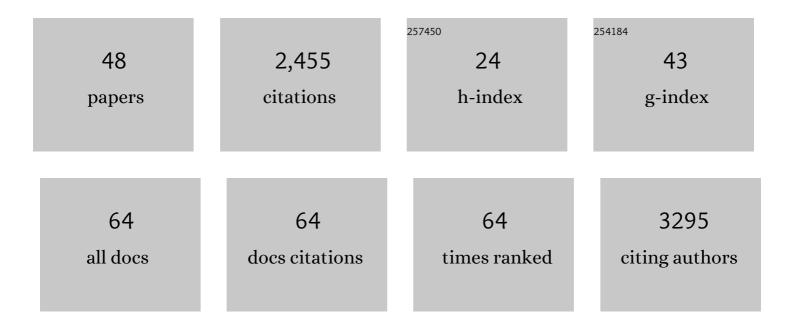
Kaiming Zhang

List of Publications by Year in descending order

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KAIMING ZHANG

#	Article	IF	CITATIONS
1	Designer nanoscale DNA assemblies programmed from the top down. Science, 2016, 352, 1534-1534.	12.6	500
2	Measurement of atom resolvability in cryo-EM maps with Q-scores. Nature Methods, 2020, 17, 328-334.	19.0	230
3	A Single Immunization with Spike-Functionalized Ferritin Vaccines Elicits Neutralizing Antibody Responses against SARS-CoV-2 in Mice. ACS Central Science, 2021, 7, 183-199.	11.3	134
4	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. Nature Methods, 2020, 17, 699-707.	19.0	119
5	Cryo-EM and antisense targeting of the 28-kDa frameshift stimulation element from the SARS-CoV-2 RNA genome. Nature Structural and Molecular Biology, 2021, 28, 747-754.	8.2	91
6	Cryo-EM structure of a 40ÂkDa SAM-IV riboswitch RNA at 3.7 à resolution. Nature Communications, 2019, 10, 5511.	12.8	90
7	Ultra-thermostable RNA nanoparticles for solubilizing and high-yield loading of paclitaxel for breast cancer therapy. Nature Communications, 2020, 11, 972.	12.8	86
8	Automated Sequence Design of 3D Polyhedral Wireframe DNA Origami with Honeycomb Edges. ACS Nano, 2019, 13, 2083-2093.	14.6	77
9	Cryo-EM Structures of Human Drosha and DGCR8 in Complex with Primary MicroRNA. Molecular Cell, 2020, 78, 411-422.e4.	9.7	75
10	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	19.0	73
11	Controllable Selfâ€Assembly of RNA Tetrahedrons with Precise Shape and Size for Cancer Targeting. Advanced Materials, 2016, 28, 7501-7507.	21.0	70
12	Resolving individualÂatoms of protein complex by cryo-electron microscopy. Cell Research, 2020, 30, 1136-1139.	12.0	69
13	Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1ÂÃ resolution. Nature, 2021, 596, 603-607.	27.8	59
14	A Novel Mechanism for Small Heat Shock Proteins to Function as Molecular Chaperones. Scientific Reports, 2015, 5, 8811.	3.3	56
15	Fabrication of RNA 3D Nanoprisms for Loading and Protection of Small RNAs and Model Drugs. Advanced Materials, 2016, 28, 10079-10087.	21.0	54
16	Cryo-EM advances in RNA structure determination. Signal Transduction and Targeted Therapy, 2022, 7, 58.	17.1	54
17	Structure of the 30ÂkDa HIV-1 RNA Dimerization Signal by a Hybrid Cryo-EM, NMR, and Molecular Dynamics Approach. Structure, 2018, 26, 490-498.e3.	3.3	52
18	Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. Nature Structural and Molecular Biology, 2019, 26, 1094-1105.	8.2	52

