

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	Reconstitution and structure of a plant NLR resistosome conferring immunity. <i>Science</i> , 2019, 364, .	12.6	551
2	Ligand-triggered allosteric ADP release primes a plant NLR complex. <i>Science</i> , 2019, 364, .	12.6	334
3	Structural and biochemical basis for induced self-propagation of NLRC4. <i>Science</i> , 2015, 350, 399-404.	12.6	282
4	A magnetic protein biocompass. <i>Nature Materials</i> , 2016, 15, 217-226.	27.5	250
5	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
6	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
7	Cryo-EM structure of the exocyst complex. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 139-146.	8.2	119
8	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
9	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
10	Single particle cryo-EM reconstruction of 52 kDa streptavidin at 3.2 Angstrom resolution. <i>Nature Communications</i> , 2019, 10, 2386.	12.8	106
11	Trifunctional cross-linker for mapping protein-protein interaction networks and comparing protein conformational states. <i>ELife</i> , 2016, 5, .	6.0	105
12	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
13	Architecture of the yeast Rps44 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
14	Cryo-EM structure of human mTOR complex 2. <i>Cell Research</i> , 2018, 28, 518-528.	12.0	98
15	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
16	How cryo-electron microscopy and X-ray crystallography complement each other. <i>Protein Science</i> , 2017, 26, 32-39.	7.6	90
17	Substrate-specific structural rearrangements of human Dicer. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 662-670.	8.2	89
18	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

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19	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
20	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
21	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
22	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
23	4.4 Å... Resolution Cryo-EM structure of human mTOR Complex 1. <i>Protein and Cell</i> , 2016, 7, 878-887.	11.0	69
24	Directly reconstructing principal components of heterogeneous particles from cryo-EM images. <i>Journal of Structural Biology</i> , 2015, 191, 245-262.	2.8	67
25	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
26	Cryo-EM structure of human ATR-ATRIP complex. <i>Cell Research</i> , 2018, 28, 143-156.	12.0	60
27	Structural Basis for pri-miRNA Recognition by Drosha. <i>Molecular Cell</i> , 2020, 78, 423-433.e5.	9.7	60
28	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
29	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
30	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
31	Activation of the β 2B adrenoceptor by the sedative sympatholytic dexmedetomidine. <i>Nature Chemical Biology</i> , 2020, 16, 507-512.	8.0	51
32	Structural characterization of full-length NSF and 20S particles. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 268-275.	8.2	46
33	Hybrid MoO ₃ "Polyoxometallate Sub-1 nm Nanobelt Superstructures. <i>Journal of the American Chemical Society</i> , 2020, 142, 17557-17563.	13.7	46
34	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
35	CryoEM structure of yeast cytoplasmic exosome complex. <i>Cell Research</i> , 2016, 26, 822-837.	12.0	44
36	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

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37	Cryo-EM structure of SNAP-SNARE assembly in 20S particle. <i>Cell Research</i> , 2015, 25, 551-560.	12.0	42
38	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
39	Sub-Nanometer Nanobelts Based on Titanium Dioxide/Zirconium Dioxide Polyoxometalate Heterostructures. <i>Advanced Materials</i> , 2021, 33, e2100576.	21.0	42
40	WHAMM initiates autolysosome tubulation by promoting actin polymerization on autolysosomes. <i>Nature Communications</i> , 2019, 10, 3699.	12.8	40
41	Origin of the Reflectin Gene and Hierarchical Assembly of Its Protein. <i>Current Biology</i> , 2017, 27, 2833-2842.e6.	3.9	39
42	Robust ultraclean atomically thin membranes for atomic-resolution electron microscopy. <i>Nature Communications</i> , 2020, 11, 541.	12.8	37
43	Cryo-EM structures of PAC1 receptor reveal ligand binding mechanism. <i>Cell Research</i> , 2020, 30, 436-445.	12.0	35
44	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
45	Cryo-EM Structure of a Bacterial Lipid Transporter YebT. <i>Journal of Molecular Biology</i> , 2020, 432, 1008-1019.	4.2	31
46	Non-coding Y RNAs as tethers and gates. <i>RNA Biology</i> , 2013, 10, 1602-1608.	3.1	30
47	Structural engineering of graphene for high-resolution cryo-electron microscopy. <i>SmartMat</i> , 2021, 2, 202-212.	10.7	24
48	Au-Polyoxometalates A ₂ B ₂ A ₂ B ₂ Type Copolymer Analogue Sub-1 nm Nanowires. <i>Small</i> , 2021, 17, e2006260.	10.0	22
49	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
50	Polymorphism of structural forms of C-reactive protein. <i>International Journal of Molecular Medicine</i> , 2002, 9, 665-71.	4.0	21
51	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
52	Mechanisms of distinctive mismatch tolerance between Rad51 and Dmc1 in homologous recombination. <i>Nucleic Acids Research</i> , 2021, 49, 13135-13149.	14.5	17
53	Challenges and opportunities in cryo-EM with phase plate. <i>Current Opinion in Structural Biology</i> , 2019, 58, 175-182.	5.7	16
54	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

