



Hong-Wei Wang

Dean, Professor, School of Life Sciences, Tsinghua University

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Contact

Mailing address	Room 353, Life Science Building School of Life Sciences, Tsinghua University Haidian District, Beijing 100084, China
Phone	86-10-62789094 86-10-62792083 (Administrative Assistant)
Email	hongweiwang@tsinghua.edu.cn

Professional Positions

2016.04 - present	Dean, School of Life Sciences, Tsinghua University, Beijing, China.
2014.01 - present	Adjunct Associate Professor, Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT, USA.
2011.07 - present	Principle Investigator, Tsinghua-Peking Center for Life Sciences, Tsinghua University, Beijing, China.
2010.12 - present	Professor, School of Life Sciences, Tsinghua University, Beijing, China.
2009.01 - 2011.12	Assistant Professor, Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, CT, USA.
2006.05 - 2008.12	Research Scientist, Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA.
2001.08 - 2006.05	Postdoctoral fellow, Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA, USA.

Education

1996 - 2001	Ph.D. in Biophysics, Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing, China.
1992 - 1996	B.S. in Biological Sciences & Biotechnology, Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing, China.

Awards and Honors

2019	Chair-Elected, Gordon Research Conference of Three-Dimensional Electron Microscopy
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Curriculum Vitae

Hong-Wei Wang

2012	Youth One-Thousand Talent Program, State Council of China.
2009	Smith Family Award for Excellence in Biomedical Research, the Smith Family Foundation.
2005	National Award of Natural Science (2nd rank) by State Council of China.
2005	Outstanding Performance Award, Lawrence Berkeley National Laboratory.
2001	Distinguished Ph.D. Dissertation Award, Tsinghua University.
1996	Distinguished Graduation Award, Tsinghua University.

Professional Experience

2015 - present	Editorial Board, <i>Biophysics Report</i> .
2013 - present	Council Member, Chinese Biophysics Society.
2012 - present	Council Member, Chinese Electron Microscopy Society.
2009 - present	Member and Reviewer, Faculty of 1000, Cytoskeleton Section.
2009 - present	Member of American Physical Society.
2005 - present	Member, Sigma Xi Society.
2002 - present	Member, Biophysics Society. Ad Hoc Reviewers for Human Frontier Science Program; Netherland Organization for Scientific Research; Jeffress Research Grant; Indo-US Science and Technology Forum; <i>Cell</i> , <i>Nature</i> , <i>Science</i> , <i>Nature Structural & Molecular Biology</i> , <i>Genes & Development</i> , <i>PNAS</i> , <i>Journal of Molecular Biology</i> , <i>Structure</i> , <i>Journal of Structural Biology</i> , <i>Experimental Cell Research</i> .

Research Interests

In the very crowded inner environment of a cell, most macromolecules function in the form of complexes, many being described as “molecular machines.” To understand the machines’ structures and structural changes that occur during the working cycle, we employ cryo-electron microscopy to visualize them as “single particles” or ordered functional assemblies. The micrographs are analyzed by computational image processing to reveal the structures and conformational variations of these molecules. We then combine the structural information with data from accompanying biophysical and biochemical techniques to elucidate the mechanisms of these large macromolecular machines.

Our current research focuses on:

- (1) Methodology development for more efficient and high resolution cryo-electron microscopy
- (2) The coordination mechanisms of cytoskeleton and membrane systems.
- (3) The mechanism and regulations of nucleic acid quality control.



