BIOGRAPHICAL SKETCH

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NAME: Wang, Qinzhe

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

POSITION TITLE: POST DOC RESEARCH ASSOCIATE

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
Northwest University, China	B.S.	07/2009	Biotechnology
Northwest University, China	M.S.	07/2012	Biochemistry and Molecular Biology
University of Toledo, USA	Ph.D.	05/2017	Chemistry and Biochemistry
University of Utah, USA	Postdoc		Structural Biology

A. Personal Statement

As a M.S. student with Zheng Li at Northwest University, I was trained as a biochemist in glyco-proteomics, and characterized the evolutional patterns of N-linked glycosylation sites in influenza virus glycoproteins, as well as determined the glycoproteome patterns of human saliva and from cell models and tissues from various cancer types.

As a Ph.D. student with Ronald Viola at the University of Toledo, I was trained as an enzymologist, and characterized multiple enzymes that related to Canavan Disease, a fatal, neurological degenerative disease of infancy.

As a postdoc in Erhu Cao's laboratory at The University of Utah, I am pursuing biochemical, biophysical and structural analyses of polycystin family of ion channels and receptors, which are key players in normal functions of cardiovascular and renal systems. I have extensive experience in molecular biology, protein biochemistry, ion channel reconstitution, and single particle electron cryo-microscopy (cryo-EM). I would like to further gain more knowledge and skills in ion channel electrophysiology, electron microscope operation and cryo-EM data processing. I hope these training experiences will support my future career plan that is having my own research lab and contributing more to biomedical research. The publications that are most relevant to the current proposal are listed below:

a. **Qinzhe Wang**, Erhu Cao (**2019**). Structural Determination of the Polycystin-2 Channel by Electron Cryomicroscopy, in Yu, Y. and Hu, J.H. (ed.) *Polycystic Kidney Disease.* ISBN: 9781138603899.
b. Xiaoyong Yang*, **Qinzhe Wang***, Erhu Cao. Structure of the human cation-chloride cotransporter NKCC1 determined by single-particle electron cryo-microscopy. *Nature Communications*, **2020**, 11, 1016 PMCID: PMC7035313
c. Kotdaji Ha, Mai Nobuhara, **Qinzhe Wang**, Rebecca V Walker, Feng Qian, Christoph Schartner, Erhu Cao, Markus Delling. The heteromeric PC-1/PC-2 polycystin complex is activated by the PC-1 N terminus. *eLife*. **2020** Nov 9;9:e60684. PMCID: PMC7728438.

B. Positions and Honors

Position/Employment

2012 – 2017 Graduate Research Assistant, Ronald Viola laboratory, Department of Chemistry and Biochemistry, The University of Toledo.
2017 – present Postdoctoral fellow, Department of Biochemistry, University of Utah School of Medicine.

Honors

2016 Travel Award from ACS Division of Biological Chemistry for 252nd ACS National Meeting, Philadelphia, PA (2016)
2020 Jared J. Grantham Research Fellowship from American Society of Nephrology

Professional Membership

American Chemical Society, since 2012
American Society for Biochemistry and Molecular Biology, since 2012
American Association for the Advancement of Science, since 2014
American Society of Nephrology, since 2019

C. Contributions to Science

1. **Glyco-proteomics: Methods and application in biomarker discovery for cancer nondestructive early detection.**

Malignant tumor usually associates with alterations in glycosylation. We developed a magnetic particle-based enrichment method for efficient glyco-peptide capture from various tissues, and I used the glycoproteomic approach to characterize the glycoproteomes from serum, saliva and cell models with aims of developing a nondestructive method for the early detection of cancer biomarkers. I discovered that the composition and abundance of glycoproteins in healthy people's saliva vary among ages and exist gender differences. This research led to two important developments: first, a following study in the same lab uncovered the glycopattern differences from saliva among age groups, explaining why saliva proteins may protect older people from influenza virus infection; second, it established saliva as a new non-invasive medium for cancer early detection.