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19	Structure of human immunoproteasome with a reversible and noncompetitive inhibitor that selectively inhibits activated lymphocytes. Nature Communications, 2017, 8, 1692.	12.8	45
20	A Small Heat Shock Protein Enables Escherichia coli To Grow at a Lethal Temperature of 50ÂC Conceivably by Maintaining Cell Envelope Integrity. Journal of Bacteriology, 2014, 196, 2004-2011.	2.2	43
21	Mapping the catalytic conformations of an assembly-line polyketide synthase module. Science, 2021, 374, 729-734.	12.6	41
22	Coupling of ssRNA cleavage with DNase activity in type III-A CRISPR-Csm revealed by cryo-EM and biochemistry. Cell Research, 2019, 29, 305-312.	12.0	40
23	Inhibition mechanisms of AcrF9, AcrF8, and AcrF6 against type I-F CRISPR–Cas complex revealed by cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7176-7182.	7.1	35
24	Cryo-EM structures of <i>Helicobacter pylori</i> vacuolating cytotoxin A oligomeric assemblies at near-atomic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6800-6805.	7.1	33
25	Photo-controlled release of paclitaxel and model drugs from RNA pyramids. Nano Research, 2019, 12, 41-48.	10.4	32
26	Structure of Calcarisporiella thermophila Hsp104 Disaggregase that Antagonizes Diverse Proteotoxic Misfolding Events. Structure, 2019, 27, 449-463.e7.	3.3	29
27	Structure of the G protein chaperone and guanine nucleotide exchange factor Ric-8A bound to Gαi1. Nature Communications, 2020, 11, 1077.	12.8	18
28	The molecular architecture of dihydropyrindine receptor/L-type Ca2+ channel complex. Scientific Reports, 2015, 5, 8370.	3.3	14
29	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, .	7.1	13
30	Molecular basis for ATPase-powered substrate translocation by the Lon AAA+ protease. Journal of Biological Chemistry, 2021, 297, 101239.	3.4	12
31	A 3.4-Ã cryo-electron microscopy structure of the human coronavirus spike trimer computationally derived from vitrified NL63 virus particles. QRB Discovery, 2020, 1, e11.	1.6	10
32	Planar 2D wireframe DNA origami. Science Advances, 2022, 8, .	10.3	10
33	Processive cleavage of substrate at individual proteolytic active sites of the Lon protease complex. Science Advances, 2021, 7, eabj9537.	10.3	9
34	A prototype protein nanocage minimized from carboxysomes with gated oxygen permeability. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
35	RNA nanotechnology to build a dodecahedral genome of single-stranded RNA virus. RNA Biology, 2021, 18, 2390-2400.	3.1	8
36	Complete three-dimensional structures of the Lon protease translocating a protein substrate. Science Advances, 2021, 7, eabj7835.	10.3	7

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#	Article	IF	CITATIONS
37	Cryo-EM, Protein Engineering, and Simulation Enable the Development of Peptide Therapeutics against Acute Myeloid Leukemia. ACS Central Science, 2022, 8, 214-222.	11.3	7
38	Bacteriophage Twort protein Gp168 is a β-clamp inhibitor by occupying the DNA sliding channel. Nucleic Acids Research, 2021, 49, 11367-11378.	14.5	6
39	The Role of Magnetoelastic Field Related to Underlayers on Magnetic Properties of FeCo Thin Films. IEEE Transactions on Magnetics, 2012, 48, 2917-2920.	2.1	5
40	3D RNA nanocage for encapsulation and shielding of hydrophobic biomolecules to improve the in vivo biodistribution. Nano Research, 2020, 13, 3241-3247.	10.4	4
41	Bacteriophage protein PEIP is a potent Bacillus subtilis enolase inhibitor. Cell Reports, 2022, 40, 111026.	6.4	4
42	Regulation of reversible conformational change, size switching, and immunomodulation of RNA nanocubes. Rna, 2021, 27, 971-980.	3.5	2
43	Structure of the Anthrax Protective Antigen D425A Dominant Negative Mutant Reveals a Stalled Intermediate State of Pore Maturation. Journal of Molecular Biology, 2022, 434, 167548.	4.2	2
44	The Function of Ile-X-Ile Motif in the Oligomerization and Chaperone-Like Activity of Small Heat Shock Protein AgsA at Room Temperature. Protein Journal, 2016, 35, 401-406.	1.6	0
45	Binding affinity analysis of the interaction between Homer EVH domain and ryanodine receptor with biosensors based on imaging ellipsometry. Analytical Methods, 2016, 8, 2936-2940.	2.7	0
46	Classification using diffraction patterns for single-particle analysis. Ultramicroscopy, 2016, 164, 46-50.	1.9	0
47	High Resolution Data Collection at S2C2, a National CryoEM Center. Microscopy and Microanalysis, 2021, 27, 1152-1154.	0.4	0
48	The structure of the complex of the cytoplasmic guanine nucleotide exchange factor Ric-8A bound to Gαi1. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a175-a175.	0.1	0