

BIOGRAPHICAL SKETCH

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NAME: Yan, Jiusheng

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

POSITION TITLE: Associate 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
Wuhan University, Wuhan, China	B.S.	07/1996	Biology
Institute of Botany, Chinese Academy of Sciences, Beijing, China	M.S.	06/2000	Botany
Purdue University, West Lafayette, Indiana	Ph.D.	12/2004	Biochem. & Mol. Biol.
The University of California, Davis, California	Postdoc	7/2007	Neuroscience
The University of Texas, Austin, Texas	Postdoc	7/2010	Neurobiology

A. Personal Statement

I have the motivation, expertise, training, and leadership necessary to successfully carry out the proposed research project. I have a broad education and training background in biochemistry, biophysics, physiology, and neurobiology with specific research expertise in mass spectrometry-based proteomics, molecular biology, protein biochemistry, and patch-clamp electrophysiology. My research focuses on exploration and understanding of structure and function of native mammalian ion channel signaling complexes with a particular interest in uncovering and characterizing novel proteins or protein-protein interactions involved in ion channel regulation. We had identified a group of leucine-rich repeat domain-containing membrane proteins as BK channel auxiliary γ subunits and a novel Sm-like (Lsm) protein Lsm12 as an NAADP receptor and a two-pore channel (TPC) auxiliary protein critical for the second messenger molecule NAADP-evoked Ca^{2+} release from acidic organelles. As PI or co-Investigator on several NIH-funded grants, I have been successful in administration of research projects, collaboration with other researchers, and being productive in research findings. The current grant application builds on our current studies on exploration of auxiliary proteins critical for function of cell volume-regulated anion channels VRAC/LRRC8 channels. I am confident that I will accomplish the proposed research project with excellent productivity within the proposed period and budget.

Ongoing and recently completed projects that I would like to highlight include:

R01 GM130814 (PI: Yan) 09/15/2018-07/31/2026
Role: PI
National Institute of General Medical Sciences (NIGMS)
Molecular basis of the NAADP-gated calcium release channel complexes

R01 NS078152 (PI: Yan) 08/01/2012-05/31/2023
Role: PI
National Institute of Neurological Disorders and Stroke (NINDS)
BK channel regulation by auxiliary LRR proteins

Citations:

1. Yan J, Aldrich RW. LRRC26 auxiliary protein allows BK channel activation at resting voltage without calcium. *Nature*. 2010 Jul 22; 466(7305):513-6. PubMed PMID: 20613726.
2. Zhang J, Guan X, Li Q, Meredith AL, Pan HL, Yan J. Glutamate-activated BK channel complexes formed with NMDA receptors. *Proc Natl Acad Sci U S A*. 2018 Sept; 115(38): E9006-14. PubMed PMID: 30181277.
3. Zhang J, Guan X, Shah K, Yan J. Lsm12 is an NAADP receptor and a two-pore channel regulatory protein required for calcium mobilization from acidic organelles. *Nat Commun*. 2021 Aug 6; 12:4739. doi: <https://doi.org/10.1038/s41467-021-24735-z>.
4. Chen G, Li Q, Webb TI, Hollywood MA, Yan J. BK channel modulation by positively charged peptides and auxiliary γ subunits mediated by the Ca^{2+} -bowl site. *J Gen Physiol* 2023 155 (6):e202213237

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2020 – 2020	NIH Peer Review Committee: Biophysics of Neural Systems (BPNS), ad hoc reviewer
2020 – 2020	NIH Peer Review Committee: Neurotoxicology and Alcohol (NAL), ad hoc reviewer
2019 – Present	Associate Professor, The University of Texas MD Anderson Cancer Center, Department of Anesthesiology and Perioperative Medicine, Houston, TX
2018 – 2020	AHA Fellowship Review Committee: Basic Cell - Proteins and Crystallography, member
2018 – Present	Editorial: Frontiers in Molecular Neuroscience, Frontiers in Physiology
2012 – 2019	Assistant Professor, The University of Texas MD Anderson Cancer Center, Department of Anesthesiology and Perioperative Medicine, Houston, TX
2010 – 2012	Research Associate, The University of Texas at Austin, Austin, TX
2016 – 2020	Member, American Heart Association
2007 – Present	Member, Society for Neurosciences
2006 – Present	Member, Biophysical Society
2003 – 2019	Member, American Society for Biochemistry and Molecular Biology

Honors

2008	AHA Postdoctoral Fellowship, American Heart Association
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C. Contribution to Science

1. Identification of novel regulatory proteins and posttranslational modifications of ion channels and receptors with affinity purification and mass spectrometry (LC-MS/MS). (a) I have recently identified a Sm-like protein Lsm12 as an NAADP receptor and a regulatory protein of two-pore channels (TPCs) for Ca^{2+} mobilization from acidic organelles. (b) I had identified NMDA receptors to be structurally and functionally coupled to BK channels within nanodomain via direct interactions in their obligatory $\text{BK}\alpha$ and GluN1 subunits. We also found that postsynaptic BK channels in medial perforant path-dentate gyrus granule cell synapses are activated by NMDA receptor-mediated Ca^{2+} influx and modulate excitatory synaptic transmission. (c) I had identified a novel auxiliary (γ 1 or LRRC26) protein of the large conductance Ca^{2+} -activated (BK) K^+ channels from prostate cancer cells. This finding provided a molecular basis in understanding BK channel activation mechanisms and function in non-excitabile cells. (d) I had comprehensively identified and characterized an unprecedented more than 30 phosphorylation sites of an ion channel protein (BK channel α subunit) from brain tissues and by collaboration identified phosphorylation sites of NMDA receptors and methylation sites of an estrogen receptor.