a. Shisheng Sun*, Fei Zhao*, **Qinzhe Wang***, Yaogang Zhong, Tanxi Cai, Peng Wu, Fuquan Yang, Zheng Li. Analysis of age and gender associated *N*-glycoproteome in human whole saliva. *Clinical Proteomics*, **2014**, 11(1): 25. (contributed equally to this work) PMCID: PMC4070402

b. **Patent Granted**: Zheng Li, Fei Zhao, **Qinzhe Wang**, Hanjie Yu, Hua Zhang, Shisheng Sun. Method for rapid nondestructive detection of liver tumor marker and test paper strip adopted by the method, Patent Number CN102854324 A, January 2013. **Granted**.

c. **Qinzhe Wang***, Shisheng Sun* (**2015**). "Enrichment of glycoprotein and glycopeptides via hydrazide chemistry", Chapter 8 in Li, Z (ed.). *Techniques in Glycomics*. Higher Education Press of China. ISBN: 978-7-04-037676-0 (Chapter and book titles are translated from Chinese) (*We didn't determine the relative contribution between authors)

2. **Evolutionary biology: Glycosylation site alteration in the evolution of influenza A virus.** Influenza is a common, sometimes deadly, threat to human health. Influenza virus escapes host immune pressure through constantly altered glycosylation patterns on its two surface glycoproteins, hemagglutinin (HA) and neuraminidase (NA). I, together with my colleagues, systematically analyzed the patterns and conservation of glycosylation sites on HA and NA of influenza A/H1N1 viruses isolated from various hosts at different time periods through a combinatory approach that include genome-based glycosylation site prediction and 3D modeling of glycoprotein structures. We uncovered trends of influenza evolution: increasing number of surface N-linked glycosylation sites to shield more protein antigen; positional conversion to cover more important surface regions by fewer glycans. We proposed five possible functions that the glycosite

migrations in human influenza viruses: to more effectively mask the antigenic sites, to more effectively protect the enzymatic cleavage sites of neuraminidase (NA), to stabilize the polymeric structures, to regulate the receptor binding and catalytic activities and to balance the binding activity of hemagglutinin (HA) with the release activity of NA.

a. **Qinzhe Wang***, Wentian Chen*, Ran Wang* (**2015**). "Bioinformatics in Glycomics", Chapter 15 in Li, Z. (ed.) *Techniques in Glycomics.* Higher Education Press of China. ISBN: 978-7-04-037676-0 (Chapter and book titles are translated from Chinese) (*We didn't determine the relative contribution among authors)

b. **Software Copyright: Qinzhe Wang**, Zishi Qin, Shisheng Sun, Zheng Li. Sequon Finder V1.0. CN Registration Number: 2010SR014428.

c. Shisheng Sun**, Qinzhe Wang**, Fei Zhao, Wentian Chen, Zheng Li. Glycosite alteration in the evolution of influenza A (H1N1) viruses. *PLoS ONE,* **2011**, 6(7): e22844. PMCID: PMC3145772

d. Shisheng Sun, **Qinzhe Wang**, Fei Zhao, Wentian Chen, Zheng Li. Prediction of Biological Functions on Glycosylation Site Migrations in Human Influenza H1N1 Viruses. *PLoS ONE*, **2011**, 7(2): e32119. PMCID: PMC3280219

3. **Enzymology: Aspartate *N*-acetyltransferase inhibitors for the potential treatment of Canavan Disease.**

My Ph.D. work in Dr. Ronald Viola lab at The University of Toledo focused on the enzymology of two enzymes in the aspartate metabolism in human brain, aspartoacylase and aspartate Nacetyltransferase. During my Ph.D. study, I successfully expressed, purified and characterized aspartate *N*-acetyltransferase, which is a membrane protein that not only involves in Canavan disease but also in neuropsychiatric disorders with drug abuse. Together with my colleagues, we developed the first set of potent inhibitors with low nanomolar inhibition constants against aspartate *N*-acetyltransferase. Further development of these lead compounds could lead to therapeutic drugs for Canavan Disease.

