Youdong Mao

List of Publications by Year
in descending order

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44 papers	3,067 citations	257450 24 h-index	315739 38 g-index
54 all docs	54 docs citations	54 times ranked	4278 citing authors

#	Article	IF	Citations
1	Structural mechanism for NEK7-licensed activation of NLRP3 inflammasome. Nature, 2019, 570, 338-343.	27.8	467
2	Cryo-EM structure of the activated NAIP2-NLRC4 inflammasome reveals nucleated polymerization. Science, 2015, 350, 404-409.	12.6	347
3	Gating of Single Synthetic Nanopores by Proton-Driven DNA Molecular Motors. Journal of the American Chemical Society, 2008, 130, 8345-8350.	13.7	295
4	Cryo-EM structures and dynamics of substrate-engaged human 26S proteasome. Nature, 2019, 565, 49-55.	27.8	264
5	Subunit organization of the membrane-bound HIV-1 envelope glycoprotein trimer. Nature Structural and Molecular Biology, 2012, 19, 893-899.	8.2	151
6	Structural basis for dynamic regulation of the human 26S proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12991-12996.	7.1	147
7	Molecular basis of caspase-1 polymerization and its inhibition by a new capping mechanism. Nature Structural and Molecular Biology, 2016, 23, 416-425.	8.2	135
8	A deep convolutional neural network approach to single-particle recognition in cryo-electron microscopy. BMC Bioinformatics, 2017, 18, 348.	2.6	126
9	Molecular architecture of the uncleaved HIV-1 envelope glycoprotein trimer. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12438-12443.	7.1	101
10	Comparative Analysis of the Glycosylation Profiles of Membrane-Anchored HIV-1 Envelope Glycoprotein Trimers and Soluble gp140. Journal of Virology, 2015, 89, 8245-8257.	3.4	99
11	Studies of temperature-dependent electronic transduction on DNA hairpin loop sensor. Nucleic Acids Research, 2003, 31, 108e-108.	14.5	76
12	Cryo-EM structure of the DNA-PK holoenzyme. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7367-7372.	7.1	74
13	Structural mechanism for nucleotide-driven remodeling of the AAA-ATPase unfoldase in the activated human 26S proteasome. Nature Communications, 2018, 9, 1360.	12.8	74
14	Alternating-electric-field-enhanced reversible switching of DNA nanocontainers with pH. Nucleic Acids Research, 2007, 35, e33.	14.5	73
15	Structure, Dynamics and Function of the 26S Proteasome. Sub-Cellular Biochemistry, 2021, 96, 1-151.	2.4	64
16	Residues in the gp41 Ectodomain Regulate HIV-1 Envelope Glycoprotein Conformational Transitions Induced by gp120-Directed Inhibitors. Journal of Virology, 2017, 91, .	3.4	53
17	The Highly Conserved Layer-3 Component of the HIV-1 gp120 Inner Domain Is Critical for CD4-Required Conformational Transitions. Journal of Virology, 2013, 87, 2549-2562.	3.4	49
18	Massively parallel unsupervised single-particle cryo-EM data clustering via statistical manifold learning. PLoS ONE, 2017, 12, e0182130.	2.5	44

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19	Graphene Structures at an Extreme Degree of Buckling. ACS Nano, 2011, 5, 1395-1400.	14.6	43
20	In vivo nanomechanical imaging of blood-vessel tissues directly in living mammals using atomic force microscopy. Applied Physics Letters, 2009, 95, 013704.	3.3	38
21	USP14-regulated allostery of the human proteasome by time-resolved cryo-EM. Nature, 2022, 605, 567-574.	27.8	38
22	AAA+ ATPases in Protein Degradation: Structures, Functions and Mechanisms. Biomolecules, 2020, 10, 629.	4.0	37
23	Folding DNA into a Lipidâ€Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. Angewandte Chemie - International Edition, 2018, 57, 2072-2076.	13.8	36
24	Conformational Landscape of the p28-Bound Human Proteasome Regulatory Particle. Molecular Cell, 2017, 67, 322-333.e6.	9.7	35
25	Tunable non-equilibrium gating of flexible DNA nanochannels in response to transport flux. Nature Nanotechnology, 2007, 2, 366-371.	31.5	24
26	Characterization of a core fragment of the rhesus monkey TRIM5Î± protein. BMC Biochemistry, 2011, 12, 1.	4.4	20
27	Asymmetric Structures and Conformational Plasticity of the Uncleaved Full-Length Human Immunodeficiency Virus Envelope Glycoprotein Trimer. Journal of Virology, 2021, 95, e0052921.	3.4	20
28	Reply to Subramaniam, van Heel, and Henderson: Validity of the cryo-electron microscopy structures of the HIV-1 envelope glycoprotein complex. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4178-82.	7.1	19
29	A Twin-Cysteine Motif in the V2 Region of gp120 Is Associated with SIV Envelope Trimer Stabilization. PLoS ONE, 2013, 8, e69406.	2.5	19
30	Reversibly switchable DNA nanocompartment on surfaces. Nucleic Acids Research, 2004, 32, e144-e144.	14.5	16
31	DNA Origami as Scaffolds for Selfâ€Assembly of Lipids and Proteins. ChemBioChem, 2019, 20, 2422-2431.	2.6	13
32	Evaluation of the contribution of the transmembrane region to the ectodomain conformation of the human immunodeficiency virus (HIV-1) envelope glycoprotein. Virology Journal, 2017, 14, 33.	3.4	11
33	Folding DNA into a Lipidâ€Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. Angewandte Chemie, 2018, 130, 2094-2098.	2.0	11
34	Unsupervised Cryo-EM Data Clustering through Adaptively Constrained K-Means Algorithm. PLoS ONE, 2016, 11, e0167765.	2.5	7
35	USING EVOLUTIONARY ALGORITHM TO CALCULATE THE GROUND-STATE ENERGY OF DOUBLE-ELECTRON ATOMS IN A UNIFORM MAGNETIC FIELD (B â‰ 109G). International Journal of Modern Physics C, 2000, 11, 183-194.	1.7	6
36	Understanding Thermodynamic Competitivity between Biopolymer Folding and Misfolding under Large-Scale Intermolecular Interactions. Journal of the American Chemical Society, 2012, 134, 631-639.	13.7	5

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37	Robustness of signal detection in cryo-electron microscopy via a bi-objective-function approach. BMC Bioinformatics, 2019, 20, 169.	2.6	4
38	Monte Carlo simulation of melting transition on DNA nanocompartment. Journal of Physics: Conference Series, 2006, 29, 18-26.	0.4	3
39	Using an evolutionary algorithm based on cell division operation to calculate ground-state energies of double-electron systems in magnetic fields. Chinese Physics B, 2001, 10, 1118-1123.	1.3	0
40	The Realization of a Fast and Effective Optimization Method on Atomic Structure. Journal of the Physical Society of Japan, 2002, 71, 762-766.	1.6	0
41	Reversibly switchable DNA nanocompartment on surfaces: experiments, applications, and theory. Frontiers of Physics in China, 2008, 3, 74-87.	1.0	0
42	Frontispiz: Folding DNA into a Lipidâ€Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. Angewandte Chemie, 2018, 130, .	2.0	0
43	Frontispiece: Folding DNA into a Lipidâ€Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. Angewandte Chemie - International Edition, 2018, 57, .	13.8	0
44	Abstract B134:Cryo-EMstructure of the activated NAIP2-NLRC4 inflammasome reveals nucleated polymerization. , 2016, , .		0