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Curriculum Vitae

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Publications

1. Liu T, Dai A, Cao Y, Zhang R, Dong MQ, **Wang HW***. (2017) Structural Insights of WHAMM's Interaction with Microtubules by Cryo-EM. *J. Mol. Biol.*, 429:1352-1363
2. Xu J, Zhao L, Xu Y, Zhao W, Sung P*, **Wang HW***. (2017) Cryo-EM structures of human RAD51 recombinase filaments during catalysis of DNA-strand exchange. *Nat. Struct. Mol. Biol.*, 24:40-46
3. **Wang HW***, Wang JW. (2017) How cryo-electron microscopy and X-ray crystallography complement each other. *Protein Sci.*, 26:32-39 (Review)
4. **Wang HW***, Lei J*, Shi Y*. (2017) Biological cryo-electron microscopy in China. *Protein Sci.*, 26:16-31 (Review)
5. Yang H, Wang J, Liu M, Chen X, Huang M, Tan D, Dong MQ, Wong CC, Wang J*, Xu Y*, **Wang HW***. (2016) 4.4 Å Resolution Cryo-EM structure of human mTOR Complex 1. *Protein Cell*, 7:878-887
6. Agrawal RK*, **Wang HW***, Belfort M*. (2016) Forks in the tracks: Group II introns, spliceosomes, telomeres and beyond. *RNA Biol.*, 13:1218-1222
7. Gong X, Qian H, Shao W, Li J, Wu J, Liu JJ, Li W, **Wang HW**, Espenshade P*, Yan N*. (2016) Complex structure of the fission yeast SREBP-SCAP binding domains reveals an oligomeric organization. *Cell Research*, 26:1197-1211
8. Liu JJ, Niu CY, Wu Y, Tan D, Wang Y, Ye MD, Liu Y, Zhao W, Zhou K, Liu QS, Dai J, Yang X, Dong MQ, Huang N, **Wang HW***. (2016) CryoEM structure of yeast cytoplasmic exosome complex. *Cell Research*, 26:822-837
9. Qu G, Kaushal PS, Wang J, Shigematsu H, Piazza CL, Agrawal RK*, Belfort M*, **Wang HW***. (2016) Structure of a group II intron in complex with its reverse transcriptase. *Nat. Struct. Mol. Biol.*, 23:549-557
10. Wang J*, Chai J, **Wang HW**. (2016) Structure of the mouse Toll-like receptor 13 ectodomain in complex with a conserved sequence from bacterial 23S ribosomal RNA. *FEBS J.*, 283:1631-1635
11. Tan D, Li Q, Zhang MJ, Liu C, Ma C, Zhang P, Ding YH, Fan SB, Tao L, Yang B, Li X, Ma S, Liu J, Feng B, Liu X, **Wang HW**, He SM, Gao N, Ye K, Dong MQ* Lei X*. (2016) Trifunctional cross-linker for mapping protein-protein interaction networks and comparing protein conformational states. *Elife*, pii: e12509



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12. Qin S, Yin H, Yang C, Dou Y, Liu Z, Zhang P, Yu H, Huang Y, Feng J, Hao J, Hao J, Deng L, Yan X, Dong X, Zhao Z, Jiang T, **Wang HW**, Luo SJ, Xie C*. (2016) A magnetic protein biocompass. *Nat Mater.*, 15:217-226
13. Jia N, Liu N, Cheng W, Jiang YL, Sun H, Chen LL, Peng J, Zhang Y1, Ding YH, Zhang ZH, Wang X, Cai G, Wang J, Dong MQ, Zhang Z, Wu H, **Wang HW***, Chen Y*, Zhou CZ*. (2016) Structural basis for receptor recognition and pore formation of a zebrafish aerolysin-like protein. *EMBO Reports*, 17:235-248
14. Wang J, Wang W, Song W, Han Z, Zhang H, Chai J*, **Wang HW***, Wang J*. (2015) An improved method for phasing crystal structures with low non-crystallographic symmetry using cryo-electron microscopy data. *Protein Cell*, 6:919-923 (Letter)
15. **Wang HW***. (2015) Opening new doors for understanding eukaryotic RNA splicing. *Sci China Life Sci.*, 58:1171-1172 (Editorial Material)
16. Hu Z, Zhou Q, Zhang C, Fan S, Cheng W, Zhao Y, Shao F, **Wang HW**, Sui SF*, Chai J*. (2015) Structural and biochemical basis for induced self-propagation of NLRC4. *Science*, 350:399-404
17. Tomko RJ Jr*, Taylor DW, Chen ZA, **Wang HW**, Rappaport J, Hochstrasser M*. (2015) A single α helix drives extensive remodeling of the proteasome lid and completion of regulatory particle assembly. *Cell*, 163:432-444
18. Song W, Wang J, Han Z, Zhang Y, Zhang H, Wang W, Chang J, Xia B, Fan S, Zhang D, Wang J*, **Wang HW***, Chai J*. (2015) Structural basis for specific recognition of single-stranded RNA by Toll-like receptor 13. *Nat. Struct. Mol. Biol.*, 22:782-787
19. Chang HY, Liao CY, Su GC, Lin SW, **Wang HW**, Chi P*. (2015) Functional Relationship of ATP Hydrolysis, Presynaptic Filament Stability, and Homologous DNA Pairing Activity of the Human Meiotic Recombinase DMC1. *J. Biol. Chem.*, 290:19863-19873
20. Tagare HD*, Kucukelbir A, Sigworth FJ, **Wang HW**, Rao M. (2015) Directly reconstructing principal components of heterogeneous particles from cryo-EM images. *J. Struct. Biol.*, 191:245-262
21. **Wang HW***. (2015) Cryo-electron microscopy for structural biology: current status and future perspectives. *Sci. China Life Sci.*, 58:750-756 (Review)
22. Zhou Q, Huang X, Sun S, Li X, **Wang HW***, Sui SF*. (2015) Cryo-EM structure of SNAP-SNARE assembly in 20S particle. *Cell Research*, 25:551-560



