Yuan SHANG, PH.D.

CURRICULUM VITAE

Contact Information	
The University of Arizona Center for Innovation in Brain Science 1230 N. Cherry Avenue, PO Box 210242 Tucson, Arizona 85721-0242	Telephone: (520) 626-3318 E-mail: yshang@arizona.edu Mobile: (520) 312-6696

EDUCATION

2020	M.S (expected in 2020 Dec) , University of Arizona, Arizona Statistics
2014	Ph.D., Hong Kong University of Science and Technology, Hongkong Biochemistry
2009	B.A., Shanghai Jiao Tong University, Shanghai Bioinformatics

ACADEMIC APPOINTMENTS

2020 – Present	Research Assistant Professor, Neurology, University of Arizona
2020 - Present	Assistant Scientific Investigator, The Center for Innovation in Brain Science, University of Arizona
2017 - 2019	Principle Research Specialist, The Center for Innovation in Brain Science, University of Arizona
2017 - Present	Principle Research Specialist, The Center for Biomedical Informatics and Biostatistics, University of Arizona
2014 - 2016	Research Associate, Hong Kong University of Science and Technology, Hongkong

SKILLS

Programming: Proficient in R, Python; Basic in MySQL, Matlab, Perl, VBA, C++, Java.

- ✧ I mainly use R in my daily research, including data processing, statistical modeling and simulations.
- ✧ I built my own MySQL database to store biological names of homologs from different species.
- ✧ I use Python for machine learning related projects, familiar with Keras based DNN, CNN,LSTM, auto-encoder/decoder data modeling and training.

Bioinformatics: Proficient in various omics data analysis including processing, normalization, integration, correlation network, and presentation.

Machine learning & Statistics: Deep learning models, Google cloud computing

Biology: Molecular Biology including protein structures, protein-drug interactions; Computational Biology.

HONORS AND AWARDS

2019	Alzheimer's Drug Discovery Foundation ,ADDF Young Investigator Scholarship
2014	Best Thesis Award, Division of Life Science, School of Science, HKUST
2011	Annual Research Award for Postgraduate Students, Division of Life Science, School of Science, HKUST
2011	Best Poster Award, 17th International Biophysics Congress
2008	National Scholarship
2007	First Prize, National Undergraduate Mathematical Modeling Competition
2007	Barclays' Scholarship
2006	Secondary Prize, National Undergraduate Mathematical Modeling Competition
2004	First Prize, National Chemistry Competition for Senior High School Students
2004	Second Prize, National Mathematics Competition for Senior High School Students
2003	First Prize, National Chemistry Competition for Senior High School Students

PROFESSIONAL SERVICE

REVIEWER:

BMC Bioinformatics PeerJ

TEACHING EXPERIENCE

2009 - 2014 Teaching Assistant, Biochemistry, Hong Kong University of Science and Technology, Hongkong

RESEARCH FUNDING

2020 AllOfUs Research Workshop Planning grant

2007 - 2009 National University Student Innovation Program
Sterile Phenotype-Related Insertion Mutants in RGRC database

RESEARCH SUMMARY

Current work: New therapies for Alzheimer's Disease.
My current research is mainly focusing on computational biology, searching for new therapeutic opportunities for Alzheimer's Disease:

- Develop multi-scale network integration methods to explore potential beneficial mechanisms in drug development. I integrated all previous accumulated various omics data of both animal models and phase I clinic trial human datasets in the lab, and found potential mechanisms of how that drug could improve the patients. Network approach explains very well how our drug works. Together with all our other results, our phase 2 clinic trial was approved ($37million) in August 2019.
- Explore new drug targets for Alzheimer's Disease. My current effort is mainly focusing on disease classification based on various publicly available datasets (including genomics,

epigenomics, transcriptomics, proteomics and metabolomics). Alzheimer's has distinct pathologies based on the multi-omics network, and I'm building prediction model based on network and machine learning techniques. This work would definitely advance the field of personalized medicine and would lead to new drug targets for specific Alzheimer's subtype.

- Develop Novel factors that affect Alzheimer's Disease progressions. Our data showed that life style and medicine treatment could affect AD progression dramatically. With the early access to the clinic data in AllOfUs dataset, together with UKbiobank dataset, I'm now actively exploring novel factors that affect the progressions of Alzheimer's disease using machine learning approaches.