a. **Qinzhe Wang***, Mojun Zhao*, Gwenn G. Parungao, Ronald E. Viola. Purification and characterization of aspartate *N*-acetyltransferase: A critical enzyme in brain metabolism. *Protein Expression and Purification*, **2016**, 119: 11-18. (contributed equally to this work) PMID: 26550943

b. **Patent Granted:** Ronald Viola, Bharani Thangavelu, Vinay Mutthamsetty, **Qinzhe Wang,** Pravin Bhansali. Potent phthalate inhibitors of aspartate N-acetyltransferase and selective aspartate pathway inhibitors, Patent Number US10449168B2, October 2019. **Granted**.

c. **Patent application:** Ronald Viola, **Qinzhe Wang**, Mojun Zhao, Gwenn G. Parungao. Purification of a Soluble and Active Form of Aspartate *N*-Acetyltransferase, US. Application no. 62/216,700, filed September 10, 2015

4. **Enzymology: Characterization of human aspartoacylase, the defective enzyme in Canavan Disease.**

Aspartoacylase is the defective enzyme in a fatal neurodegenetive disease, Canavan disease. I explained the *N*-glycosylation site that is at close proximity to the enzyme active site is not essential for enzyme activity, reconciled a long-time debate about the effect of post-translational glycosylation on this crucial metabolic enzyme.

a. **Qinzhe Wang**, Ronald E Viola. Reexamination of aspartoacylase: Is this human enzyme really a glycoprotein? *Archives of Biochemistry and Biophysics*, **2014**, 548:66-73. PMID: 24632142

5. **Structural Biology: Structure of the human cation-chloride cotransporter NKCC1 determined by single-particle electron cryo-microscopy.**

The secondary active cation-chloride cotransporters (CCCs) utilize the existing Na^+ and/or K^+ gradients to move Cl^- into or out of cells. NKCC1 is an intensively studied member of the CCC family and plays fundamental roles in regulating trans-epithelial ion movement, cell volume, chloride homeostasis and neuronal excitability. Together with my colleagues, we reported the first human NKCC1 structure captured in a partially loaded,

inward-open state solved by singleparticle electron cryo-microscopy. The human NKCC1 structure provides a blueprint for further probing structure-function relationships of NKCC1 and other CCCs.

a. Xiaoyong Yang*, **Qinzhe Wang***, Erhu Cao. Structure of the human cation-chloride cotransporter NKCC1 determined by single-particle electron cryo-microscopy. *Nature Communications.* accepted (contributed equally to this work)

D. Additional Information: Research Support and/or Scholastic Performance

Currently I am a postdoc fellow in Erhu Cao's lab at the University of Utah. In addition to the research support from lab, I have a Jared J. Grantham Research Fellowship from American Society of Nephrology to support my research.

BIOGRAPHICAL SKETCH
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NAME: Cao, Erhu

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

POSITION TITLE: Assistant Professor

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
Huazhong Agricultural University, China	B.S.	07/1996	Plant Biology
Albert Einstein College of Medicine, USA	Ph.D.	03/2007	Biomedical Science
University of California, San Francisco, USA	Postdoctoral	08/2015	Molecular Pharmacology

A. Personal Statement

As a joint Ph.D. student with Steven Almo and Stanley Nathenson at the Albert Einstein College of Medicine, I trained as biochemist and structural biologist, and determined multiple X-ray crystal structures of immunoglobulin family receptors, ligands, and their complexes, including the first structure of the complex between PD-1 and its ligand PD-L2. These studies contributed significantly to our understanding of cellular immunity. As a postdoc in David Julius' laboratory at UCSF, I pursued biochemical, biophysical and structural analyses of transient receptor potential (TRP) ion channels, which are key players in sensory signaling and in the detection of noxious stimuli. My work there included biophysical, pharmacological and structural studies of the TRPV1 ion channel. Consequently, I have extensive experience in molecular biology, protein biochemistry, ion channel reconstitution into liposomes, ion channel electrophysiology, single-particle electron cryo-microscopy (cryo-EM), and protein X-ray crystallography. As an independent faculty member at the University of Utah, my goal is to elucidate the structure, pharmacology, function, and pathophysiology of ion channels, receptors, and transporters that play pivotal roles in renal physiology and which, when mutated, cause kidney diseases in humans. We employ a multidisciplinary approach that includes molecular biology, protein biochemistry, pharmacology, ion channel electrophysiology (patch clamp recording), ion flux assays, X-ray crystallography, and single-particle cryo-EM to achieve a comprehensive and in-depth understanding of sensory and transport mechanisms in the kidneys. The publications that are most relevant to the current proposal are listed below:

