BIOGRAPHICAL SKETCH

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NAME: Ren, Gang (Gary)

eRA COMMONS USER NAME (credential, e.g., agency login): gangren

POSITION TITLE: Career Staff Scientist (P.I.)

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Lanzhou University, China	B.S	06/1990	Theoretical Physics
Lanzhou University, China	M.S.	06/1993	Theoretical Physics
Univ. of Science and Technology Beijing, China	Ph.D.	06/1997	Material Physics (Electron Microscopy)
The Scripps Research Institute, La Jolla, CA, USA	Postdoctoral	06/1997-01/ 2004	Cell Biology (Cryo-Elect. Microscopy)

A. Personal Statement

The goal of the proposed research is to investigate the structure and function of protein by using our reported electron microscopy techniques, including optimized negative-staining (OpNS, *JLR, 2010*,51:1228-36; *JLR*, *2011*,52:175-84), cryo-positive-staining (Cryo-PS, *Nat. Chem. Biol., 2012*, 8(4):342-349) and individual particle electron tomography (IPET, *PLoS One, 2012*, 7(1):30249). I have the expertise and motivation necessary to successfully carry out the proposed work since I have a solid background in both theory and experimentation. My previous remarkable contributions include computing the electron scattering factors, which collected in the *International Tables of Crystallography*, Vol. C since 2004; and determined the first near-atomic structure of transmembrane protein that embedded in vitreous ice (others' embedded in glucose), *i.e.* 3.7Å resolution of aquaporin 1 (AQP1) water-channel by cryo-electron crystallography (*PNAS*, *2001*, 98:1398-1403). I launched my career in flexible protein structure and function studies after my working with Dr. Wah Chiu at the National Center of Macromolecular Imaging (Baylor College of Medicine, TX), where we reported a structural model of LDL and HDL by conventional single-particle cryo-electron microscopy (*PNAS, 2010*, 107:1059-1064, *PNAS, 2008*, 105, 12176-12181). As a principal investigator at UCSF (as a keck fellow), and later at LBNL (as a staff scientist), I laid the groundwork to develop the cryo-electron tomography (cryo-ET) technique for expanding the electron tomography capability in protein structure determination of heterogeneous, asymmetric and small protein, such as HDL and antibody. As a result, we developed the OpNS protocol, reported cryo-PS method, and invented IPET reconstruction algorithm. IPET allowed us to determine the 3D structure of an individual particle of protein (without average) at 1-3 nanometer resolution, such as the 3D structural dynamics and thermal fluctuation of IgG1 (*Sci. Rep.*, 2015, 5:8741), neuron proteins (*JBC* , 2016, 291(46):24133-24147; *JBC*, 2014, 289(50):34530-42) and DNA (*Nat. Comm.*, 2016, 7:11083; *Nat. Comm.*, 2018, 9:592). I have successfully administered various projects (*e.g.* in staffing, research protections, and budget), collaborated with other researchers, and produced more than 28 peer-reviewed publications in last five years, leading more than 21 publications in prestigious journals (include *NCB*, *NC*, *PNAS*, *et. al.*). In summary, I have a demonstrated record of successful and productive research projects, and my expertise and experience have prepared me to support this proposed project.

1. 3D Structural Dynamics of DNA Origami Mechanisms and Machines Using Individual-Particle Electron Tomography, D. Lei, A. Marras, J. Liu, C. Huang, L. Zhou, C. Castro, H.J. Su, **G. Ren**, *Nature Communications*, (2018), 9:592
2. Three Dimensional Structural Dynamics and Fluctuations of DNA Nanogold Conjugates by Individual Particle Electron Tomography, L. Zhang, D. Lei, J. M. Smith, M. Zhang, H. Tong, X. Zhang, Z. Lu, J. Liu, P. Alivisatos & **G. Ren**, *Nature Communications*, (2016), 7:11083. doi: 10.1038/ncomms11083.