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23. Chang S, Sun D, Liang H, Wang J, Li J, Guo L, Wang X, Guan C, Boruah BM, Yuan L, Feng F, Yang M, Wang L, Wang Y, Wojdyla J, Li L, Wang J, Wang M, Cheng G, **Wang HW***, Liu Y*. (2015) Cryo-EM Structure of Influenza Virus RNA Polymerase Complex at 4.3 Å Resolution. *Mol Cell*, 57:925-935
24. Liu Z, Wang J, Li G*, **Wang HW***. (2015) Structure of precursor microRNA's terminal loop regulates human Dicer's dicing activity by switching DExH/D domain. *Protein Cell*, 6:185-193
25. Liu JJ, Bratkowski MA, Liu X, Niu CY, Ke A*, **Wang HW***. (2014) Visualization of distinct substrate-recruitment pathways in the yeast exosome by EM. *Nat. Struct. Mol. Biol.*, 21:95-102
26. Zhao W, Saro D, Hammel M, Kwon Y, Xu Y, Rambo RP, Williams GJ, Chi P, Lu L, Pezza RJ, Camerini-Otero RD, Tainer JA, **Wang HW**, Sung P*. (2014) Mechanistic insights into the role of Hop2-Mnd1 in meiotic homologous DNA pairing. *Nucleic Acids Res.*, 42:906-917
27. Yin P, Li Q, Yan C, Liu Y, Liu J, Yu F, Wang Z, Long J, He J, **Wang HW**, Wang J, Zhu JK, Shi Y, Yan N*. (2013) Structural basis for the modular recognition of single-stranded RNA by PPR proteins. *Nature*, 504:168-171
28. Wolin SL*, Belair C, Bocitto M, Chen X, Sim S, Taylor DW, **Wang HW**. (2013) Non-coding Y RNAs as tethers and gates: Insights from bacteria. *RNA Biol.*, 10:1602-1608
29. Busygina V, Gaines WA, Xu Y, Kwon Y, Williams GJ, Lin SW, Chang HY, Chi P, **Wang HW**, Sung P*. (2013) Functional attributes of the *Saccharomyces cerevisiae* meiotic recombinase Dmc1. *DNA Repair (Amst)*, 12:707-712
30. Li Y, Hsin J, Zhao L, Cheng Y, Shang W, Huang KC, **Wang HW**, Ye S*. (2013) FtsZ protofilaments use a hinge-opening mechanism for constrictive force generation. *Science*, 341:392-295
31. Taylor DW, Ma E, Shigematsu H, Cianfrocco MA, Noland CL, Nagayama K, Nogales E, Doudna JA*, **Wang HW***. (2013) Substrate-specific structural rearrangements of human Dicer. *Nat. Struct. Mol. Biol.*, 20:662-670
32. Chen X, Taylor DW, Fowler CC, Galan JE, **Wang HW**, Wolin SL*. (2013) An RNA degradation machine sculpted by Ro autoantigen and noncoding RNA. *Cell*, 153:166-177
33. Li B, Li N, Wang F, Guo L, Huang Y, Liu X, Wei T, Zhu D, Liu C, Pan H, Xu S, **Wang HW**, Gu L*. (2012) Structural insight of a concentration-dependent mechanism by which



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YdiV inhibits Escherichia coli flagellum biogenesis and motility. *Nucleic Acids Res.*, 40:11073-11085

