

Youdong Mao

List of Publications by Year in descending order

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44
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293460

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54
all docs

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docs citations

54
times ranked

4817
citing authors

#	ARTICLE	IF	CITATIONS
1	USP14-regulated allostery of the human proteasome by time-resolved cryo-EM. <i>Nature</i> , 2022, 605, 567-574.	13.7	38
2	Asymmetric Structures and Conformational Plasticity of the Uncleaved Full-Length Human Immunodeficiency Virus Envelope Glycoprotein Trimer. <i>Journal of Virology</i> , 2021, 95, e0052921.	1.5	20
3	Structure, Dynamics and Function of the 26S Proteasome. <i>Sub-Cellular Biochemistry</i> , 2021, 96, 1-151.	1.0	64
4	AAA+ ATPases in Protein Degradation: Structures, Functions and Mechanisms. <i>Biomolecules</i> , 2020, 10, 629.	1.8	37
5	Structural mechanism for NEK7-licensed activation of NLRP3 inflammasome. <i>Nature</i> , 2019, 570, 338-343.	13.7	467
6	Robustness of signal detection in cryo-electron microscopy via a bi-objective-function approach. <i>BMC Bioinformatics</i> , 2019, 20, 169.	1.2	4
7	DNA Origami as Scaffolds for Self-Assembly of Lipids and Proteins. <i>ChemBioChem</i> , 2019, 20, 2422-2431.	1.3	13
8	Cryo-EM structures and dynamics of substrate-engaged human 26S proteasome. <i>Nature</i> , 2019, 565, 49-55.	13.7	264
9	Frontispiz: Folding DNA into a Lipid-Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. <i>Angewandte Chemie</i> , 2018, 130, .	1.6	0
10	Structural mechanism for nucleotide-driven remodeling of the AAA-ATPase unfoldase in the activated human 26S proteasome. <i>Nature Communications</i> , 2018, 9, 1360.	5.8	74
11	Frontispiece: Folding DNA into a Lipid-Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. <i>Angewandte Chemie - International Edition</i> , 2018, 57, .	7.2	0
12	Folding DNA into a Lipid-Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. <i>Angewandte Chemie</i> , 2018, 130, 2094-2098.	1.6	11
13	Folding DNA into a Lipid-Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 2072-2076.	7.2	36
14	Residues in the gp41 Ectodomain Regulate HIV-1 Envelope Glycoprotein Conformational Transitions Induced by gp120-Directed Inhibitors. <i>Journal of Virology</i> , 2017, 91, .	1.5	53
15	Conformational Landscape of the p28-Bound Human Proteasome Regulatory Particle. <i>Molecular Cell</i> , 2017, 67, 322-333.e6.	4.5	35
16	Cryo-EM structure of the DNA-PK holoenzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7367-7372.	3.3	74
17	Evaluation of the contribution of the transmembrane region to the ectodomain conformation of the human immunodeficiency virus (HIV-1) envelope glycoprotein. <i>Virology Journal</i> , 2017, 14, 33.	1.4	11
18	Massively parallel unsupervised single-particle cryo-EM data clustering via statistical manifold learning. <i>PLoS ONE</i> , 2017, 12, e0182130.	1.1	44