- a. Zhang J, Guan X, Shah K, Yan J. Lsm12 is an NAADP receptor and a two-pore channel regulatory protein required for calcium mobilization from acidic organelles. *Nat Commun*. 2021 Aug 6; 12:4739. doi: <https://doi.org/10.1038/s41467-021-24735-z>.
 - b. Zhang J, Guan X, Li Q, Meredith AL, Pan HL, Yan J. Glutamate-activated BK channel complexes formed with NMDA receptors. *Proc Natl Acad Sci U S A*. 2018 Sept; 115(38): E9006-14. PubMed PMID: 30181277.
 - c. Yan J, Aldrich RW. LRRC26 auxiliary protein allows BK channel activation at resting voltage without calcium. *Nature*. 2010 Jul 22; 466(7305):513-6. PubMed PMID: 20613726.
 - d. Yan J, Olsen JV, Park KS, Li W, Bildl W, Schulte U, Aldrich RW, Fakler B, Trimmer JS. Profiling the phospho-status of the BKCa channel alpha subunit in rat brain reveals unexpected patterns and complexity. *Mol Cell Proteomics*. 2008 Nov; 7(11):2188-98. PubMed PMID: 18573811; PubMed Central PMCID: PMC2577206.
2. Studies of NAADP-evoked Ca^{2+} release and molecular mechanisms of two-pore channels (TPCs). I have recently identified a Sm-like protein Lsm12 as an NAADP receptor and a regulatory protein of two-pore channels (TPCs) for Ca^{2+} mobilization from acidic organelles. We found that Lsm12 binds to NAADP via its Lsm domain and is essential and immediately participates in NAADP-evoked TPC activation and Ca^{2+} mobilization from acidic stores. These findings provide a molecular basis for understanding the mechanisms of NAADP signaling. We had identified YM201636 and PI-103 as new and potent pore blocker of TPC2 channel.
- a. Zhang J, Guan X, Shah K, Yan J. Lsm12 is an NAADP receptor and a two-pore channel regulatory protein required for calcium mobilization from acidic organelles. *Nat Commun*. 2021 Aug 6; 12:4739. doi: <https://doi.org/10.1038/s41467-021-24735-z>.
 - b. Shah KR, Guan X, Yan J. Diversity of two-pore channels and the accessory NAADP receptors in intracellular Ca^{2+} signaling. *Cell Calcium*. 2022 Jun; 104:102594. doi: 10.1016/j.ceca.2022.102594
 - c. Du C, Guan X, Yan J. Two-pore channel blockade by phosphoinositide kinase inhibitors YM201636 and PI-103 determined by a histidine residue near pore-entrance. *Commun Biol*. 2022 July; 5(1):738, e-Pub 7/2022. PMCID: PMC9308409
3. Studies of molecular mechanisms of BK channel regulation by auxiliary γ subunits. I have led research on BK channel regulation by auxiliary γ subunits by: (a) establishing a group of LRR containing membrane proteins as auxiliary proteins of BK channels and systematically investigated their structure and function in BK channel regulation; (b) unraveling the molecular basis of the 4 γ subunits' differential modulatory effects on voltage-dependence of BK channel gating, and identifying the single transmembrane segment as the key molecular determinant for modulatory function of the auxiliary γ subunit; (c) establishing a competitive relationship between γ subunits and a small molecule activator mallotoxin on BK channel modulation; (d) revealing the function of the LRR domains in auxiliary γ subunits.
- a. Yan J*, Aldrich RW*. BK potassium channel modulation by leucine-rich repeat-containing proteins. *Proc Natl Acad Sci U S A*. 2012 May 15; 109(20):7917-22. PubMed PMID: 22547800; PubMed Central PMCID: PMC3356614. (* corresponding author)
 - b. Li Q, Fan F, Kwak HR, Yan J. Molecular basis for differential modulation of BK channel voltage-dependent gating by auxiliary γ subunits. *J Gen Physiol*. 2015 Jun; 145(6):543-54. PubMed PMID: 26009545; PubMed Central PMCID: PMC4442785.
 - c. Xin G, Li Q, Yan J. Relationship between auxiliary gamma subunits and mallotoxin on BK channel modulation. *Sci Rep*. 2017 Feb; 7: 42240. PubMed PMID: 28165042. PubMed Central PMCID: PMC5292707.
 - d. Chen G, Li Q, Yan J. The leucine-rich repeat domains of BK channel auxiliary γ subunits regulate their expression, trafficking, and channel-modulation functions. *J Biol Chem* 2022 Jan 30; 101664. e-Pub 1/2022. PMID: 35104503.
4. Studies of gating mechanisms of BK channel activation by voltage and Ca^{2+} . I have contributed to our understanding of the structure-function relationships of BK channel gating mechanisms by: (a) identification and characterization of a deep pore site that caused constitutively opening of the channels upon most

mutations at this site, which is helpful in localizing BK channel activation gate and understanding its gating mechanisms, (b) identification of a unique closed-state-coupled C-type inactivation and proposition of a novel concept that the closed-state represents an early step of C-type inactivation in BK channels, and (c) identification of molecular determinants of Ca^{2+} sensitivity at the intersubunit interface of the BK channel gating ring.