3. Structure basis of transfer between lipoproteins by cholesteryl ester transfer protein. Zhang, L., F. Yan, S. Zhang, D. Lei, M. A. Charles, G. Cavigiolio, M. Oda, R. M. Krauss, K. H. Weisgraber, K.A. Rye, H.J. Pownall, X. Qiu & G. Ren. *Nature Chemical Biology*, (2012), 8(4):342-349.
4. Model of Human Low Density Lipoprotein and Bound Receptor Based on Cryo-EM. **Ren, G**., G. Rudenko, S.J. Ludtke, J. Deisenhofer, W. Chiu, H.J. Pownall, *Proc. Natl. Acad. Sci. USA.* (2010), 107(3):1059–1064
5. Visualization of a water-selective pore by electron crystallography in vitreous ice. **Ren, G.**, Reddy, V. S., Cheng, A., Melnyk, P., and Mitra, A. K. *Proc. Natl. Acad. Sci. USA*. (2001), 98: 1398-1403.

B. Positions and Honors

Positions and Employment

1999-2001 American Heart Association Postdoctoral Fellow, Department of Cell Biology, The Scripps Research Institute, La Jolla, CA
2001-2004 University of California AIDS Research Postdoctoral Fellow, Department of Cell Biology, The Scripps Research Institute, La Jolla, CA
2004-2006 Research Associate, The National Center for Macromolecular Imaging, Baylor College of Medicine, Houston, TX
2006-2010 Keck Fellow (Principal Investigator), Department of Biochemistry and Biophysics, University of California, San Francisco, CA
2010-2015 Career-track Staff Scientist (Principal Investigator), The Molecular Foundry, Lawrence Berkeley National Laboratory, Berkeley, CA
2015- Career Staff Scientist (Principal Investigator), The Molecular Foundry, Lawrence Berkeley National Laboratory, Berkeley, CA

Other Experience and Professional Memberships

1998- Member, American Heart Association
1998- Member, American Biophysical Society
2006- Member, American Chemical Society
2011- Editorial board member, Journal of Physical Chemistry & Biophysics
2015- Editorial board member, Scientific Reports
2016- Associate director, California Separation Science Society (CASSS)
2016- Board member of Institutional Biosafety Committee (IBC), Lawrence Berkeley National Laboratory

Honors

1986-90 Outstanding student awards for academic excellence in physics, Lanzhou University, China.
1988 First place award, University-wide competition in mathematics, Lanzhou University, China
1989 First place award, University-wide competition in physics, Lanzhou University, China.
1992 Second place award, Gansu Province boxing competition, China.
1999-01 Fellowship award, American Heart Association.
2002-04 Fellowship award, Univ. of California (University-wide AIDS Research Program).
2004- Research results collected by the *International Tables of Crystallography*, Vol. C
2006 Travel award, Gordon Conference (Lipoprotein Metabolism)
2012 Irvine H. Page Research Award (finalist), American Heart Association
2012 NIH R01 Award, National Health Institute, NHLBI, #1R01HL115153
2013 NIH R01 Award, National Health Institute, NIGMS, #1R01GM104427
2017 NIH R01 Award, National Health Institute, NHLBI, #2R01HL115153

C. Contribution to Science

1. **Parameterization of elastic and absorptive electron atomic scattering factors:** We computed the electron scattering factors and parameterized the factors of > 90 elements. The fitted parameters have been collected in the *International Tables of Crystallography, Volume C* since 2004. *International Tables* for *Crystallography* is the definitive resource and reference work for *crystallography* and structural science.
   a) Electron Diffraction. Colliex, C., J. M. Cowley, S. L. Dudarev, M. Fink, J. Gjonnes, R. Hilderbrandt, A. Howie, D. F. Lynch, L. M. Peng, **G. Ren**, A. W. Ross, V. H. Smith Jr, J. C. H. Spence, J. W. Steeds, J. Wang, M. J. Whelan and B. B. Zvyagin, *International Tables For Crystallography*. Volume C: Mathematical, physical and chemical tables, Edited by E.Prince, Fourth Edition, Published by Kluwer Academic Publishers (2006) Chapter 4.3, pp259-429.

b) Robust Parameterization of Elastic and Absorptive Electron Atomic Scattering Factors, Peng L. -M, **G. Ren**, S.L. Dudarev and M.J. Whelan, *Acta Cryst. A* (1996), A52: 257-276.
c) Debye-Waller Factors and Absorptive Scattering Factors of Elemental Crystals, Peng L.-M., G. Ren, S.L. Dudarev and M.J. Whelan, *Acta Cryst. A.* (1996), A52: 456-470.
d) Accurate Measurements of Crystal Structure Factors Using a FEG Electron Microscope Using Digital Micrographs, **Ren G.** , J. M. Zuo and L.-M. Peng, *Micron*, (1997) 28: 459-467.

