i>Synechocystis</i> sp. PCC 6803. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	58
13	Structural and mechanistic insights into guanylylation 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
14	On the interpretation of electron microscopic maps of biological macromolecules. Protein Science, 2017, 26, 122-129.	3.1	47
15	Crystal Structure Determination ofEscherichia coliClpP Starting from an EM-Derived Mask. Journal of Structural Biology, 1998, 124, 151-163.	1.3	46
16	Structural Changes in the Oxygen-Evolving Complex of PhotosystemÂll Induced by the S ₁ to S ₂ Transition: A Combined XRD and QM/MM Study. Biochemistry, 2014, 53, 6860-6862.	1.2	46
17	Insights into Base Selectivity from the 1.8 Ã Resolution Structure of an RB69 DNA Polymerase Ternary Complex. Biochemistry, 2011, 50, 581-590.	1.2	43
18	Structure of HIV-1 reverse transcriptase cleaving RNA in an RNA/DNA hybrid. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 507-512.	3.3	39

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19	Correction of X-ray intensities from single crystals containing lattice-translocation defects. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 67-74.	2.5	38
20	Structural Insights into Complete Metal Ion Coordination from Ternary Complexes of B Family RB69 DNA Polymerase. Biochemistry, 2011, 50, 9114-9124.	1.2	35
21	Structure of a monomeric photosystem II core complex from a cyanobacterium acclimated to far-red light reveals the functions of chlorophylls d and f. Journal of Biological Chemistry, 2022, 298, 101424.	1.6	32
22	Hoogsteen base-pairing in DNA replication?. Nature, 2005, 437, E6-E7.	13.7	29
23	RNA stabilization by a poly(A) tail 3′-end binding pocket and other modes of poly(A)-RNA interaction. Science, 2021, 371, .	6.0	29
24	A Twisted Four-Sheeted Model for an Amyloid Fibril. Structure, 2005, 13, 1279-1288.	1.6	27
25	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
26	RB69 DNA Polymerase Mutants with Expanded Nascent Base-Pair-Binding Pockets Are Highly Efficient but Have Reduced Base Selectivity. Biochemistry, 2009, 48, 6940-6950.	1.2	24
27	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
28	On the appearance of carboxylates in electrostatic potential maps. Protein Science, 2017, 26, 396-402.	3.1	24
29	A Corrected Quaternary Arrangement of the Peptidase HslV and ATPase HslU in a Cocrystal Structure. Journal of Structural Biology, 2001, 134, 15-24.	1.3	23
30	Experimental charge density from electron microscopic maps. Protein Science, 2017, 26, 1619-1626.	3.1	23
31	Correction of X-ray intensities from an HslV–HslU co-crystal containing lattice-translocation defects. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 932-941.	2.5	22
32	Identification of ions in experimental electrostatic potential maps. IUCrJ, 2018, 5, 375-381.	1.0	22
33	Opportunities and challenges for assigning cofactors in cryo-EM density maps of chlorophyll-containing proteins. Communications Biology, 2020, 3, 408.	2.0	21
34	Estimation of the quality of refined protein crystal structures. Protein Science, 2015, 24, 661-669.	3.1	19
35	Variation in Mutation Rates Caused by RB69pol Fidelity Mutants Can Be Rationalized on the Basis of Their Kinetic Behavior and Crystal Structures. Journal of Molecular Biology, 2011, 406, 558-570.	2.0	18
36	Probing Minor Groove Hydrogen Bonding Interactions between RB69 DNA Polymerase and DNA. Biochemistry, 2012, 51, 4343-4353.	1.2	17

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37	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
38	Xâ€ray radiationâ€induced addition of oxygen atoms to protein residues. Protein Science, 2016, 25, 1407-1419.	3.1	17
39	On contribution of known atomic partial charges of protein backbone in electrostatic potential density maps. Protein Science, 2017, 26, 1098-1104.	3.1	17
40	Insights into Photosystem II from Isomorphous Difference Fourier Maps of Femtosecond X-ray Diffraction Data and Quantum Mechanics/Molecular Mechanics Structural Models. ACS Energy Letters, 2017, 2, 397-407.	8.8	16
41	Structure of a photosystem I-ferredoxin complex from a marine cyanobacterium provides insights into far-red light photoacclimation. Journal of Biological Chemistry, 2022, 298, 101408.	1.6	16
42	Two-Metal-Ion Catalysis: Inhibition of DNA Polymerase Activity by a Third Divalent Metal Ion. Frontiers in Molecular Biosciences, 2022, 9, 824794.	1.6	15
43	Crystallographic identification of spontaneous oxidation intermediates and products of protein sulfhydryl groups. Protein Science, 2019, 28, 472-477.	3.1	13
44	Crystallographic evidence for twoâ€metalâ€ion catalysis in human pol Î∙. Protein Science, 2019, 28, 439-447.	3.1	13
45	Structural analyses of an RNA stability element interacting with poly(A). Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	13
46	Oxygen additions in serial femtosecond crystallographic protein structures. Protein Science, 2016, 25, 1797-1802.	3.1	12
47	Chlorophyll a with a farnesyl tail in thermophilic cyanobacteria. Photosynthesis Research, 2017, 134, 175-182.	1.6	12
48	Mechanism of Inhibition of the Reproduction of SARS-CoV-2 and <i>Ebola</i> Viruses by Remdesivir. Biochemistry, 2021, 60, 1869-1875.	1.2	12
49	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. Biochemistry, 2022, 61, 785-794.	1.2	12
50	Determination of chemical identity and occupancy from experimental density maps. Protein Science, 2018, 27, 411-420.	3.1	11
51	Do crystallographic XFEL data support binding of a water molecule to the oxygen-evolving complex of photosystem II exposed to two flashes of light?. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	11
52	Structural Basis for Differential Insertion Kinetics of dNMPs Opposite a Difluorotoluene Nucleotide Residue. Biochemistry, 2012, 51, 1476-1485.	1.2	10
53	Structural models of the membrane anchors of envelope glycoproteins E1 and E2 from pestiviruses. Virology, 2014, 454-455, 93-101.	1.1	10
54	Computational insights into the membrane fusion mechanism of SARS-CoV-2 at the cellular level. Computational and Structural Biotechnology Journal, 2021, 19, 5019-5028.	1.9	10