Peter S. Shen[#], Xiaoyong Yang[#], Paul G. Decaen, Xiaowen Liu, David Bulkley, David E. Clapham*, and **Erhu Cao***. The structure of the polycystic kidney disease 2 channel in lipid nanodiscs. *Cell* (2016) 167: 763-773. PMCID: PMC6055481 [#] Co-first authors * Corresponding authors

Wang Zheng[#], Xiaoyong Yang[#], Ruikun Hu, Ruiqi Cai, Laura Hofmann, Zhifei Wang, Qiaolin Hu, Xiong Liu, David Bulkey, Yong Yu, Jingfeng Tang*, Veit Flockerzi, Ying Cao, **Erhu Cao**[*], and Xing-Zhen Chen[*]. Hydrophobic pore gates regulate ion permeation in polycystic kidney disease 2 and 2L1 channels. *Nature Communications* (2018) 9:2302. PMCID: PMC5998024. [#] Co-first authors * Corresponding authors

Thuy N. Vien[#], Jinliang Wang[#], Leo C.T. Ng, **Erhu Cao**, and Paul DeCaen. Molecular dysregulation of ciliary polycystin-2 channels caused by variants in the TOP domain. *Proceedings of the National Academy of Sciences*. 2020 May 12;11(1):2359. PMCID: PMC7229662. [#] Co-first authors.

Kotdaji Ha, Mai Nobuhara, Qinzhe Wang, Rebecca V Walker, Feng Qian, Christoph Schartner, **Erhu Cao**, Markus Delling. The heteromeric PC-1/PC-2 polycystin complex is activated by the PC-1 N-terminus. *eLife*. 2020 Nov 9;9:e60684. PMCID: PMC7728438.

B. Positions and Honors

Position/Employment

1999 – 2001 Research Assistant, Youxin Jin lab, Shanghai Institute of Biochemistry, Shanghai, China.
2001 – 2007 Graduate Student, Steven Almo and Stanley Nathenson laboratories, Albert Einstein College of Medicine.
2007 – 2015 Postdoctoral Fellow, David Julius Laboratory, Department of Physiology, UCSF.
2015 – present Assistant Professor, Department of Biochemistry, University of Utah School of Medicine.

Honors

2007 Julius Marmur Research Award (Albert Einstein College of Medicine Highest Award given to the best graduate students)
2008 – 2010 Damon Runyon Cancer Research Foundation Postdoctoral Fellowship
2017 – 2021 Pew Scholar Award (a highly competitive award that recognizes ~ 20 junior faculty members nationwide each year)

Professional Membership

2010 Biophysical Society
2014 American Heart Association
2015 American Society of Nephrology

C. Contributions to Science

1. **Independent Investigator – structural mechanisms of polycystic kidney disease proteins.**

One of our research areas concerns the 11-transmembrane (TM)-spanning PKD1 receptor and tetrameric 6-TM-spanning PKD2 channel, which are sites of mutations that cause the prevalent and life-threatening human genetic disorder autosomal dominant polycystic kidney disease (ADPKD). PKD2 shows distant sequence similarity with the TRPV1 channel whose properties I characterized and structures I determined as a postdoctoral fellow. In 2016, we reported the first cryo-EM structure of the PKD2 channel in a closed state in lipidic nanodiscs at 3.0 Å resolution, which represents the second near-atomic reconstruction of a membrane protein in nanodiscs; the first such technical breakthrough was achieved with TRPV1, whose structures my colleagues and I also determined in nanodiscs (see below). To understand the gating mechanisms (i.e., the process that a channel opens and closes) of PKD2, we then determined the structure of a gain-of-function PKD2 mutant (F604P) captured in a partially open state, providing initial insights into activation-associated conformational changes in PKD2. To understand pathogenic mechanisms of disease-associated PKD2 variants, we recently reported a structure of PKD2 C331S, demonstrating that this pathogenic variant maintains the tetrameric architecture, but exhibits decreased stability caused by disruption of a conserved disulfide bond formed between C331 and C343. In collaboration with Paul Decaen at Northwestern University, we showed that C331S and many other PKD2 disease-associated variants show diminished voltage sensitivity, establishing that ADPKD is not only a ciliopathy as widely appreciated, but also a channelopathy in which defects in channel biogenesis and/or gating are the root cause. Most recently, in collaboration with Markus Delling at UCSF, we showed that the large ectodomain of PKD1 (> 3000 amino acids) functions as an agonist for activation of the PKD1/PKD2 complex, providing initial insights into regulation of this enigmatic receptor/ion channel complex.