2. **First-time in vitrified ice determined the near-atomic structure of membrane protein, AQP1 by electron crystallography (others' determinations embedded in glucose):** Determined the first near-atomic structure of transmembrane protein that embedded in vitreous ice, i.e. 3.7Å resolution of aquaporin 1 (AQP1) water-channel by cryo-electron crystallography. This is the first membrane protein has been determined by electron microscopy in USA and the third membrane protein determined by electron microscopy in the world. The research work was cited by the advanced information of 2003 Nobel Prize in Chemistry. The paper has been cited for about 200 times.
   a) Visualization of a water-selective pore by electron crystallography in vitreous ice. **Ren, G.**, Reddy, V. S., Cheng, A., Melnyk, P., and Mitra, A. K. *Proc. Natl. Acad. Sci. USA*. (2001), 98: 1398-1403. PMID: 11171962
   b) Three-dimensional fold of the human AQP1 water channel determined at 4-Å resolution by electron crystallography of 2-dimensional crystals embedded in ice. **Ren, G.**, Cheng, A., Reddy, V., Melnyk, P., and Mitra, A. K. *J. Mol. Biolo.* (2000), 301: 369-387
   c) Polymorphism in the packing of Aquaporin-1 tetramers in 2-D crystals. **Ren, G.**, Cheng, A., Melnyk, P., and Mitra, A. K.. *J. Struct. Biol.* (2000). 130: 45-53

3. **Discovered the tunnel mechanism of cholesterol ester transfer protein:** Human cholesteryl ester transfer protein (CETP) mediates the net transfer of cholesteryl ester mass from atheroprotective high-density lipoproteins to atherogenic low-density lipoproteins. Four CETP inhibitors for treating cardiovascular diseases have been submitted to large scale clinical trials. However, the first two inhibitors failure in Phase III resulted more than 20 billion market volume evaporated, partially due to unknow mechanism of CETP. We used our developed optimized negative-staining (OpNS) discovered a tunnel mechanism, in which, CETP bridges a ternary complex with its N-terminal b-barrel domain penetrating into high-density lipoproteins and its C-terminal domain interacting with low-density lipoprotein or very-low-density lipoprotein. The related news was reported on the front page of DOE, the office of science on April 9, 2012. *http://science.energy.gov/news/featured-articles/2012/04-09-12/*
   a) Structure basis of transfer between lipoproteins by cholesteryl ester transfer protein. Zhang, L., F. Yan, S. Zhang, D. Lei, M. A. Charles, G. Cavigiolio, M. Oda, R. M. Krauss, K. H. Weisgraber, K.A. Rye, H.J. Pownall, X. Qiu & **G. Ren**. *Nature Chemical Biology*, (2012), 8(4):342-349. PMID: 22344176
   b) Structural Features of Cholesteryl Ester Transfer Protein: A Molecular Dynamics Simulation Study. Dongsheng Lei, Xing Zhang, Shengbo Jiang, Zhaodi Cai, Matthew J. Rames, Lei Zhang, Gang Ren*, and Shengli Zhang*. *Proteins*, (2013), 81:415–425.
   c) HDL surface lipids mediate CETP binding as revealed by electron microscopy and molecular dynamics simulation,M. Zhang, R. Charles, H. Tong, L. Zhang, M. Patel, F. Wang, M.J. Rames, A. Ren, K.A. Rye, X. Qiu, D.G. Johns, M.A. Charles, **G. Ren**. *Scientific Reports*, (2015), 5:8741; PMID: 25737239
   d) Structural basis of the lipid transfer mechanism of phospholipid transfer protein (PLTP), Meng Zhang, Xiaobo Zhai, Jinping Li, John J. Albers, Simona Vuletic, **Gang Ren**, ***BBA Lipids***, (2018), 2018), 1863(9), 1082-1094, DOI: 10.1016/j.bbalip.2018.06.001
   e) Patent: Cholesterol ester transfer protein (CETP) inhibitor polypeptide antibodies for prophylactic and therapeutic anti-atherosclerosis treatments, **Ren, G.**, L. Zhang, WO 2013075040 A1, US 20140328851