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55	Synaptotagmin-7 is a key factor for bipolar-like behavioral abnormalities in mice. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 4392-4399.	7.1	15
56	Three epitope-distinct human antibodies from RenMab mice neutralize SARS-CoV-2 and cooperatively minimize the escape of mutants. Cell Discovery, 2021, 7, 53.	6.7	14
57	Structural Insights of WHAMM's Interaction with Microtubules by Cryo-EM. Journal of Molecular Biology, 2017, 429, 1352-1363.	4.2	13
58	Structure of Rift Valley Fever Virus RNA-Dependent RNA Polymerase. Journal of Virology, 2022, 96, JVI0171321.	3.4	13
59	Functional Relationship of ATP Hydrolysis, Presynaptic Filament Stability, and Homologous DNA Pairing Activity of the Human Meiotic Recombinase DMC1. Journal of Biological Chemistry, 2015, 290, 19863-19873.	3.4	12
60	Forks in the tracks: Group II introns, spliceosomes, telomeres and beyond. RNA Biology, 2016, 13, 1218-1222.	3.1	12
61	Trimeric ring-like structure of ArsA ATPase. FEBS Letters, 2000, 469, 105-110.	2.8	9
62	Cryo-Electron Microscopic Study of the Enzymatic Mechanism of the RNA 2'-O-Methyltransferase Box CD sRNP. Microscopy and Microanalysis, 2014, 20, 1284-1285.	0.4	9
63	Particle segmentation algorithm for flexible single particle reconstruction. Biophysics Reports, 2017, 3, 43-55.	0.8	9
64	Assembly of Tetraspanin-enriched macrodomains contains membrane damage to facilitate repair. Nature Cell Biology, 2022, 24, 825-832.	10.3	9
65	Cryo-electron microscopy for structural biology: current status and future perspectives. Science China Life Sciences, 2015, 58, 750-756.	4.9	8
66	Determining the RAD51-DNA Nucleoprotein Filament Structure and Function by Cryo-Electron Microscopy. Methods in Enzymology, 2018, 600, 179-199.	1.0	8
67	The Balance between Actin-Bundling Factors Controls Actin Architecture in Pollen Tubes. IScience, 2019, 16, 162-176.	4.1	8
68	Hydrophilic, Clean Graphene for Cell Culture and Cryo-EM Imaging. Nano Letters, 2021, 21, 9587-9593.	9.1	7
69	Cryo-EM structure of L-fucokinase/GDP-fucose pyrophosphorylase (FKP) in Bacteroides fragilis. Protein and Cell, 2019, 10, 365-369.	11.0	6
70	Exon and protein positioning in a pre-catalytic group II intron RNP primed for splicing. Nucleic Acids Research, 2020, 48, 11185-11198.	14.5	6
71	Cryo-EM structure of Nma111p, a unique HtrA protease composed of two protease domains and four PDZ domains. Cell Research, 2017, 27, 582-585.	12.0	5
72	Voices in methods development. Nature Methods, 2019, 16, 945-951.	19.0	5

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73	Atomically Thin Bilayer Janus Membranes for Cryo-electron Microscopy. <i>ACS Nano</i> , 2021, 15, 16562-16571.	14.6	5
74	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
75	Biological cryo-electron microscopy in China. <i>Protein Science</i> , 2017, 26, 16-31.	7.6	3
76	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
77	A Link between Intronic Polyadenylation and HR Maintenance Discovered. <i>Biochemistry</i> , 2019, 58, 1835-1836.	2.5	1
78	Cryo-Electron Microscopy of Endogenous Yeast Exosomes. <i>Methods in Molecular Biology</i> , 2020, 2062, 401-415.	0.9	1
79	Contributory presentations/posters. <i>Journal of Biosciences</i> , 1999, 24, 33-198.	1.1	0
80	Opening new doors for understanding eukaryotic RNA splicing. <i>Science China Life Sciences</i> , 2015, 58, 1171-1172.	4.9	0
81	Inside Front Cover: Volume 2 Issue 2. <i>SmartMat</i> , 2021, 2, iii.	10.7	0