a. Peter S. Shen[#], Xiaoyong Yang[#], Paul G. Decaen, Xiaowen Liu, David Bulkley, David E. Clapham*, and **Erhu Cao***. The structure of the polycystic kidney disease 2 channel in lipid nanodiscs. *Cell* (2016) 167: 763-773. PMCID: PMC6055481 [#] Co-first authors * Corresponding authors

b. Wang Zheng[#], Xiaoyong Yang[#], Ruikun Hu, Ruiqi Cai, Laura Hofmann, Zhifei Wang, Qiaolin Hu, Xiong Liu, David Bulkey, Yong Yu, Jingfeng Tang*, Veit Flockerzi, Ying Cao, **Erhu Cao**[*], and Xing-Zhen Chen[*]. Hydrophobic pore gates regulate ion permeation in polycystic kidney disease 2 and 2L1 channels. *Nature Communications* (2018) 9:2302. PMCID: PMC5998024. [#] Co-first authors * Corresponding authors

c. Thuy N. Vien[#], Jinliang Wang[#], Leo C.T. Ng, **Erhu Cao**, and Paul DeCaen. Molecular dysregulation of ciliary polycystin-2 channels caused by variants in the TOP domain. *Proceedings of the National Academy of Sciences*. 2020 May 12;11(1):2359. PMCID: PMC7229662. [#] Co-first authors.

d. Kotdaji Ha, Mai Nobuhara, Qinzhe Wang, Rebecca V Walker, Feng Qian, Christoph Schartner, **Erhu Cao**, Markus Delling. The heteromeric PC-1/PC-2 polycystin complex is activated by the PC-1 N-terminus. *eLife*. 2020 Nov 9;9:e60684. PMCID: PMC7728438.

2. **Independent Investigator – structures and pharmacology of cation-chloride cotransporters.**

More recently, we have started to take a holistic view of the fascinating sensory and transport systems in the kidneys. We were drawn to the cation-chloride cotransporters (CCCs) because two family members (NKCC2 and NCC) are fundamental in salt reabsorption in the kidneys, and, consequently, contribute to maintenance of blood volume and pressure. Several members of the CCC family also play pivotal roles in inhibitory synaptic transmission in the nervous system and are implicated in brain disorders and psychiatric diseases. Pharmacologically targeting CCCs thus represents a promising therapeutic strategy for the treatment of numerous human diseases. Indeed, loop and thiazide diuretics inhibit NKCC2 and NCC, respectively, and are widely prescribed to treat hypertension and edema decades before their molecular targets were finally cloned in 1990s. Our contributions in this area so far include a published structure of human NKCC1 captured in a partially loaded, dephosphorylated (inactive), inward open state (and unpublish results detailed in this proposal).

a. Xiaoyong Yang[#], Qinzhe Wang[#], and **Erhu Cao**. Structure of the human cation-chloride cotransporter NKCC1 determined by single-particle electron cryo-microscopy. *Nature Communications.* 2020 Feb 21;11(1):1016. PMCID: PMC7035313. [#] Co-first authors

3. **Postdoctoral studies – structural and functional insights into the mechanisms of TRPV1 activation and drug action.**

My postdoctoral work in the Julius lab at UCSF focused on the structure and physiology of sensory TRP channels, particularly the TRPV1 channel. TRPV1 is a major player in the pain pathway, and is capable of detecting and integrating a wide range of pain-producing physiological and environmental stimuli. These include noxious heat, proton, pro-inflammatory agents, as well as natural products (e.g., capsaicin from chili pepper and peptide toxins present in spider venoms) that have evolved as defense mechanisms to discourage herbivory or to deter predators.