4. **Developed a method for first-time 3D reconstruction of an individual/single macromolecule (without averaging) at near one nanometer resolution** Structural study on flexible, dynamic and heterogeneous macromolecules is challenging by current structural determination techniques, including X-ray crystallography, nuclear magnetic resonance (NMR) spectrum, small angle scattering and electron microscopy (EM) single-particle reconstruction due to the "signal" used to determine the structure by these techniques is the signal averaged from thousands to millions of different macromolecules. We reported an approach to determine the 3D structure of a single-instance macromolecule at near a nanometer resolution, termed individual-particle electron tomography (IPET). IPET does not require a pre-given initial model, class averaging of multiple molecules or an extended ordered lattice, but can tolerate small tilt-errors and sample heterogeneity. Through the structure determination of each individual macromolecule, the structural comparison of these macromolecules provides a new opportunity to reveal the

soft-/bio-macromolecular dynamic character, equilibrium fluctuation, mechanism and even the intermediate-state 3D structure of chemical reaction.

a) IPET and FETR: experimental approach for studying molecular structure dynamics by cryo-electron tomography of a single-molecule structure. Zhang, L. and **G. Ren**. *PLoS ONE*, (2012), 7(1):30249. PMID: 22291925).
b) An Algorithm for Enhancing the Image Contrast of Electron Tomography, Hao Wu, Xiaobo Zhai, Dongsheng Lei, Jianfang Liu, Yadong Yu, Rongfang Bie, **Gang Ren**, *Scientific Reports*., (2018), 8(1):16711, PMID: 30420636
c) Fully Mechanically Controlled Automated Electron Microscopic Tomography, Jinxin Liu, Hongchang Li, Lei Zhang, Matthew Rames, Meng Zhang, Yadong Yu, Bo Peng, César Díaz Celis, April Xu, Qin Zou, Xu Yang, Xuefeng Chen, **G. Ren**, *Scientific Reports*, (2016) 6:29231 | DOI: 10.1038/srep29231
d) *3D Structural Dynamics of DNA Origami Mechanisms and Machines Using Individual-Particle Electron Tomography*, Dongsheng Lei, Alex Marras, Jianfang Liu, Chaomin Huang, Lifeng Zhou, Carlos Castro, Hai-Jun Su, **Gang Ren**, *Nature Communications*, (2018), 9:592, DOI:10.1038/s41467-018-03018-0
e) *Three-Dimensional Structural Dynamics and Fluctuations of DNA-Nanogold Conjugates by Individual-Particle Electron Tomography*, Lei Zhang, Dongsheng Lei, J. M. Smith, H. Tong, X. Zhang, Z. Lu, P. Alivisatos and **G. Ren**. *Nature Communications* (2016)7:11083. doi: 10.1038/ncomms11083.

