

# 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  | USP14-regulated allostery of the human proteasome by time-resolved cryo-EM. <i>Nature</i> , 2022, 605, 567-574.  | 27.8 | 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.         | 3.4  | 20        |
| 3  | Structure, Dynamics and Function of the 26S Proteasome. <i>Sub-Cellular Biochemistry</i> , 2021, 96, 1-151.  | 2.4  | 64        |
| 4  | AAA+ ATPases in Protein Degradation: Structures, Functions and Mechanisms. <i>Biomolecules</i> , 2020, 10, 629.  | 4.0  | 37        |
| 5  | Structural mechanism for NEK7-licensed activation of NLRP3 inflammasome. <i>Nature</i> , 2019, 570, 338-343.   | 27.8 | 467       |
| 6  | Robustness of signal detection in cryo-electron microscopy via a bi-objective-function approach. <i>BMC Bioinformatics</i> , 2019, 20, 169.  | 2.6  | 4         |
| 7  | DNA Origami as Scaffolds for Self-Assembly of Lipids and Proteins. <i>ChemBioChem</i> , 2019, 20, 2422-2431.   | 2.6  | 13        |
| 8  | Cryo-EM structures and dynamics of substrate-engaged human 26S proteasome. <i>Nature</i> , 2019, 565, 49-55.   | 27.8 | 264       |
| 9  | Frontispiz: Folding DNA into a Lipid-Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. <i>Angewandte Chemie</i> , 2018, 130, .   | 2.0  | 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.                               | 12.8 | 74        |
| 11 | Frontispiece: Folding DNA into a Lipid-Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. <i>Angewandte Chemie - International Edition</i> , 2018, 57, .                      | 13.8 | 0         |
| 12 | Folding DNA into a Lipid-Conjugated Nanobarrel for Controlled Reconstitution of Membrane Proteins. <i>Angewandte Chemie</i> , 2018, 130, 2094-2098.  | 2.0  | 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.                           | 13.8 | 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, .                       | 3.4  | 53        |
| 15 | Conformational Landscape of the p28-Bound Human Proteasome Regulatory Particle. <i>Molecular Cell</i> , 2017, 67, 322-333.e6.  | 9.7  | 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.   | 7.1  | 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. | 3.4  | 11        |
| 18 | Massively parallel unsupervised single-particle cryo-EM data clustering via statistical manifold learning. <i>PLoS ONE</i> , 2017, 12, e0182130.   | 2.5  | 44        |

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|----|--|------|-----------|
| 19 | A deep convolutional neural network approach to single-particle recognition in cryo-electron microscopy. BMC Bioinformatics, 2017, 18, 348.  | 2.6  | 126       |
| 20 | 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       |
| 21 | 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       |
| 22 | Unsupervised Cryo-EM Data Clustering through Adaptively Constrained K-Means Algorithm. PLoS ONE, 2016, 11, e0167765.   | 2.5  | 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. Journal of Virology, 2015, 89, 8245-8257.   | 3.4  | 99        |
| 25 | Cryo-EM structure of the activated NAIP2-NLRC4 inflammasome reveals nucleated polymerization. Science, 2015, 350, 404-409.   | 12.6 | 347       |
| 26 | 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        |
| 27 | 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        |
| 28 | 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       |
| 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 | Subunit organization of the membrane-bound HIV-1 envelope glycoprotein trimer. Nature Structural and Molecular Biology, 2012, 19, 893-899.   | 8.2  | 151       |
| 31 | Understanding Thermodynamic Competitiveness between Biopolymer Folding and Misfolding under Large-Scale Intermolecular Interactions. Journal of the American Chemical Society, 2012, 134, 631-639.   | 13.7 | 5         |
| 32 | Graphene Structures at an Extreme Degree of Buckling. ACS Nano, 2011, 5, 1395-1400.  | 14.6 | 43        |
| 33 | Characterization of a core fragment of the rhesus monkey TRIM5 $\alpha$ protein. BMC Biochemistry, 2011, 12, 1.  | 4.4  | 20        |
| 34 | 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        |
| 35 | Reversibly switchable DNA nanocompartment on surfaces: experiments, applications, and theory. Frontiers of Physics in China, 2008, 3, 74-87.   | 1.0  | 0         |
| 36 | Gating of Single Synthetic Nanopores by Proton-Driven DNA Molecular Motors. Journal of the American Chemical Society, 2008, 130, 8345-8350.  | 13.7 | 295       |

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|----|---|------|-----------|
| 37 | Alternating-electric-field-enhanced reversible switching of DNA nanocontainers with pH. Nucleic Acids Research, 2007, 35, e33.  | 14.5 | 73        |
| 38 | Tunable non-equilibrium gating of flexible DNA nanochannels in response to transport flux. Nature Nanotechnology, 2007, 2, 366-371.   | 31.5 | 24        |
| 39 | Monte Carlo simulation of melting transition on DNA nanocompartment. Journal of Physics: Conference Series, 2006, 29, 18-26.  | 0.4  | 3         |
| 40 | Reversibly switchable DNA nanocompartment on surfaces. Nucleic Acids Research, 2004, 32, e144-e144.   | 14.5 | 16        |
| 41 | Studies of temperature-dependent electronic transduction on DNA hairpin loop sensor. Nucleic Acids Research, 2003, 31, 108e-108.  | 14.5 | 76        |
| 42 | 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         |
| 43 | 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         |
| 44 | USING EVOLUTIONARY ALGORITHM TO CALCULATE THE GROUND-STATE ENERGY OF DOUBLE-ELECTRON ATOMS IN A UNIFORM MAGNETIC FIELD ( $B \approx 10^9$ G). International Journal of Modern Physics C, 2000, 11, 183-194. | 1.7  | 6         |