In one research direction, I reconstituted purified TRPV1 into giant liposomes and characterized its intrinsic properties by patch clamp recording. By taking this reductionist approach, I showed that TRPV1 is directly activated by heat without the requirement for any other cellular factors. Moreover, I demonstrated that TRPV1 is directly inhibited by PIP_2, thereby providing a mechanistic explanation for how TRPV1 is sensitized by numerous pro-inflammatory agents that lead to phospholipase C (PLC) activation and consequent PIP_2 degradation. Analogous liposome reconstitution approaches will be extremely powerful in deciphering the functions and mechanisms of PKD proteins, which are the focus of this proposal.

In addition, I collaborated with Maofu Liao in Yifan Cheng' lab at UCSF, and together we determined structures of the TRPV1 channel locked in three distinct functional states (i.e. closed, partially activated, and fully activated) by single particle cryo-EM. These structures revealed a unique two-gate mechanism of channel activation, which includes an unusually dynamic outer pore region, which participates in channel sensitization by tissue acidosis and possibly by other pro-inflammatory agents as well. We also resolved binding sites for pain-producing spider toxins and pungent natural products, and determined how these sites relate to mechanisms of channel activation.

This work represented a seminal achievement in the field because it provided a landmark blueprint for future biophysical and pharmacological studies of TRP channels. Delineation of TRPV1 structure to near atomic resolution without the need to obtain protein crystals also represented a technical breakthrough in single particle cryo-EM. Our success had significant ramifications for the future of membrane protein structure determination because it opened the way for determining receptor and ion channel structures in the many cases where material is limiting or conformationally heterogeneous. Indeed, our TRPV1 structures ushered in a new era of membrane protein structural biology in which membrane protein structures can be routinely determined by single-particle cryo-EM. The summary in the accompanying "News and Views" highlight from Dr. Richard Henderson read: "Structures of the heat-sensitive TRPV1 ion channel have been solved using single-particle electron cryo-microscopy, representing a landmark in the use of this technique for structural biology."

a. **Erhu Cao**, Julio F. Cordero-Morales, Beiying Liu, Feng Qin, and David Julius. TRPV1 channels are intrinsically heat sensitive and negatively regulated by phosphoinositide lipids. *Neuron* (2013) February; 77:667-679. PMCID: PMC3583019.

b. ***Erhu Cao**, *Maofu Liao, Yifan Cheng, and David Julius. TRPV1 structures indistinct conformations reveal activation mechanisms. *Nature (Article with News and Views written by Richard Henderson)* (2013) 504:113-118. PMCID: PMC4023639. * Equally contributing authors

c. *Maofu Liao, ***Erhu Cao**, David Julius, and Yifan Cheng. Structure of the TRPV1 channel determined by electron cryo-microscopy. *Nature (Article with News and Views written by Richard Henderson)* (2013) 504:107-112. PMCID: PMC4078027. *Equally contributing authors

d. Yuan Gao, **Erhu Cao**, David Julius, and Yifan Cheng. TRPV1 structures in nanodiscs reveal mechanisms of ligand and lipid action. *Nature* (2016) 534:347-351. PMCID: PMC4911334.