5. **Revealing the structural dynamical and fluctuation of flexible antibody:** Commonly used methods for determining protein structure, including X-ray crystallography and single-particle reconstruction, often provide a single and unique three-dimensional (3D) structure. However, in these methods, the protein dynamics and flexibility/fluctuation remain mostly unknown. In this paper, we utilized advances in electron tomography (ET) to study the antibody flexibility and fluctuation through structural determination of individual antibody particles rather than averaging multiple antibody particles together. Through determined 120 ab-initio 3D density maps at an intermediate resolution (~1 – 3 nm) from 120 individual IgG1 antibody particles by IPET, we used these maps as a constraint and derived 120 conformations of the antibody via structural flexible docking of the crystal structure to these maps by targeted molecular dynamics simulations. Statistical analysis of the various conformations disclosed the antibody 3D conformational flexibility through the distribution of its domain distances and orientations. This is the first time to reveal the 3D structural fluctuation from a single molecule point of view.
   a) 3D structural fluctuation of IgG1 antibody revealed by individual particle electron tomography. X. Zhang, L. Zhang, H. Tong, B. Peng, M.J. Rames, S. Zhang, **G. Ren**. *Scientific Reports,* (2015), 5:8741
   b) Peptide-Conjugation Induced Conformational Changes in Human IgG1 Observed by Optimized Negative-Staining and Individual-Particle Electron Tomography, Huimin Tong, Lei Zhang, Allan Kaspar, Matthew J Rames, Liqing Huang, Gary Woodnutt, and **G. Ren**, *Scientific Reports*, (2013), 3(1089):1-9), DOI: 10.1038/srep01089
   c) Structural and Functional Characterization of a Hole-Hole Homodimer Variant in a "Knob-Into-Hole" Bispecific Antibody, Hui-Min Zhang, Charlene Li, Ming Lei, Ho Young Lee, Milady Ninonuevo, Guanghui Han, Wendy Sandoval, Victor Lundin, Dongsheng Lei, **Gang Ren**, Jennifer Zhang and Hongbin Liu, ***Analytical Chemistry***, (2017) , 89(24):13494-13501. doi: 10.1021/acs.analchem.7b03830

D. Research Support

Ongoing Research Support

NIH 2R01 HL115153 (PI: Ren) 12/01/2017 – 11/31/2021

NIH/NHLBI

"Structure-Function Relationship Studies of the Plasma Lipid Transfer Proteins CETP and PLTP"

The major goals of this project are to "see" how CETP and PLTP "transfer" by a unique combination of electron microscopy and animal experiments.

Department of Energy, #DE-AC02-05CH11231 08/2010 - ongoing

Imaging and Manipulation of Nanostructures Facility, Overview, the Molecular Foundry

The Molecular Foundry provides support to researchers from around the world whose work can benefit from or contribute to nanoscience. Through unparalleled access to state-of-the-art instruments, materials, technical expertise and training, the Foundry provides researchers with the tools to enhance the development and understanding of the synthesis, characterization and theory of nanoscale materials. Gang Ren is one of the PIs supported by this program.

NIH R01 DK042667 (PI: Dahms) 1/01/2016 – 12/31/2024

NIH/NIDDK

"Structural Analysis of the Mannose 6-Phosphate Receptors"

The major goals of this project are to determine the three-dimensional structure of the ligand binding sites of the mannose 6-phosphate receptors by X-ray crystallographic, NMR and TEM approaches, and the role of individual amino acids in carbohydrate recognition by the mannose 6-phosphate receptors. Gang Ren is one of the Co-PIs supported by this program.

NIH R01 NS097326 (PI: Rudenko) 8/01/2018 – 7/31/2022

NIH/NINDS

"Multidisciplinary Approaches to CNTNAP2 Structure, Dynamics and Mechanism"

The major goals of this project are to determine the CNTNAP2 structure, dynamics and function by the combination of multidisciplinary approaches, including X-ray, biochemistry and electron microscopy. Gang Ren is the Co-PI supported by this program.

Pending Research Support

NIH R01 AI127808-01 (PI: Ren) 11/01/2018– 12/31/2022

NIH/NIAID

"Antibody 3D Structure and Dynamics by Individual Particle Electron Tomography"

The major goals of this project are to "see" the 3D structure of each antibody and its complex for structural analyses of the antibody dynamics, aggregation and function using our developed novel and high-throughput approach, individual particle electron tomography. Gang Ren is the single PI in the project.

Completed Research Support

NIH R01 GM104427 (PI: Ren) 5/01/2013 – 4/30/2017

NIH/NIGMS

*"*Lipoprotein Structure and Function by Individual Particle Electron Tomography"

The major goal of this project is to develop novel and high throughput approach, individual particle electron tomography, to "see" each molecule's building block of LDL and HDL. Gang Ren is the single PI in the project.

NIH R01 HL115153 (PI: Ren) 8/01/2012 – 7/31/2017

NIH/NHLBI

"Cholesterol Metabolism Related Protein Structure and Function by Electron Microscopy"

The major goals of this project are to "see" how CETP "converts" good cholesterol to bad cholesterol by a unique combination of electron microscopy and computational similarity. Gang Ren is the single PI in the project.