- a. Chen X, Yan J, Aldrich RW. BK channel opening involves side-chain reorientation of multiple deep-pore residues. *Proc Natl Acad Sci U S A*. 2014 Jan 7; 111(1):E79-88. PubMed PMID: 24367115; PubMed Central PMCID: PMC3890798.
 - b. Yan J*, Li Q, Aldrich RW*. Closed-state-coupled C-type inactivation in BK channels. *Proc Natl Acad Sci U S A*. 2016 Jun 13; 113(25):6991-6. PubMed PMID: 27298368. (* corresponding author)
 - c. Li Q, Li Y, Wei H, Pan HM, Vouga AG, Rothberg BS, Wu Y, Yan J. Molecular determinants of Ca^{2+} sensitivity at the intersubunit interface of the BK channel gating ring. *Sci Rep*. 2018 Jan; 8(1): 509. PubMed PMID: 29323236.
 - d. Vouga AG, Rockman ME, Yan J, Jacobson MA, Rothberg BS. State-dependent inhibition of BK channels by the opioid agonist loperamide. *J Gen Physiol* 2021 Aug 6; 153(9):e202012834. PMCID: PMC8352719.
5. Early studies of structure and function of cytochrome complex and energy-transducing membranes. I have advanced research in this field by analyzing structure and function-relationship of the cytochrome b_6f complex with a focus on its electron transport mechanisms, inhibitor bindings and actions, and novel structure and properties of prosthetic groups using molecular biological, biochemical, structural and other biophysical approaches.
- a. Yan J, Cramer WA. Functional insensitivity of the cytochrome b_6f complex to structure changes in the hinge region of the Rieske iron-sulfur protein. *J Biol Chem*. 2003 Jun 6; 278(23):20925-33. PubMed PMID: 12672829.
 - b. Yan J, Cramer WA. Molecular control of a bimodal distribution of quinone-analogue inhibitor binding sites in the cytochrome b_6f complex. *J Mol Biol*. 2004 Nov 19; 344(2):481-93. PubMed PMID: 15522300.
 - c. Yan J, Kurisu G, Cramer WA. Intraprotein transfer of the quinone analogue inhibitor 2,5-dibromo-3-methyl-6-isopropyl-p-benzoquinone in the cytochrome b_6f complex. *Proc Natl Acad Sci U S A*. 2006 Jan 3; 103(1):69-74. PubMed PMID: 16371475; PubMed Central PMCID: PMC1324977.
 - d. Yan J, Dashdorj N, Baniulis D, Yamashita E, Savikhin S, Cramer WA. On the structural role of the aromatic residue environment of the chlorophyll a in the cytochrome b_6f complex. *Biochemistry*. 2008 Mar 25; 47(12):3654-61. PubMed PMID: 18302324.

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BIOGRAPHICAL SKETCH

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NAME: Shah, Kunal

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

POSITION TITLE: Postdoctoral Fellow

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)	START DATE MM/YYYY	COMPLETION DATE MM/YYYY	FIELD OF STUDY
St. Xavier's College, Gujarat University, Ahmedabad, Gujarat	BS	06/2001	04/2005	Biochemistry
The University of Western Australia, Perth, Western Australia	MS	07/2008	08/2009	Biochemistry
The Maharaja Sayajirao University of Baroda, Vadodara, Gujarat	PHD	06/2012	01/2018	Biochemistry
University of Oregon, Eugene, Oregon	Postdoctoral Fellow	08/2018	07/2019	Biochemistry
The University of Texas M D Anderson Cancer Center, Houston, Texas	Postdoctoral Fellow	07/2019	present	Biochemistry/Structural Biology of Ion Channels

A. Personal Statement

I have a broad education and training background in biochemistry, biophysics, and structural biology with specific research expertise in molecular biology, protein biochemistry, protein expression and purification, protein-protein and protein-small molecule interaction. X-Ray Crystallography and Cryo-EM. My current research focuses on using protein biochemistry and structural biology tools to explore and understand the ion channel signaling complexes and uncovering underlying mechanism which regulates many important physiological processes. We had identified a novel Sm-like (Lsm) protein Lsm12 as an NAADP receptor and a two-pore channel (TPC) auxiliary protein essential for the NAADP induced Ca²⁺ release from the acidic organelles. As a Postdoctoral fellow I am playing an import role in generating data for several NIH funded grants and being part of the team to generate preliminary data which serves as a basis for new project applications for funding from different agencies.

