

Hong-Wei Wang

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

4,744
citations

101543

36
h-index

110387

64
g-index

122
all docs

122
docs citations

122
times ranked

7426
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of Rift Valley Fever Virus RNA-Dependent RNA Polymerase. <i>Journal of Virology</i> , 2022, 96, JVI0171321.	3.4	13
2	Assembly of Tetraspanin-enriched macrodomains contains membrane damage to facilitate repair. <i>Nature Cell Biology</i> , 2022, 24, 825-832.	10.3	9
3	Sub-Nanometer Nanobelts Based on Titanium Dioxide/Zirconium Dioxide-Polyoxometalate Heterostructures. <i>Advanced Materials</i> , 2021, 33, e2100576.	21.0	42
4	Inside Front Cover: Volume 2 Issue 2. <i>SmartMat</i> , 2021, 2, iii.	10.7	0
5	Molecular basis of cross-species ACE2 interactions with SARS-CoV-2-like viruses of pangolin origin. <i>EMBO Journal</i> , 2021, 40, e107786.	7.8	46
6	Structural engineering of graphene for high-resolution cryo-electron microscopy. <i>SmartMat</i> , 2021, 2, 202-212.	10.7	24
7	Three epitope-distinct human antibodies from RenMab mice neutralize SARS-CoV-2 and cooperatively minimize the escape of mutants. <i>Cell Discovery</i> , 2021, 7, 53.	6.7	14
8	Atomically Thin Bilayer Janus Membranes for Cryo-electron Microscopy. <i>ACS Nano</i> , 2021, 15, 16562-16571.	14.6	5
9	Au-Polyoxometalates Type Copolymer Analogue Sub-1 nm Nanowires. <i>Small</i> , 2021, 17, e2006260.	10.0	22
10	Cross-species recognition of SARS-CoV-2 to bat ACE2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	73
11	Structure of PDE3A-SLFN12 complex and structure-based design for a potent apoptosis inducer of tumor cells. <i>Nature Communications</i> , 2021, 12, 6204.	12.8	19
12	Hydrophilic, Clean Graphene for Cell Culture and Cryo-EM Imaging. <i>Nano Letters</i> , 2021, 21, 9587-9593.	9.1	7
13	Mechanisms of distinctive mismatch tolerance between Rad51 and Dmc1 in homologous recombination. <i>Nucleic Acids Research</i> , 2021, 49, 13135-13149.	14.5	17
14	Cryo-EM Structure of a Bacterial Lipid Transporter YebT. <i>Journal of Molecular Biology</i> , 2020, 432, 1008-1019.	4.2	31
15	Broad host range of SARS-CoV-2 and the molecular basis for SARS-CoV-2 binding to cat ACE2. <i>Cell Discovery</i> , 2020, 6, 68.	6.7	132
16	Exon and protein positioning in a pre-catalytic group II intron RNP primed for splicing. <i>Nucleic Acids Research</i> , 2020, 48, 11185-11198.	14.5	6
17	Hybrid MoO ₃ -Polyoxometallate Sub-1 nm Nanobelt Superstructures. <i>Journal of the American Chemical Society</i> , 2020, 142, 17557-17563.	13.7	46
18	Activation of the β 2 adrenoceptor by the sedative sympatholytic dexmedetomidine. <i>Nature Chemical Biology</i> , 2020, 16, 507-512.	8.0	51