WF009766 (PI: Ren) 8/01/2013 – 7/31/2015

Pfizer Inc.

"Cryo-electron tomography analysis on antibody structure before and after drug conjugation"

The major goal of this project is to "see" the conformational changes of each individual antibody before and after conjugated the peptide using in-house developed individual particle electron tomography approach. Gang Ren is the single PI in the project.

WF010583 (PI: Ren) 10/14/2014 – 1/13/2015

Roche/Genentech Inc.

"Genentech Antibody Structural Changes caused by Light-stress and Oxidation using individual-particle Electron tomography"

The major goal of this project is to investigate the conformational change of antibody after light stress and oxidation using in-house developed individual particle electron tomography. Gang Ren is the single PI in the project.

LKRD105435 (PI: Ren) 5/01/2013 – 4/30/2015

Merck Sharp & Dohme Corp.

"How Different CETP Inhibitors Effect on CETP Conformation and its Function in CE Transfer among Various Lipoproteins"

The major goal of this project is to investigate how the CETP inhibitors change the CETP structure and function at molecular level. Gang Ren is the single PI in the project.

PROFESSIONAL SOCIETIES:

Member of Biophysical Society
Member of American Chemical Society
Member of American Society for Biochemistry and Molecular Biology
Member of American Heart Association

SELECTED LECTURES AND SEMINARS:

1. Oct. 2019, Invited talk, *Single Molecule 3D Image: An Approach to Reveal Antibody Structural Dynamics & Conformational Changes*, World ADC San Diego Summit, San Diego, CA
2. Aug. 2019, Seminar, *Understanding Pharmaceutical Antibody Functional Deficiency by Single-Molecule 3D Imaging*, Merck Research Laboratories, South San Francisco, CA
3. Mar, 2019, Seminar, *Single-Macromolecule 3D Structure Determination*, Nankai University, Tianjing, China
4. Feb, 2019, Seminar, *Individual-Particle Electron Tomography and applications*, Lanzhou University, China
5. Sept. 2018, Invited talk, The Center for Integrated Nanotechnologies (CINT) Annual Meeting, Santa Fe, NM, USA
6. Jul. 2018, Talk, Soft-/biomaterials structure and Dynamics, Princeton - Nature Conference: Frontiers in Electron Microscopy for the Physical and Life Sciences, Princeton University, Princeton, NJ, USA
7. May, 2018, Seminar, Individual-Particle Electron Tomography, Lanzhou University, China
8. May, 2018, Seminar, Individual-Particle Electron Tomography, Beijing University, China
9. Mar. 2018, Invited talk, Single DNA origami 3D imaging and dynamics. Protein and Peptide Annual Meeting, Miami
10. Mar. 2018, Invited talk, CETP mechanism and inhibitor development. Nanjing University
11. Sept. 2017, Invited talk, DNA Origami and Dynamics. DOE Nanoscale Science Research Centers workshop, Santa Fe, NM
12. Sept. 2017, Seminar, Single protein 3D imaging and molecular drug analysis. Chinese Academic of Science and Technology, Shenzhen, China
13. Aug. 2017, Seminar, Single protein 3D structure and dynamics. Fudan University, China
14. Jul. 2017, Seminar, Single protein 3D imaging. Northwest University, Xi'an, China
15. Jul. 2017, Seminar, Single protein 3D imaging and its applications. Sun Yat-sen University, Guangzhou, China