B. Positions and Honors**Positions and Scientific Appointments**

2022 - Member, Biophysical society
2022 - 2023 Postdoctoral Association, Policy Sub-committee chair , The University of Texas M D Anderson Cancer Center
2013 - 2020 Member, Indian Crystallography Society

C. Contribution to Science

1. Mechanism of NAADP evoked Ca²⁺ release and mechanism of Two-pore channels (TPCs). We have identified a Sm-like protein Lsm12 as an NAADP receptor and a regulatory protein of two-pore channels (TPCs) for Ca²⁺ mobilization from acidic organelles. Lsm12 is part of an unique sub-class of Sm like protein consists of N-terminal Lsm domain and Anticodon binding domain (AD) at C-terminus. We found

that LSM12 binds to NAADP via its N-terminal LSM domain and is essential and instantly involved in NAADP-evoked TPC activation and mobilization of Ca²⁺ from acidic stores. These findings provide the molecular basis for mechanism of NAADP signaling.

- a. Shah KR, Guan X, Yan J. Diversity of two-pore channels and the accessory NAADP receptors in intracellular Ca²⁺ signaling. *Cell Calcium*. 2022 Jun;104:102594. PubMed Central PMCID: PMC9645597.
 - b. Zhang J, Guan X, Shah K, Yan J. LSM12 is an NAADP receptor and a two-pore channel regulatory protein required for calcium mobilization from acidic organelles. *Nat Commun*. 2021 Aug 6;12(1):4739. PubMed Central PMCID: PMC8346516.
2. Many plants maintain an elaborate RNA-editing machine that allows them to correct accumulated errors in their organellar genomes by specifically editing the RNA transcripts of the affected genes. A portable and adaptable version of this molecular machine would have significant biotechnological value, providing the ability to correct genetic errors, and to intervene in gene regulation without permanently altering a genome. Our lab previously identified Pentatricopeptide Repeat (PPR) proteins, a huge family of 450 proteins involved in controlling the gene expression in mitochondria and chloroplast. Proteins of the PPR superfamily are characterized by tandem arrays of a degenerate 35-amino-acid α -hairpin motif. A modular, predictable code for sequence-specific binding of RNA by PPR proteins has recently been revealed, which opens the door to the de novo design of bespoke proteins with specific RNA targets, with widespread biotechnological potential. In this project we carried out the design and production of a synthetic PPR protein based on a consensus sequence and the determination of its crystal structure to 2.2 Å resolution. The crystal structure displays helical disorder, resulting in electron density representing an infinite superhelical PPR protein. A structural comparison with related tetratricopeptide repeat (TPR) proteins, and with native PPR proteins, reveals key roles for conserved residues in directing the structure and function of PPR proteins. The designed proteins have high solubility and thermal stability, and can form long tracts of PPR repeats. Thus, consensus-sequence synthetic PPR proteins could provide a suitable backbone for the design of bespoke RNA-binding proteins with the potential for high specificity.
- a. Gully BS, Shah KR, Lee M, Shearston K, Smith NM, Sadowska A, Blythe AJ, Bernath-Levin K, Stanley WA, Small ID, Bond CS. The design and structural characterization of a synthetic pentatricopeptide repeat protein. *Acta Crystallogr D Biol Crystallogr*. 2015 Feb;71(Pt 2):196-208. PubMed PMID: 25664731.
3. A highly efficient coding system is necessary to allow cells to communicate swiftly through complex surface recognition and interactions. Complex carbohydrate surpasses amino acids and nucleotides in their information storing capacity and serves as important ligand throughout the process of recognition in a living system. Ability to decipher the biological code written in carbohydrate moieties is one of the biggest strength of lectins and other carbohydrate binding proteins. During my graduate degree, we were able to characterize two different class of proteins from different species for their carbohydrate recognition capacity and role of their glycan binding properties in their potential dual functional roles.
- a. Patel DK, Shah KR, Pappachan A, Gupta S, Singh DD. Cloning, expression and characterization of a mucin-binding GAPDH from *Lactobacillus acidophilus*. *Int J Biol Macromol*. 2016 Oct;91:338-46. PubMed PMID: 27180300.
 - b. Shah KR, Patel DK, Pappachan A, Prabha CR, Singh DD. Characterization of a Kunitz-type serine protease inhibitor from *Solanum tuberosum* having lectin activity. *Int J Biol Macromol*. 2016 Feb;83:259-69. PubMed PMID: 26645142.