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19	A deep convolutional neural network approach to single-particle recognition in cryo-electron microscopy. <i>BMC Bioinformatics</i> , 2017, 18, 348.	1.2	126
20	Molecular basis of caspase-1 polymerization and its inhibition by a new capping mechanism. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 416-425.	3.6	135
21	Structural basis for dynamic regulation of the human 26S proteasome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12991-12996.	3.3	147
22	Unsupervised Cryo-EM Data Clustering through Adaptively Constrained K-Means Algorithm. <i>PLoS ONE</i> , 2016, 11, e0167765.	1.1	7
23	Abstract B134:Cryo-EM structure of the activated NAIP2-NLRC4 inflammasome reveals nucleated polymerization. , 2016, , .		0
24	Comparative Analysis of the Glycosylation Profiles of Membrane-Anchored HIV-1 Envelope Glycoprotein Trimers and Soluble gp140. <i>Journal of Virology</i> , 2015, 89, 8245-8257.	1.5	99
25	Cryo-EM structure of the activated NAIP2-NLRC4 inflammasome reveals nucleated polymerization. <i>Science</i> , 2015, 350, 404-409.	6.0	347
26	Reply to Subramaniam, van Heel, and Henderson: Validity of the cryo-electron microscopy structures of the HIV-1 envelope glycoprotein complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4178-82.	3.3	19
27	The Highly Conserved Layer-3 Component of the HIV-1 gp120 Inner Domain Is Critical for CD4-Required Conformational Transitions. <i>Journal of Virology</i> , 2013, 87, 2549-2562.	1.5	49
28	Molecular architecture of the uncleaved HIV-1 envelope glycoprotein trimer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12438-12443.	3.3	101
29	A Twin-Cysteine Motif in the V2 Region of gp120 Is Associated with SIV Envelope Trimer Stabilization. <i>PLoS ONE</i> , 2013, 8, e69406.	1.1	19
30	Subunit organization of the membrane-bound HIV-1 envelope glycoprotein trimer. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 893-899.	3.6	151
31	Understanding Thermodynamic Competitiveness between Biopolymer Folding and Misfolding under Large-Scale Intermolecular Interactions. <i>Journal of the American Chemical Society</i> , 2012, 134, 631-639.	6.6	5
32	Graphene Structures at an Extreme Degree of Buckling. <i>ACS Nano</i> , 2011, 5, 1395-1400.	7.3	43
33	Characterization of a core fragment of the rhesus monkey TRIM5 α protein. <i>BMC Biochemistry</i> , 2011, 12, 1.	4.4	20
34	In vivo nanomechanical imaging of blood-vessel tissues directly in living mammals using atomic force microscopy. <i>Applied Physics Letters</i> , 2009, 95, 013704.	1.5	38
35	Reversibly switchable DNA nanocompartment on surfaces: experiments, applications, and theory. <i>Frontiers of Physics in China</i> , 2008, 3, 74-87.	1.0	0
36	Gating of Single Synthetic Nanopores by Proton-Driven DNA Molecular Motors. <i>Journal of the American Chemical Society</i> , 2008, 130, 8345-8350.	6.6	295

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37	Alternating-electric-field-enhanced reversible switching of DNA nanocontainers with pH. <i>Nucleic Acids Research</i> , 2007, 35, e33.	6.5	73
38	Tunable non-equilibrium gating of flexible DNA nanochannels in response to transport flux. <i>Nature Nanotechnology</i> , 2007, 2, 366-371.	15.6	24
39	Monte Carlo simulation of melting transition on DNA nanocompartment. <i>Journal of Physics: Conference Series</i> , 2006, 29, 18-26.	0.3	3
40	Reversibly switchable DNA nanocompartment on surfaces. <i>Nucleic Acids Research</i> , 2004, 32, e144-e144.	6.5	16
41	Studies of temperature-dependent electronic transduction on DNA hairpin loop sensor. <i>Nucleic Acids Research</i> , 2003, 31, 108e-108.	6.5	76
42	The Realization of a Fast and Effective Optimization Method on Atomic Structure. <i>Journal of the Physical Society of Japan</i> , 2002, 71, 762-766.	0.7	0
43	Using an evolutionary algorithm based on cell division operation to calculate ground-state energies of double-electron systems in magnetic fields. <i>Chinese Physics B</i> , 2001, 10, 1118-1123.	1.3	0
44	USING EVOLUTIONARY ALGORITHM TO CALCULATE THE GROUND-STATE ENERGY OF DOUBLE-ELECTRON ATOMS IN A UNIFORM MAGNETIC FIELD ($B \approx 10^9$ G). <i>International Journal of Modern Physics C</i> , 2000, 11, 183-194.	0.8	6