16. Jun. 2017, Talk, Single protein 3D imaging and its applications. Shanghai Tech Univ., Shanghai, China
17. Mar. 2017, Workshop talk, *Three-Dimensional Electron Tomographic for Hard and Soft Materials Research*. Materials Research Society, Spring meeting, Phoenix, AZ, U.S
18. Mar. 2017, Workshop talk, *Individual-Particle Electron Tomography (IPET): an approach to study flexible soft-/bio-molecular structure and dynamics*. National Institute of Standard Technology (NIST), Gaithersburg, MD, U.S
19. Nov. 2016, Seminar, *3D image of a single protein*. National Institute of Standard Tech. (NIST), Gaithersburg, MD, U.S
20. Sept. 2016, Seminar, 3D image of a single macromolecule. NIBS, Beijing, China
21. Jun. 2016, Invited Talk, *The physics in Biology*. Lanzhou University, Lanzhou China
22. Jun. 2016, Seminar, *Image process techniques in biological research*. Beijing Normal University, Beijing, China
23. Jun. 2016, Seminar, *3D image of a single macromolecule Chinese Aca. of Sci.*, Inst. of Modern Physics, Lanzhou, China
24. May 2016, Seminar, *IPET: an approach to study protein dynamics and aggregation*. Mercer University, Macon, GA, US
25. Apr. 2016, invited talk, *Individual-particle electron tomography (IPET): an approach to study protein mechanism, dynamics and aggregation*. 21st Annual Sealy Center for Structural Biology Symposium, Galveston, TX
26. Apr. 2016, invited talk, *3D structural dynamics of DNA-nanogold conjugates,* NanoWorld Conference, Boston, MA
27. Apr. 2016, Invited talk, *Individual-particle electron tomography (IPET): an approach to study protein mechanism, dynamics and aggregation*. The Higher Order Structure 2014, An Intl. Separation Science Society, Long Beach, CA
28. Mar. 2016, Seminar, *Individual-particle electron tomography (IPET): an approach to study the flexible protein structure, dynamics, mechanism and aggregation*. Medical College of Wisconsin, Milwaukee, WC
29. Oct. 2015, seminar, *Individual-particle electron tomography (IPET): an approach to study protein mechanism, dynamics and aggregation*. Eli Lilly, Indianapolis, IN
30. Aug. 2015, seminar, *Individual-particle electron tomography (IPET): an approach to study antibody structure, dynamics and aggregation*. Eli Lilly, San Diego, CA
31. Jul. 2015, seminar, *Individual-particle electron tomography (IPET): an approach to study the flexible protein structure, dynamics, mechanism and aggregation*. Biogen Inc., Boston, MA
32. April. 2015, seminar*, Individual-particle electron tomography (IPET): an approach to study the protein mechanism and dynamics*. University of Science and Technology China, Hefei, China.
33. April. 2015, invited talk, *IgG1 antibody structural dynamics and fluctuation*. 7th Annual International Congress of Antibodies-2015, Nanjing, China
34. Feb. 2014, invited talk, *IgG1 antibody structural dynamics and fluctuation*. The Higher Order Structure 2014, An International Separation Science Society, Arlington, Virginia
35. Sept. 2013, seminar, *Individual-particle electron tomography (IPET).* Dept. of Chemistry, Univ of Cali, Berkeley, CA
36. Jun. 2013, seminar, *Individual-particle electron tomography (IPET): an approach to study antibody structure, dynamics and aggregation*. Genentech, South San Francisco, CA