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<https://www.ncbi.nlm.nih.gov/myncbi/kunal.shah.2/bibliography/public/>

BIOGRAPHICAL SKETCH

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NAME: Chen, Guanxing

eRA COMMONS USER NAME (credential, e.g., agency login): GCHEN4

POSITION TITLE: Research Investigator

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)	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
Inner Mongolia Normal University	BS	9/2006	7/2010	Biotechnology
Capital Normal University	PHD	9/2010	7/2015	Genetics/Proteomics
Kansas State University	Postdoctoral Fellow	6/2016	3/2017	Neuroscience
University of Texas MD Anderson Cancer Center	Postdoctoral Fellow/ Research Investigator	4/2017	Present	Ion channel /Neuroscience

A. Personal Statement

From my B.Sc. and Ph.D. degree, I had nine years' training in molecular biology, cell biology, genetics, and proteomics analysis. The work of my Ph.D. thesis "Starch synthesis analysis using genetics, proteomics, and phosphoproteomics" was accomplished in September of 2015. Meantime, during my Ph.D. time, I published 4 papers with my name listed as the first author and eight papers as second author or co-first author. Because I want to get more challenges and gain more achievements. I, as a postdoctoral fellow, went to Kansas State University to studying "Gene regulations in Parkinson Disease" in June 2016. I learned the yeast two-hybrid, yeast genome-wide screen, spotting assay, cell culture, transfection, co-immunoprecipitation, etc. Late on, I transferred to Dr. Cui's lab at MD Anderson Cancer Center April 2017 to study "Analgesic lipid molecules suppress chemotherapy-induced neuropathic pain" and "Morphine caused cancer cells apoptosis". I have further learned flow cytometry, Chip-seq, rodent cell primary culture, immunocytochemistry, immunohistochemistry, behavioral tests for pain assessment, animal surgery, etc. during my post-doctoral time. In March 2019, because Dr. Cui's project was ended, I transferred to Dr. Yan's lab, and the projects were ion channels related both in vivo and in vitro. In Dr. Yan's Lab, I am studying the structure, function and regulation of mammalian ion channels related to pain, and neurological diseases, with multidisciplinary approaches and tools including mass spectrometry-based proteomics, electrophysiology (patch-clamp recording), protein expression and structural analyses, mammalian cell culture and animal models.

1. Q Li, **G Chen**, J Yan (2024) Transmembrane determinants of voltage-gating differences between BK (Slo1) and Slo3 channels. Biophysical Journal 123: 1-V13.
2. L Li, Q Ru, Y Lu, A Saifullah, **G Chen**, A Saifullah, C Yao, K Talias (2023) Tiam1 coordinates synaptic structural and functional plasticity underpinning the pathophysiology of neuropathic pain. Neuron 111: 2038-V2050.

3. **G Chen**, Q Li, J Yan (2023) BK channel modulation by the β -subunit positively charged peptides via electrostatic interactions with the calcium-bowl site. *Journal of General Physiology*. 155 (6): e202213237.
4. **G Chen**, Q Li, J Yan (2022) The leucine-rich repeat domains of BK channel auxiliary β subunits regulate their expression, trafficking, and channel-modulation functions. *Journal of Biological Chemistry*. 298(3): 101664.
5. Y Gwak, **G Chen**, S Abdi, He Kim (2021) Calcium-independent phospholipase A2 inhibitor produces an analgesic effect in a rat model of neuropathic pain by reducing central sensitization in the dorsal horn. *NEUROLOGICAL RESEARCH* 43 (8): 683-692.
6. Y Ji, **G Chen**, Q Zhong, M Zhang, Z Wu, M Liu (2019) Comprehensive transcriptome profiling reveals an opposite regulatory mechanism of root and leaf in tomato after restraining the synthesis of gibberellin. *International journal of molecular sciences* 20 (13): 3307.
7. J Cui, **G Chen**, A Perry, S Abdi (2018) Transient Cell-to-Cell Signaling before Mitosis in Cultures of human Bone Marrow-Derived Mesenchymal Stem/Stromal Cells. *Stem Cells and Development* 28 (2): 120-128.
8. Y Xiong, S Neifert, S Karuppagounder, J Stankowski, B Lee, J Grima, **Chen G**, H Ko, Y Lee, D Swing, L Tessarollo, T Dawson, V Dawson (2017) Overexpression of Parkinson's Disease-associated mutation LRRK2 G2019S in mouse forebrain induces behavioral deficits and α -synuclein pathology. *eNeuro* 17: 4(2).
9. **G Chen**, Y Liu, S Zhen, X Yan, M Zhang, Y Yan (2017) In vivo phosphoproteome characterization reveals key starch granule-binding phosphoproteins involved in wheat water-deficit response. *BMC Plant Biology* 17:168-181.
10. D Lv, S Zhen, G Zhu, Y Bian, **G Chen**, C Han, Z Yu, Y Yan (2016) High-Throughput sequencing reveals H2O2 stress-associated MicroRNAs and a potential regulatory network in *Brachypodium distachyon* seedlings. *Frontiers in plant science* 7, 1567.
11. **G Chen**, J Zhou, Y Liu, X Lu, C Han, X Li and Y Yan (2016) Biosynthesis and regulation of wheat amylose and amylopectin from proteomic and phosphoproteomic characterization of granule-binding proteins. *Scientific Reports* 6: 33111-33126.
12. Y Liu, S Wang, C Wang, **G Chen**, H Cao, Y Wang, W Ma, Y Hu, Y Yan (2016) Comparative proteomic analysis of wheat developing grains between Chinese Spring and 1Sl/1B substitution line. *Cereal research communications* 44 (1), 13-23.
13. C Zhu., N Luo, M He, **G Chen**, J Zhu, G Yin, X Li, Y Hu, J Li and Y Yan (2014) Molecular Characterization and Expression Profiling of the Protein Disulfide Isomerase Gene Family in *Brachypodium distachyon* L. *PLoS One* 9 (4), e94704.
14. M Cao, **G Chen**, C Wang, S Zhen, X Li, W Zhang, F Zeller, S Hsam, Y Hu and Y Yan (2015) 1Sl(1B) Chromosome substitution in Chinese Spring wheat promotes starch granule development and starch biosynthesis. *Crop & Pasture Science* 66: 894-903.
15. P Hao, J Zhu, A Gu, D Lv, P Ge, **G Chen**, X Li and Y Yan (2015) An integrative proteome analysis of different seedling organs in tolerant and sensitive wheat cultivars under drought stress and recovery. *Proteomics* 15: 1544-1563.
16. M Zhang, **G Chen**, D Lv, X Li, and Y Yan (2015) N-Linked Glycoproteome Profiling of Seedling Leaf in *Brachypodium distachyon* L. *Journal of Proteome Research* 14(4): 1727-1738.
17. H Cao, X Yan, **G Chen**, J Zhou, X Li, W Ma and Y Yan (2015) Comparative proteome analysis of A- and B-type starch granule-associated proteins in bread wheat (*Triticum aestivum* L.) and *Aegilops crassa*. *Journal of Proteomics* 112: 95-112.
18. C Ma, J Zhou, **G Chen**, Y Bian, D Lv, X Li, Z Wang and Y Yan (2014) iTRAQ-based quantitative proteome and phosphoprotein characterization reveals the central metabolism changes involved in wheat grain development. *BMC Genomics* 15(1): 1029.
19. **G Chen**, J Zhu, J Zhou, S Subburaj, M Zhang, C Han, P Hao, X Li and Y Yan (2014) Dynamic development of starch granules and the regulation of starch biosynthesis in *Brachypodium distachyon*: comparison with common wheat and *Aegilops peregrine*. *BMC Plant Biology* 14(1):198-213.
20. J Zhu, P Hao, **G Chen**, C Han, X Li, F Zeller, S Hsam, Y Hu and Y Yan (2014) Molecular cloning, phylogenetic analysis, and expression profiling of endoplasmic reticulum molecular chaperone BiP genes from bread wheat (*Triticum aestivum* L.). *BMC Plant Biology* 14(1): 260.
21. M Zhang, D Lv, P Ge, Y Bian, **G Chen**, G Zhu, X Li and Y Yan (2014) Phosphoproteome analysis reveals new drought response and defense mechanisms of seedling leaves in bread wheat (*Triticum aestivum* L.). *Journal of Proteomics* 109: 290-308.