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55	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. Biochemistry, 2022, 61, 424-432.	1.2	10
56	On the validation of crystallographic symmetry and the quality of structures. Protein Science, 2015, 24, 621-632.	3.1	9
57	Identification of Mg ²⁺ ions next to nucleotides in cryo-EM maps using electrostatic potential maps. Acta Crystallographica Section D: Structural Biology, 2021, 77, 534-539.	1.1	9
58	Bidentate and tridentate metalâ€ion coordination states within ternary complexes of RB69 DNA polymerase. Protein Science, 2012, 21, 447-451.	3.1	8
59	Systematic analysis of residual density suggests that a major limitation in wellâ€refined Xâ€ray structures of proteins is the omission of ordered solvent. Protein Science, 2017, 26, 1012-1023.	3.1	8
60	Heterogeneous Composition of Oxygen-Evolving Complexes in Crystal Structures of Dark-Adapted Photosystem II. Biochemistry, 2021, 60, 3374-3384.	1.2	8
61	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. Biochemistry, 2012, 51, 4609-4617.	1.2	7
62	Effects of aligned αâ€helix peptide dipoles on experimental electrostatic potentials. Protein Science, 2017, 26, 1692-1697.	3.1	7
63	On the relationship between cumulative correlation coefficients and the quality of crystallographic data sets. Protein Science, 2017, 26, 2410-2416.	3.1	7
64	Misreading chaperone–substrate complexes from random noise. Nature Structural and Molecular Biology, 2018, 25, 989-990.	3.6	7
65	Calcium-dependent conformational transition of calmodulin determined by Fourier transform infrared spectroscopy. International Journal of Biological Macromolecules, 2013, 56, 57-61.	3.6	6
66	Visualization of H atoms in the Xâ€ray crystal structure of photoactive yellow protein: Does it contain Iowâ€barrier hydrogen bonds?. Protein Science, 2019, 28, 1966-1972.	3.1	6
67	Quantitative assessment of chlorophyll types in cryo-EM maps of photosystem I acclimated to far-red light. BBA Advances, 2021, 1, 100019.	0.7	6
68	Comment on "Crystal structures of translocator protein (TSPO) and mutant mimic of a human polymorphism― Science, 2015, 350, 519-519.	6.0	5
69	Destructionâ€andâ€diffraction by Xâ€ray freeâ€electron laser. Protein Science, 2016, 25, 1585-1592.	3.1	5
70	On the damage done to the structure of the <i>Thermoplasma acidophilum</i> proteasome by electron radiation. Protein Science, 2018, 27, 2051-2061.	3.1	5
71	Identification of a Na ⁺ -Binding Site near the Oxygen-Evolving Complex of Spinach Photosystem II. Biochemistry, 2020, 59, 2823-2831.	1.2	5
72	Structural and biochemical insights into inhibition of human primase by citrate. Biochemical and Biophysical Research Communications, 2018, 507, 383-388.	1.0	4

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73	Exploiting large non-isomorphous differences for phase determination of a G-segment invertase–DNA complex. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 685-693.	2.5	4
74	Exploiting subtle structural differences in heavy-atom derivatives for experimental phasing. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1873-1883.	2.5	3
75	Reduced Occupancy of the Oxygen-Evolving Complex of Photosystem II Detected in Cryo-Electron Microscopy Maps. Biochemistry, 2018, 57, 5925-5929.	1.2	3
76	Crystal structure of the C-terminal domain of DENR. Computational and Structural Biotechnology Journal, 2020, 18, 696-704.	1.9	3
77	Structure of New Binary and Ternary DNA Polymerase Complexes From Bacteriophage RB69. Frontiers in Molecular Biosciences, 2021, 8, 704813.	1.6	3
78	Structural insights into the oligomerization of FtsH periplasmic domain from Thermotoga maritima. Biochemical and Biophysical Research Communications, 2018, 495, 1201-1207.	1.0	2
79	Glycerol binding at the narrow channel of photosystem II stabilizes the low-spin S2 state of the oxygen-evolving complex. Photosynthesis Research, 2022, , 1.	1.6	1