4. **Ph.D. graduate studies - structural mechanisms of regulation of cellular immunity by NTB-A, TIM-3 and PD-1 receptors.**

NTB-A, TIM-3, and PD-1 all belong to the immunoglobulin (Ig) superfamily of receptors that are capable of stimulating or inhibiting a variety of immune cells (e.g. T cells, B cells, and natural killer cells) upon engaging their cognate ligands via extracellular Ig domains. Notably, tumor cells often exploit the immunosuppressive interactions between PD-1 and its ligands (PD-L1 and PD-L2) to evade immune surveillance. Indeed, antibodies that block the inhibitory PD-1/PD-L1 pathway can boost immune responses against malignant cells in patients, and this advance was honored with the 2018 Nobel Prize in Medicine to Honjo and Allison. In my graduate work, I determined crystal structures of NTB-A, TIM-3, and PD-1 in complex with PD-L2, and performed associated biochemical analyses. Together, these findings provide structural blueprints for understanding ligand recognition by these receptors and suggest sites or hot spots that can be targeted for the development of novel immunotherapies to treat cancer and other immune related diseases.

a. Xuewu Zhang, Jean-Claude D. Schwartz, Xiaoling Guo, Sumeena Bhatia, **Erhu Cao**, Michael Lorenz, Michael Cammer, Lieping Chen, Zhong-Yin Zhang, Michael A. Edidin, Stanley G. Nathenson, and Steven C. Almo. Structural and functional analysis of the costimulatory receptor programmed death-1. *Immunity* (2004) 20: 337-47. PMID: 15030777.

b. **Erhu Cao**, Udupi A. Ramagopal, Alexander Fedorov, Elena Fedorov, Qingrong Yan, Jeffrey W. Lary, James L. Cole, Stanley G. Nathenson, and Steven C. Almo. NTB-A Receptor Crystal Structure: Insights into Homophilic Interactions in the Signaling Lymphocytic Activation Molecule Receptor Family. *Immunity* (2006) 25: 559-70. PMID: 17045824.

c. **Erhu Cao**, Xingxing Zang, Udupi A. Ramagopal, Arunika Mukhopadhaya, Alexander Fedorov, Elena Fedorov, Wendy D. Zencheck, Jeffrey W. Lary, James L. Cole, Haiteng Deng, Teresa P. DiLorenzo, James P. Allison, Stanley G. Nathenson, and Steven C. Almo. T Cell Immunoglobulin Mucin-3 Crystal Structure Reveals a Galectin-9- independent Ligand-Binding Surface. *Immunity* (2007) 26: 311-321. PMID: 17363302.

d. *Eszter Lázár-Molnár, *Qingrong Yan, ***Erhu Cao**, Udupi Ramagopal, Stanley G. Nathenson and Steven C. Almo. Crystal structure of the complex between programmed death-1 (PD-1) and its ligand PD-L2. *Proc Natl Acad Sci U S A.* (2008) 105: 10483-8. PMCID: PMC2492495. * Equally contributing authors

Complete List of Published Work in MyBibliography
https://www.ncbi.nlm.nih.gov/myncbi/erhu.cao.1/bibliography/public/

D. Research Support

Ongoing Research Support

R01 DK110575 Cao (PI) 09/01/2016 – 12/31/2021
National Institutes of Health
Structures and Mechanisms of Polycystic Kidney Disease Proteins

The goal of this proposal is to elucidate the structural principles and fundamental biophysical properties of polycystic kidney disease proteins, which are the sites of mutations that cause autosomal dominant polycystic kidney disease. Treatment options for this prevalent genetic disorder are currently limited, in large part because the molecular mechanisms of the relevant proteins are only poorly understood. Successful outcomes will provide structural and biochemical insights that will inform the development of novel therapeutic strategies.

Pew Scholar Award Cao (PI) 08/01/2017 – 08/01/2022
The Pew Charity Trust
This award is meant to support exploratory and highly risky research efforts in the Cao lab.

Completed Research Support

Seed Grant Cao (PI) 07/01/2016 – 06/30/2017
University of Utah Research Foundation
Pharmacology of Polycystic Kidney Disease Proteins
Role: PI

DoD Discovery Grant Cao (PI) 08/01/2016 – 01/31/2019
Department of Defense
Pharmacology of Polycystic Kidney Disease Proteins
The major aim of this project is to develop pharmacological tools (e.g., small chemical compounds, peptide toxins from venomous animals, and conformation-sensitive, functional antibodies) for dissecting structures and physiology of polycystic kidney disease proteins. Such pharmacological studies of PKD proteins will also help to establish therapeutic principles for treating autosomal dominant polycystic kidney disease.