22. G Zhu, **G Chen**, J Zhu, Y Zhu, X Lu, X Li, Y Hu and Y Yan (2015) Molecular Characterization and Expression Profiling of NAC Transcription Factors in *Brachypodium distachyon* L. PLoS One 10(10): e0139794.
23. **G Chen**, D Lv, W Li, S Subburaj, Z Yu, Y Wang, X Li, K Wang, X Ye, W Ma and Y Yan (2013) The α -gliadin genes from *Brachypodium distachyon* L. provide evidence for a significant gap in the current genome assembly. Functional & Integrative Genomics 14(1): 149-160.
24. S Subburaj, **G Chen**, C Han, D Lv, X Li, F Zeller, S Hsam and Y Yan (2013) Molecular characterisation and evolution of HMW glutenin subunit genes in *Brachypodium distachyon* L. Journal of Applied genetics 55(1): 27-42.
25. C Han, Z Yu, S Feng, D Lv, X Yan, **G Chen**, X Li, W Ma, Y Yan (2013) Applications of capillary electrophoresis for rapidly separating and characterizing water-soluble proteins of wheat grains. Cereal Research Communications 41 (4), 601-612.
26. Z Yu, C Han, S Wang, D Lv, **G Chen**, X Li, GL Jiang, Y Yan (2013) Fast separation and characterization of water-soluble proteins in wheat grains by reversed-phase ultra performance liquid chromatography (RP-UPLC). Journal of cereal science 57 (3), 288-294.
27. S Wang, K Wang, **G Chen**, D Lv, X Han, Z Yu, X Li, X Ye, S Hsam, W Ma, R Appels and Y Yan (2012) Molecular characterization of LMW-GS genes in *Brachypodium distachyon* L. reveals highly conserved Glu-3 loci in *Triticum* and related species. BMC Plant Biology 12(1): 221.