34. Shen QT, Hsiue PP, Sindelar CV, Welch MD, Campellone KG*, **Wang HW***. (2012) Structural insight into WHAMM-mediated cytoskeletal coordination during membrane remodeling. *J. Cell Biol.*, 199:111-124
35. Nam KH, Haitjema C, Liu X, Ding F, **Wang HW**, DeLisa MP*, Ke A*. (2012) Cas5d protein processes pre-crRNA and assemblies into a Cascade-like interference complex in subtype I-C/Dvulg CRISPR-Cas system. *Structure*, 20:1574-1584
36. Bower-Phipps KR, Taylor DW, **Wang HW**, Baserga SJ*. (2012) The box C/D sRNP dimeric architecture is conserved across domain Archaea. *RNA*, 18:1527-1540
37. Shi L, Shen QT, Kiel A, Wang J, **Wang HW**, Melia TJ, Rothman JE*, Pincet F*. (2012) One to fuse and three to keep the nascent fusion pore open. *Science*, 335:1355-1359
38. Chang LF, Chen S, Liu CC, Pan XJ, Jian JS, Bai XC, Xie X, **Wang HW**, Sui SF*. (2012) Structural characterization of full-length NSF and 20S particles. *Nature Struct. Mol. Biol.*, 19:268-275
39. Zhou K, Kanai R, Lee P, **Wang HW***, Modis Y*. (2012) Toll-like receptor 5 forms asymmetric dimers in the absence of flagellin. *J. Struct. Biol.*, 177:402-409
40. Chandramouli P, Hernandez-Lopez R, **Wang HW**, Leschziner AE*. (2011) Validation of the orthogonal tilt reconstruction method with a biological test sample. *J. Struct. Biol.*, 175:85-96
41. Liu XQ, **Wang HW***. (2011) Single particle electron microscopy reconstruction of the exosome complex using the random conical tilt method. *J. Vis. Exp.*, doi: 10.3791/2574
42. Ramey VH, **Wang HW**, Nakajima Y, Wong A, Liu J, Drubin D, Barnes G, Nogales E*. (2011) The Dam1 ring binds to the E-hook of tubulin and diffuses along the microtubule. *Mol. Biol. Cell*, 22:457-466
43. Wu X, Shen QT, Stokes N, Lu C, Zheng Q, Polak L, **Wang HW**, Fuchs E*. (2011) Skin stem cells orchestrate directional migration by regulating microtubule-ACF7 connections through GSK3 β . *Cell*, 144:341-352
44. Yang H, Wang J, Jia X, McNatt M, Zang T, Pan B, Meng W, **Wang HW**, Bieniasz P, Xiong Y*. (2010) Structural insight into the mechanisms of enveloped virus tethering by Tetherin. *Proc. Natl. Acad. Sci. USA*, 107:18428-18432



45. Nogales E*, Ramey VH, **Wang HW**. (2010) Cryo-EM studies of microtubule structural intermediates and kinetochore-microtubule interactions. *Methods Cell Biol.*, 95:129-156 (Review; Book Chapter)
46. **Wang HW***, Noland C, Siridechadilok B, Taylor DW, Ma E, Felderer K, Doudna JA*, Nogales E*. (2009) Structural insights into RNA processing by the human RISC-loading complex. *Nat. Struct. Mol. Biol.*, 16:1148-1153
47. Wu Z, **Wang HW**, Mu W, Quyang Z, Nogales E, Xing J*. (2009) Simulations of tubulin sheet polymers as possible structural intermediates in microtubule assembly. *PLoS One*, 4:e7291
48. Ramey VH, **Wang HW**, Nogales E*. (2009) Ab initio reconstruction of helical samples with heterogeneity, disorder and coexisting symmetries. *J. Struct. Biol.*, 167:97-105
49. Shen QT, Bai XC, Chang LF, Wu Y, **Wang HW**, Sui SF*. (2009) Bowl-shaped oligomeric structures on membranes as DegP's new functional forms in protein quality control. *Proc. Natl. Acad. Sci. USA*, 106:4858-4863
50. **Wang HW**, Long S, Ciferri C, Westermann S, Drubin DG, Barnes G, Nogales E*. (2008) Architecture and flexibility of the yeast Ndc80 kinetochore complex. *J. Mol. Biol.*, 383:894-903
51. **Wang HW***, Wang J, Ding F, Callahan K, Bratkowski MA, Butler JS, Nogales E, Ke A*. (2007) Architecture of the yeast Rrp44-exosome complex suggests routes of RNA recruitment for 3'-end processing. *Proc. Natl. Acad. Sci. USA*, 104:16844-16849
52. **Wang HW**, Ramey VH, Westermann S, Leschziner AE, Welburn JPI, Nakajima Y, Drubin DG, Barnes G, Nogales E*. (2007) Architecture of the Dam1 kinetochore ring complex and implications for microtubule-driven assembly and force-coupling mechanisms. *Nat. Struct. Mol. Biol.*, 14:721-726
53. Nogales E*, **Wang HW**. (2006) Structural mechanisms underlying nucleotide-dependent self-assembly of tubulin and its relatives. *Curr. Opin. Struct. Biol.*, 16:221-229 (Review)
54. Nogales E*, **Wang HW**. (2006) Structural intermediates in microtubule assembly and disassembly: how and why? *Curr. Opin. Cell Biol.*, 18:179-284 (Review)
55. Westermann S, **Wang HW**, Avila-Sakar A, Drubin DG, Nogales E, Barnes G*. (2006) The kinetochore ring complex moves processively on depolymerizing microtubule ends. *Nature*, 440:565-563