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19	Structural Basis for pri-miRNA Recognition by Drosha. <i>Molecular Cell</i> , 2020, 78, 423-433.e5.	9.7	60
20	Cryo-EM structures of PAC1 receptor reveal ligand binding mechanism. <i>Cell Research</i> , 2020, 30, 436-445.	12.0	35
21	Synaptotagmin-7 is a key factor for bipolar-like behavioral abnormalities in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4392-4399.	7.1	15
22	Robust ultraclean atomically thin membranes for atomic-resolution electron microscopy. <i>Nature Communications</i> , 2020, 11, 541.	12.8	37
23	Cryo-Electron Microscopy of Endogenous Yeast Exosomes. <i>Methods in Molecular Biology</i> , 2020, 2062, 401-415.	0.9	1
24	WHAMM initiates autolysosome tubulation by promoting actin polymerization on autolysosomes. <i>Nature Communications</i> , 2019, 10, 3699.	12.8	40
25	Challenges and opportunities in cryo-EM with phase plate. <i>Current Opinion in Structural Biology</i> , 2019, 58, 175-182.	5.7	16
26	The Balance between Actin-Bundling Factors Controls Actin Architecture in Pollen Tubes. <i>IScience</i> , 2019, 16, 162-176.	4.1	8
27	Single particle cryo-EM reconstruction of 52 kDa streptavidin at 3.2 Angstrom resolution. <i>Nature Communications</i> , 2019, 10, 2386.	12.8	106
28	A Link between Intronic Polyadenylation and HR Maintenance Discovered. <i>Biochemistry</i> , 2019, 58, 1835-1836.	2.5	1
29	Ligand-triggered allosteric ADP release primes a plant NLR complex. <i>Science</i> , 2019, 364, .	12.6	334
30	Reconstitution and structure of a plant NLR resistosome conferring immunity. <i>Science</i> , 2019, 364, .	12.6	551
31	Voices in methods development. <i>Nature Methods</i> , 2019, 16, 945-951.	19.0	5
32	Structural basis of antagonism of human APOBEC3F by HIV-1 Vif. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1176-1183.	8.2	21
33	Cryo-EM structure of L-fucokinase/GDP-fucose pyrophosphorylase (FKP) in <i>Bacteroides fragilis</i> . <i>Protein and Cell</i> , 2019, 10, 365-369.	11.0	6
34	Cryo-EM Structure of Human Dicer and Its Complexes with a Pre-miRNA Substrate. <i>Cell</i> , 2018, 173, 1191-1203.e12.	28.9	117
35	Cryo-EM structure of human ATR-ATRIP complex. <i>Cell Research</i> , 2018, 28, 143-156.	12.0	60
36	Cryo-EM structure of the exocyst complex. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 139-146.	8.2	119

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37	Cryo-EM structure of human mTOR complex 2. <i>Cell Research</i> , 2018, 28, 518-528.	12.0	98
38	The application of CorrSight [™] in correlative light and electron microscopy of vitrified biological specimens. <i>Biophysics Reports</i> , 2018, 4, 143-152.	0.8	2
39	Determining the RAD51-DNA Nucleoprotein Filament Structure and Function by Cryo-Electron Microscopy. <i>Methods in Enzymology</i> , 2018, 600, 179-199.	1.0	8
40	Cryo-EM structure of Nma111p, a unique HtrA protease composed of two protease domains and four PDZ domains. <i>Cell Research</i> , 2017, 27, 582-585.	12.0	5
41	Structural Insights of WHAMM's Interaction with Microtubules by Cryo-EM. <i>Journal of Molecular Biology</i> , 2017, 429, 1352-1363.	4.2	13
42	Cryo-EM structures of human RAD51 recombinase filaments during catalysis of DNA-strand exchange. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 40-46.	8.2	109
43	Near-Atomic Resolution Structure Determination in Over-Focus with Volta Phase Plate by Cs-Corrected Cryo-EM. <i>Structure</i> , 2017, 25, 1623-1630.e3.	3.3	34
44	Architecture of the ATG2B-WDR45 complex and an aromatic Y/HF motif crucial for complex formation. <i>Autophagy</i> , 2017, 13, 1870-1883.	9.1	90
45	Origin of the Reflectin Gene and Hierarchical Assembly of Its Protein. <i>Current Biology</i> , 2017, 27, 2833-2842.e6.	3.9	39
46	Cryo-EM structures of the ATP-bound Vps4E233Q hexamer and its complex with Vta1 at near-atomic resolution. <i>Nature Communications</i> , 2017, 8, 16064.	12.8	42
47	Cryo-EM structure and biochemical analysis reveal the basis of the functional difference between human PI3KC3-C1 and -C2. <i>Cell Research</i> , 2017, 27, 989-1001.	12.0	44
48	Particle segmentation algorithm for flexible single particle reconstruction. <i>Biophysics Reports</i> , 2017, 3, 43-55.	0.8	9
49	Biological cryo-electron microscopy in China. <i>Protein Science</i> , 2017, 26, 16-31.	7.6	3
50	How cryo-electron microscopy and X-ray crystallography complement each other. <i>Protein Science</i> , 2017, 26, 32-39.	7.6	90
51	Trifunctional cross-linker for mapping protein-protein interaction networks and comparing protein conformational states. <i>ELife</i> , 2016, 5, .	6.0	105
52	4.4 Å.. Resolution Cryo-EM structure of human mTOR Complex 1. <i>Protein and Cell</i> , 2016, 7, 878-887.	11.0	69
53	CryoEM structure of yeast cytoplasmic exosome complex. <i>Cell Research</i> , 2016, 26, 822-837.	12.0	44
54	Structure of a group II intron in complex with its reverse transcriptase. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 549-557.	8.2	102