B. Positions, Scientific Appointments and Honors

Positions and Scientific Appointments

2022 – Research Investigator, University of Texas MD Anderson Cancer Center
 2017 – 2021 Postdoctoral Fellowship, University of Texas MD Anderson Cancer Center
 2016 – 2017 Postdoctoral Fellowship, Kansas State University
 2015 – 2016 Research assistant fellow, Beijing Vegetable Research Center of BAAFS

Honors

2nd studentship - Department of Biology, Inner Mongolia Normal University. China, 2007.
 3rd studentship - Department of Biology, Inner Mongolia Normal University. China, 2008.
 2nd studentship - Department of Biology, Inner Mongolia Normal University. China, 2009.
 2nd PhD studentship - Department of Biology, Capital Normal University. China, 2013.
 1st PhD studentship - Department of Biology, Capital Normal University. China, 2014.

C. Contributions to Science

1. **Graduate Career:** My graduate research contributions focused on the biosynthesis and regulation of plant starch by using proteomic, phosphoproteomic, and glycosylation methods. We had identified multiple proteins that can resist drought and provided important information regarding how starch synthesis responds to drought conditions. Our results shed important insight on how plants adapt to droughts and can recover from adverse environmental conditions.
 - a. **G Chen**, Y Liu, S Zhen, X Yan, M Zhang, Y Yan (2017) In vivo phosphoproteome characterization reveals key starch granule-binding phosphoproteins involved in wheat water-deficit response. BMC Plant Biology 17:168-181.
 - b. D Lv, S Zhen, G Zhu, Y Bian, **G Chen**, C Han, Z Yu, Y Yan (2016) High-Throughput sequencing reveals H₂O₂ stress-associated MicroRNAs and a potential regulatory network in *Brachypodium distachyon* seedlings. Frontiers in plant science 7, 1567.
 - c. **G Chen**, J Zhou, Y Liu, X Lu, C Han, X Li and Y Yan (2016) Biosynthesis and regulation of wheat amylose and amylopectin from proteomic and phosphoproteomic characterization of granule-binding proteins. Scientific Reports 6: 33111-33126.
 - d. Y Liu, S Wang, C Wang, **G Chen**, H Cao, Y Wang, W Ma, Y Hu, Y Yan (2016) Comparative proteomic analysis of wheat developing grains between Chinese Spring and 1SI/1B substitution line. Cereal research communications 44 (1), 13-23.

- e. C Zhu., N Luo, M He, **G Chen**, J Zhu, G Yin, X Li, Y Hu, J Li and Y Yan (2014) Molecular Characterization and Expression Profiling of the Protein Disulfide Isomerase Gene Family in *Brachypodium distachyon* L. PLoS One 9 (4), e94704.
 - f. M Cao, **G Chen**, C Wang, S Zhen, X Li, W Zhang, F Zeller, S Hsam, Y Hu and Y Yan (2015) 1S1(1B) Chromosome substitution in Chinese Spring wheat promotes starch granule development and starch biosynthesis. Crop & Pasture Science 66: 894-903.
 - g. P Hao, J Zhu, A Gu, D Lv, P Ge, **G Chen**, X Li and Y Yan (2015) An integrative proteome analysis of different seedling organs in tolerant and sensitive wheat cultivars under drought stress and recovery. Proteomics 15: 1544-1563.
 - h. M Zhang, **G Chen**, D Lv, X Li, and Y Yan (2015) N-Linked Glycoproteome Profiling of Seedling Leaf in *Brachypodium distachyon* L. Journal of Proteome Research 14(4): 1727-1738.
 - i. H Cao, X Yan, **G Chen**, J Zhou, X Li, W Ma and Y Yan (2015) Comparative proteome analysis of A- and B-type starch granule-associated proteins in bread wheat (*Triticum aestivum* L.) and *Aegilops crassa*. Journal of Proteomics 112: 95-112.
 - j. C Ma, J Zhou, **G Chen**, Y Bian, D Lv, X Li, Z Wang and Y Yan (2014) iTRAQ-based quantitative proteome and phosphoprotein characterization reveals the central metabolism changes involved in wheat grain development. BMC Genomics 15(1): 1029.
 - k. **G Chen**, J Zhu, J Zhou, S Subburaj, M Zhang, C Han, P Hao, X Li and Y Yan (2014) Dynamic development of starch granules and the regulation of starch biosynthesis in *Brachypodium distachyon*: comparison with common wheat and *Aegilops peregrine*. BMC Plant Biology 14(1):198-213.
 - l. J Zhu, P Hao, **G Chen**, C Han, X Li, F Zeller, S Hsam, Y Hu and Y Yan (2014) Molecular cloning, phylogenetic analysis, and expression profiling of endoplasmic reticulum molecular chaperone BiP genes from bread wheat (*Triticum aestivum* L.). BMC Plant Biology 14(1): 260.
 - m. M Zhang, D Lv, P Ge, Y Bian, **G Chen**, G Zhu, X Li and Y Yan (2014) Phosphoproteome analysis reveals new drought response and defense mechanisms of seedling leaves in bread wheat (*Triticum aestivum* L.). Journal of Proteomics 109: 290-308.
 - n. G Zhu, **G Chen**, J Zhu, Y Zhu, X Lu, X Li, Y Hu and Y Yan (2015) Molecular Characterization and Expression Profiling of NAC Transcription Factors in *Brachypodium distachyon* L. PLoS One 10(10): e0139794.
 - o. **G Chen**, D Lv, W Li, S Subburaj, Z Yu, Y Wang, X Li, K Wang, X Ye, W Ma and Y Yan (2013) The $\text{E}\text{-}$ gliadin genes from *Brachypodium distachyon* L. provide evidence for a significant gap in the current genome assembly. Functional & Integrative Genomics 14(1): 149-160.
 - p. S Subburaj, **G Chen**, C Han, D Lv, X Li, F Zeller, S Hsam and Y Yan (2013) Molecular characterisation and evolution of HMW glutenin subunit genes in *Brachypodium distachyon* L. Journal of Applied genetics 55(1): 27-42.
 - q. C Han, Z Yu, S Feng, D Lv, X Yan, **G Chen**, X Li, W Ma, Y Yan (2013) Applications of capillary electrophoresis for rapidly separating and characterizing water-soluble proteins of wheat grains. Cereal Research Communications 41 (4), 601-612.
 - r. Z Yu, C Han, S Wang, D Lv, **G Chen**, X Li, GL Jiang, Y Yan (2013) Fast separation and characterization of water-soluble proteins in wheat grains by reversed-phase ultra performance liquid chromatography (RP-UPLC). Journal of cereal science 57 (3), 288-294.
 - s. S Wang, K Wang, **G Chen**, D Lv, X Han, Z Yu, X Li, X Ye, S Hsam, W Ma, R Appels and Y Yan (2012) Molecular characterization of LMW-GS genes in *Brachypodium distachyon* L. reveals highly conserved Glu-3 loci in *Triticum* and related species. BMC Plant Biology 12(1): 221.
2. **Postdoctoral Career:** As a postdoctoral fellow, one of my research projects demonstrated that Tiam1-coordinated synaptic functional and structural plasticity underlies the pathophysiology of neuropathic pain and that intervening in Tiam1-mediated maladaptive synaptic plasticity has long-lasting consequences for neuropathic pain management. In another research project, we found that the LRR domains play key roles in the regulation of the expression, cell surface trafficking, and channel-modulation functions of the BK channel γ subunits. Additionally, we discovered that BK channels can be modulated by positively charged peptides and auxiliary γ subunits mediated by the Ca^{2+} -bowl site.
- a. Q Li, **G Chen**, J Yan (2024) Transmembrane determinants of voltage-gating differences between BK (Slo1) and Slo3 channels. Biophysical Journal 123: 1jV13.

