

# Zhong Ren

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

1,590  
citations

586496

16  
h-index

536525

29  
g-index

40  
all docs

40  
docs citations

40  
times ranked

1965  
citing authors

#	ARTICLE	IF	CITATIONS
1	On-chip Crystallization and Large-Scale Serial Diffraction at Room Temperature. <i>Journal of Visualized Experiments</i> , 2022, , .	0.2	1
2	Assembly of $\pi$ -Stacking Helical Peptides into a Porous and Multivariable Proteomimetic Framework. <i>Journal of the American Chemical Society</i> , 2022, 144, 7001-7009.	6.6	16
3	Light-induced protein structural dynamics in bacteriophytochrome revealed by time-resolved x-ray solution scattering. <i>Science Advances</i> , 2022, 8, .	4.7	10
4	Photoinduced isomerization sampling of retinal in bacteriorhodopsin. , 2022, 1, .		3
5	Crystal structure of a far-red $\lambda$ -sensing cyanobacteriochrome reveals an atypical bilin conformation and spectral tuning mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
6	Dimer Asymmetry and Light Activation Mechanism in <i>Brucella</i> Blue-Light Sensor Histidine Kinase. <i>MBio</i> , 2021, 12, .	1.8	12
7	An automated platform for <i>in situ</i> serial crystallography at room temperature. <i>IUCr</i> , 2020, 7, 1009-1018.	1.0	8
8	Ultrafast Structural Changes Decomposed from Serial Crystallographic Data. <i>Journal of Physical Chemistry Letters</i> , 2019, 10, 7148-7163.	2.1	8
9	Structural basis of molecular logic OR in a dual-sensor histidine kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19973-19982.	3.3	16
10	Modes of Cholesterol Binding in Membrane Proteins: A Joint Analysis of 73 Crystal Structures. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1135, 67-86.	0.8	13
11	Crystal-on-crystal chips for <i>in situ</i> serial diffraction at room temperature. <i>Lab on A Chip</i> , 2018, 18, 2246-2256.	3.1	25
12	The role of dimer asymmetry and protomer dynamics in enzyme catalysis. <i>Science</i> , 2017, 355, .	6.0	155
13	Crystal Structures of Bacterial (6 $\lambda$ ) Photolyase Mutants with Impaired DNA Repair Activity. <i>Photochemistry and Photobiology</i> , 2017, 93, 304-314.	1.3	12
14	Photoactivation mechanism of a carotenoid-based photoreceptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6286-6291.	3.3	64
15	Angular-split/temporal-delay approach to ultrafast protein dynamics at XFELs. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 871-882.	1.1	2
16	Transmembrane Helices Tilt, Bend, Slide, Torque, and Unwind between Functional States of Rhodopsin. <i>Scientific Reports</i> , 2016, 6, 34129.	1.6	24
17	Molecular events during translocation and proofreading extracted from 200 static structures of DNA polymerase. <i>Nucleic Acids Research</i> , 2016, 44, gkw555.	6.5	16
18	How Does Photoreceptor UVR8 Perceive a UV $\alpha$ Signal?. <i>Photochemistry and Photobiology</i> , 2015, 91, 993-1003.	1.3	17

#	ARTICLE	IF	CITATIONS
19	Dynamic crystallography reveals early signalling events in ultraviolet photoreceptor LVR8. <i>Nature Plants</i> , 2015, 1, .	4.7	48
20	Towards time-resolved serial crystallography in a microfluidic device. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 823-830.	0.4	29
21	<i>In situ</i> serial Laue diffraction on a microfluidic crystallization device. <i>Journal of Applied Crystallography</i> , 2014, 47, 1975-1982.	1.9	29
22	Signal to noise considerations for single crystal femtosecond time resolved crystallography of the Photoactive Yellow Protein. <i>Faraday Discussions</i> , 2014, 171, 439-455.	1.6	19
23	Resolution of structural heterogeneity in dynamic crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 946-959.	2.5	32
24	Reaction Trajectory Revealed by a Joint Analysis of Protein Data Bank. <i>PLoS ONE</i> , 2013, 8, e77141.	1.1	16
25	Reverse Engineering the Cooperative Machinery of Human Hemoglobin. <i>PLoS ONE</i> , 2013, 8, e77363.	1.1	12
26	Cooperative macromolecular device revealed by meta-analysis of static and time-resolved structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 107-112.	3.3	42
27	Temperature-scan cryocrystallography reveals reaction intermediates in bacteriophytochrome. <i>Nature</i> , 2011, 479, 428-432.	13.7	155
28	Application of Singular Value Decomposition to the Analysis of Time-Resolved Macromolecular X-Ray Data. <i>Biophysical Journal</i> , 2003, 84, 2112-2129.	0.2	146
29	Protein Conformational Relaxation and Ligand Migration in Myoglobin: A Nanosecond to Millisecond Molecular Movie from Time-Resolved Laue X-ray Diffraction. <i>Biochemistry</i> , 2001, 40, 13802-13815.	1.2	329
30	A Molecular Movie at 1.8 Å... Resolution Displays the Photocycle of Photoactive Yellow Protein, a Eubacterial Blue-Light Receptor, from Nanoseconds to Seconds. <i>Biochemistry</i> , 2001, 40, 13788-13801.	1.2	190
31	Laue crystallography: coming of age. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 891-917.	1.0	122
32	Novel insights into the allosteric gating mechanism of MthK channel. <i>National Science Review</i> , 0, , .	4.6	0