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55	Forks in the tracks: Group II introns, spliceosomes, telomeres and beyond. <i>RNA Biology</i> , 2016, 13, 1218-1222.	3.1	12
56	Structural basis for receptor recognition and pore formation of a zebrafish aerolysin-like protein. <i>EMBO Reports</i> , 2016, 17, 235-248.	4.5	53
57	Structure of the mouse Toll-like receptor 13 ectodomain in complex with a conserved sequence from bacterial 23S ribosomal <i>scp</i> RNA. <i>FEBS Journal</i> , 2016, 283, 1631-1635.	4.7	15
58	A magnetic protein biocompass. <i>Nature Materials</i> , 2016, 15, 217-226.	27.5	250
59	An improved method for phasing crystal structures with low non-crystallographic symmetry using cryo-electron microscopy data. <i>Protein and Cell</i> , 2015, 6, 919-923.	11.0	4
60	Opening new doors for understanding eukaryotic RNA splicing. <i>Science China Life Sciences</i> , 2015, 58, 1171-1172.	4.9	0
61	Cryo-electron microscopy for structural biology: current status and future perspectives. <i>Science China Life Sciences</i> , 2015, 58, 750-756.	4.9	8
62	Cryo-EM Structure of Influenza Virus RNA Polymerase Complex at 4.3 Å Resolution. <i>Molecular Cell</i> , 2015, 57, 925-935.	9.7	79
63	Cryo-EM structure of SNAP-SNARE assembly in 20S particle. <i>Cell Research</i> , 2015, 25, 551-560.	12.0	42
64	Functional Relationship of ATP Hydrolysis, Presynaptic Filament Stability, and Homologous DNA Pairing Activity of the Human Meiotic Recombinase DMC1. <i>Journal of Biological Chemistry</i> , 2015, 290, 19863-19873.	3.4	12
65	A Single α Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly. <i>Cell</i> , 2015, 163, 432-444.	28.9	73
66	Structural and biochemical basis for induced self-propagation of NLRC4. <i>Science</i> , 2015, 350, 399-404.	12.6	282
67	Structural basis for specific recognition of single-stranded RNA by Toll-like receptor 13. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 782-787.	8.2	58
68	Directly reconstructing principal components of heterogeneous particles from cryo-EM images. <i>Journal of Structural Biology</i> , 2015, 191, 245-262.	2.8	67
69	Visualization of distinct substrate-recruitment pathways in the yeast exosome by EM. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 95-102.	8.2	53
70	Cryo-Electron Microscopic Study of the Enzymatic Mechanism of the RNA 2'-O-Methyltransferase Box CD sRNP. <i>Microscopy and Microanalysis</i> , 2014, 20, 1284-1285.	0.4	9
71	Substrate-specific structural rearrangements of human Dicer. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 662-670.	8.2	89
72	Non-coding Y RNAs as tethers and gates. <i>RNA Biology</i> , 2013, 10, 1602-1608.	3.1	30

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73	Structural characterization of full-length NSF and 20S particles. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 268-275.	8.2	46
74	Bowl-shaped oligomeric structures on membranes as DegP's new functional forms in protein quality control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4858-4863.	7.1	64
75	Structural insights into RNA processing by the human RISC-loading complex. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1148-1153.	8.2	215
76	Architecture of the yeast Rps43 exosome complex suggests routes of RNA recruitment for 3' end processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16844-16849.	7.1	98
77	Architecture of the Dam1 kinetochore ring complex and implications for microtubule-driven assembly and force-coupling mechanisms. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 721-726.	8.2	88
78	Ring-like pore structures of SecA: Implication for bacterial protein-conducting channels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 4221-4226.	7.1	69
79	Polymorphism of structural forms of C-reactive protein. <i>International Journal of Molecular Medicine</i> , 2002, 9, 665-71.	4.0	21
80	Trimeric ring-like structure of ArsA ATPase. <i>FEBS Letters</i> , 2000, 469, 105-110.	2.8	9
81	Contributory presentations/posters. <i>Journal of Biosciences</i> , 1999, 24, 33-198.	1.1	0