- b. L Li, Q Ru, Y Lu, A Saifullah, **G Chen**, A Saifullah, C Yao, K Tolias (2023) Tiam1 coordinates synaptic structural and functional plasticity underpinning the pathophysiology of neuropathic pain. *Neuron* 111: 2038;V2050.
- c. **G Chen**, Q Li, J Yan (2023) BK channel modulation by the α -subunit positively charged peptides via electrostatic interactions with the calcium-bowl site. *Journal of General Physiology*. 155 (6): e202213237.
- d. **G Chen**, Q Li, J Yan (2022) The leucine-rich repeat domains of BK channel auxiliary β subunits regulate their expression, trafficking, and channel-modulation functions. *Journal of Biological Chemistry*. 298(3): 101664.
- e. Y Gwak, **G Chen**, S Abdi, He Kim (2021) Calcium-independent phospholipase A2 inhibitor produces an analgesic effect in a rat model of neuropathic pain by reducing central sensitization in the dorsal horn. *NEUROLOGICAL RESEARCH* 43 (8): 683-692.
- f. J Cui, **G Chen**, A Perry, S Abdi (2018) Transient Cell-to-Cell Signaling before Mitosis in Cultures of human Bone Marrow-Derived Mesenchymal Stem/Stromal Cells. *Stem Cells and Development* 28 (2): 120-128.
- g. Y Xiong, S Neifert, S Karuppagounder, J Stankowski, B Lee, J Grima, **Chen G**, H Ko, Y Lee, D Swing, L Tessarollo, T Dawson, V Dawson (2017) Overexpression of Parkinson's Disease-associated mutation LRRK2 G2019S in mouse forebrain induces behavioral deficits and α -synuclein pathology. *eNeuro* 17: 4(2).

D. Scholastic Performance

YEAR	COURSE TITLE	GRADE
2006	Advanced Mathematics I	A
2006	Advanced Mathematics II	A
2006	Organic Chemistry	B
2007	Statistics	A
2007	Botany	B
2007	Zoology	B
2007	Biological Chemistry	A
2008	Genetics	A
2008	Cell Biology	B
2008	Anthropology	A
2009	Molecular Biology	B
2009	Ecology	B
2010	Proteomics	P
2010	Bioinformatics	P
2010	Seminar in Genetics	P
2010	Statistics for the Life Sciences	P
2011	Seminar in Molecular Biology	P
2011	Protein Chemistry	P
2011	Scientific paper writing	P

Except for the scientific ethics course, Georgetown University graduate courses are graded P (pass) or F (fail). Passing is C plus or better. The scientific ethics course is graded CRE (credit) or NC (no credit). Students must attend at least seven of the eight presentation/discussion sessions for credit.