56. **Wang HW***, Long S, Finley KR, Nogales E. (2005) Assembly of GMPCPP-bound tubulin into helical ribbons and tubes and effect of colchicine. *Cell Cycle*, 4:1157-1160
57. **Wang HW**, Nogales E*. (2005) Nucleotide-dependent bending flexibility of tubulin regulates microtubule assembly. *Nature*, 435:911-915
58. Westermann S, Avila-Sakar A, **Wang HW**, Niederstrasser H, Wong J, Drubin DG, Nogales E, Barnes G*. (2005) Formation of a dynamic kinetochore-microtubule interface through assembly of the Dam1 ring complex. *Mol. Cell*, 17:277-290
59. **Wang HW**, Nogales E*. (2005) An iterative Fourier-Bessel algorithm for reconstruction of helical structures with severe Bessel overlap. *J. Struct. Biol.*, 149:65-78 (Cover)
60. Chen Y, Lu YJ, **Wang HW**, Yuan S, Chang Z, Sui SF*. (2003) Two-dimensional crystallization of a small heat shock protein HSP16.3 on lipid layer. *Biochem. Biophysic. Res. Commun.*, 310:360-366
61. Wu Y, **Wang HW**, Ji SR, Sui SF*. (2003) Two-dimensional crystallization of rabbit C-reactive protein monomeric subunits. *Acta. Crystallogr. D. Biol. Crystallogr.*, 59:922-926
62. Nogales E*, **Wang HW**, Niederstrasser H. (2003) Tubulin rings: which way do they curve? *Curr. Opin. Struct. Biol.*, 13:256-261 (Review)
63. **Wang HW**, Chen Y, Yang H, Chen X, Duan MX, Tai PC*, Sui SF*. (2003) Ring-like pore structures of SecA: implication for bacteria protein-conducting channels. *Proc. Natl. Acad. Sci. USA*, 100:4221-4226
64. Wu Y, Ji SR, **Wang HW**, Sui SF*. (2002) Study of the spontaneous dissociation of rabbit C-reactive protein. *Biochemistry (Mosc.)*, 67:1377-1382
65. **Wang HW**, Wu Y, Chen Y, Sui SF*. (2002) Polymorphism of structural forms of C-reactive protein. *Int. J. Mol. Med.*, 9:665-671
66. **Wang HW**, Sui SF*. (2001) Dissociation and subunit rearrangement of membrane-bound human C-reactive protein. *Biochem. Biophysic. Res. Commun.*, 288:75-79
67. **Wang HW**, Sui SF*. (2001) Two-dimensional assembly of pentameric C-reactive proteins on lipid monolayers. *J. Struct. Biol.*, 134:46-55



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Curriculum Vitae

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68. **Wang HW**, Lu YJ, Li LJ, Liu S, Wang DN, Sui SF*. (2000) Trimeric ring-like structure of ArsA ATPase. *FEBS Lett.*, 496:105-110
69. Zhou H, **Wang HW**, Zhu K, Sui SF, Xu P, Yang SF, Li N*. (1999) The multiple roles of conserved arginine 286 of 1-aminocyclopropane-1-carboxylate synthase. Coenzyme binding, substrate binding, and beyond. *Plant Physiol.*, 121:913-919
70. **Wang HW**, Sui SF*. (1999) Pentameric two-dimensional crystallization of rabbit C-reactive protein on lipid monolayers. *J. Struct. Biol.*, 127:283-286
71. Mi LZ, **Wang HW**, Sui SF*. (1997) Interaction of Rabbit C-Reactive Protein with Phospholipid Monolayers Studied by Micro-fluorescence Film Balance with an Externally Applied Electric Field. *Biophys. J.*, 73:446-451