37. Jun. 2013, invited talk, *dsDNA structural dynamics and fluctuation.* 18th Conversation of Protein Dynamics, Albany, NY
38. April, 2013, invited talk, *catching the intermediate state 3D structure during chemical reaction by individual-particle electron tomography.* Frontiers in Structural Biology of Membrane Proteins, Birmingham, AB
39. Nov. 15, 2012, seminar, *Individual-particle electron tomography (IPET).* UAB Department of Pharmacology & Toxicology, Birmingham, AB
40. Aug. 24, 2012, seminar, *Antibody dynamics by individual-particle electron tomography (IPET).* Abbott Inc, Boston, MA
41. Apr., 2012, plenary presentation, *Tunnel mechanism of cholesteryl ester transfer protein*. Arteriosclerosis, Thrombosis, Vascular Biology Ann. Meeting, Chicago, IL,
42. Apr. 21, 2012, invited talk, *Discoidal HDL structure and dynamics*. HDL summit meeting, Chicago, IL,

SELECTE PUBLICATIONS:

1. Real-time observation of dynamic structure of liquid-vapor interface at nanometer resolution in electron irradiated sodium chloride crystals, Amy Ren, David Lu, Ed Wong, Matthew R. Hauwiller, A. Paul Alivisatos, **Gang Ren**, ***Scientific Reports***, (2020), 10, 8596, Doi: 10.1038/s41598-020-65274-9.
2. Discovery of Stable and Selective Antibody Mimetics from Combinatorial Libraries of Polyvalent, Loop-Functionalized Peptoid Nanosheets, Jae Hong Kim, Samuel C. Kim, Mark A. Kline, Elissa M. Grzincic, Blakely W. Tresca, Joshua Cardiel, Mohsen Karbaschi, Dilani C. Dehigaspitiya, Yulin Chen, Venkatareddy Udumula, Tengyue Jian, Daniel J. Murray, Lisa Yun, Michael D. Connolly, Jianfang Liu, **Gang Ren**, Chun-Long Chen, Kent Kirshenbaum, Adam R. Abate, Ronald N. Zuckermann, ***ACS Nano***, (2020), 14, 1, 185–195, Doi: 10.1021/acsnano.9b07498.
3. A DNA origami plasmonic sensor with environment-independent read-out, Valentina Masciotti, Luca Piantanida, Denys Naumenko, Heinz Amenitsch, Mattia Fanetti, Matjaž Valant, Dongsheng Lei, **Gang Ren**, and Marco Lazzarino, ***Nano Research***, (2019), 12(11):2900–2907
4. Single-Molecule 3D Image of "Hole-Hole" IgG1 Homodimers by Individual-Particle Electron Tomography, Dongsheng Lei, Jianfang Liu, Hongbin Liu, Thomas E. Cleveland, John P. Marino, Ming Lei, **Gang Ren**, ***Scientific Reports,*** (2019), 9:8864, Doi:10.1038/s41598-019-44978-7
5. Single-Molecule 3D Imaging of Human Plasma Intermediate-Density Lipoproteins Reveals a Polyhedral Structure, Dongsheng Lei, Yadong Yu, Yu-Lin Kuang, Ronald M. Krauss, **Gang Ren**, ***BBA Lipids***, (2019), 1864(3):260-270
6. Optimized negative-staining protocol for lipid-protein interactions investigated by electron microscopy, Jianfang Liu, Hao Wu, Changyu Huang, Dongsheng Lei, Meng Zhang, Wei Xie, Jinping Li and **Gang Ren**, In: Kleinschmidt J. (eds) Lipid-Protein Interactions. ***Methods in Molecular Biology***, vol 2003. Humana, New York, NY, (2019), Doi:10.1007/978-1-4939-9512-7_8.
7. An Algorithm for Enhancing the Contrast of Electron Tomography Images, Hao Wu, Xiaobo Zhai, Yadong Yu, Dongsheng Lei, Jianfang Liu, Rongfang Bie, **Gang Ren**, ***Scientific Reports,*** (2018) , 8(1):16711.
8. Structural basis of the lipid transfer mechanism of phospholipid transfer protein (PLTP), Meng Zhang, Xiaobo Zhai, Jinping Li, John J. Albers, Simona Vuletic, **Gang Ren**, ***BBA Lipids***, (2018), 2018), 1863(9), 1082-1094, DOI: 10.1016/j.bbalip.2018.06.001
9. Structural Plasticity of Neurexin 1α: Implications for its Role as Synaptic Organizer, Jianfang Liu, Anurag Misra, Sekhar Reddy, Mark Andrew White, **Gang Ren**, Gabby Rudenko, ***J. Mol. Biolo.***, (2018), in-print, DOI: doi.org/10.1016/j.jmb.2018.08.026
10. IgG Antibody 3D Structures and Dynamics, Jacob White Jay, Brinkley Bray, Yaozhi Qi, Eseosaserea Igbinigie, Hao Wu, Jinping Li, **Gang Ren**, ***Antibodies***, (2018), 7, 18; doi:10.3390/antib7020018
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PATENT:

- Cholesterol Ester Transfer Protein (CETP) Inhibitor Polypeptide Antibodies for Prophylactic and Therapeutic Anti-Atherosclerosis Treatments, Authors: **Gang Ren**, Lei Zhang; U.S. patent application no. 14/279,182, Intl. Patent Application Ser. No: PCT/US2012/065697 , Filed Date: 16-Nov-2012; Claiming priority to 61/560,751, LBNL Docket: IB-3143PCT,

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