PhD Dissertation: Molecular Mechanisms in Cell Polarity and Asymmetric Cell Division

- In my PhD period, I was interested in the molecular mechanism of cell polarity and asymmetric cell division. Through determining the aPKC/Par-3 structure, we defined the substrate binding specificity of aPKC, a key kinase in cell polarity. One of the kinase's substrates—LGN, was a key adaptor protein in cell division. We found that phosphor-LGN binds to another cell polarity related protein called Dlg, linking cell division machinery to cell polarity cues. Structural studies reveal that the phosphor-substrate binding pocket in Dlg matches aPKC's substrate profile very well. All these studies lead to an aPKC-substrate-Dlg signaling cascade. For Dlg, our work also elucidated how an ancient enzyme evolves into a phosphor-protein binding scaffold. Structure analysis and bioinformatics search further led us to predict a series new functions of the newly formed domain during the evolution. Before I leave the lab, I and labmates started working on synapse protein organization and phase separation, and this also leads to lots of high level following publications.

PEER-REVIEWED PUBLICATIONS

[See also google scholar listing at:
https://scholar.google.com/citations?user=APooktAAAAAJ&hl=en]

1. **Yuan Shang***, Aarti Mishra*, Tian Wang, Yiwei Wang, Maunil Desai, Shuhua Chen, Zisu Mao, Loi Do, Adam S. Bernstein, Theodore P. Trouard, and Roberta Brinton(2020). Evidence in Support of Chromosomal Sex Influencing Plasma Based Metabolome vs APOE Genotype Influencing Brain Metabolome Profile in Humanized APOE Male and Female Mice. PLoS One 2020 , 15(1):e0225392
2. Yiwei Wang, **Yuan Shang**, Aarti Mishra, Eliza Bacon, Fei Yin, Roberta Brinton(2020). Midlife chronological and endocrinological transitions in Brain Metabolism: System Biology Basis for increased Alzheimer's Risk in female Brain. Sci. Rep. 10: 8528 (2020)
3. Zhuangfeng Weng, **Yuan Shang**, Zeyang Ji, Fei Ye, Lin Lin, Rongguang Zhang and Jinwei Zhu (2018). Structural Basis of Highly Specific Interaction between Nephrin and MAGI1 in Slit Diaphragm Assembly and Signaling. *J. Am. Soc.* Nephrol., 29 (9), 2362-2371
4. Yue Wang, **Yuan Shang**, Jianchao Li, Weidi Chen, Gang Li, Jun Wan, Wei Liu, Mingjie Zhang (2018). Specific Eph receptor-cytoplasmic effector signaling mediated by SAM-SAM domain interactions. *eLife* 2018;7:e35677
5. Zhuangfeng Weng, **Yuan Shang**, Deqiang Yao, Jinwei Zhu, Rongguang Zhang (2018). Structural analyses of key features in the KANK1/KIF21A complex yield mechanistic insights into the crosstalk between microtubules and the cell cortex. *J Biol Chem 293 (1)*, 215-225
6. Lei Zhang, Angela Jablonski, Jelena Mojsilovic-Petrovic, Hua Ding, Steven Seeholzer, Ian Newton, Inke S. Nathke, Rachael Neve, Jinbin Zhai, **Yuan Shang**, Mingjie Zhang, and Robert Kalb (2017). SAP97 binding partner CRIPT promotes dendrite growth in vitro and in vivo.

eNeuro 4(6): ENEURO.0175-17

7. Jinwei Zhu, Qingqing Zhou, **Yuan Shang**, et al (2017). Synaptic targeting and function of SAPAPs mediated by phosphorylation-dependent binding to PSD-95 MAGUKs. *Cell Report*, 21 (13), 3781-3793
8. Vincent Gardeux, Joanne Berghout, Ikbel Achour A, Grant Schissler, Qike Li, Colleen Kenost, Jianrong Li, **Yuan Shang**, et al. (2017). A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma exacerbations. *J Am Med Inform Assoc 24*, 1116-1126.
9. Yitian Xia, **Yuan Shang**, Rongguang Zhang, Jinwei Zhu (2017). Structure of the PSD-95/MAP1A complex reveals a unique target recognition mode of the MAGUK GK domain. *Biochem J 474,* 2817-2828
10. Jinwei Zhu, **Yuan Shang***, Yitian Xia, Rongguang Zhu, et al. (2016). An Atypical MAGUK GK Target Recognition Mode Revealed by the Interaction between DLG and KIF13B. *Structure 24*,1-10.
11. Menglong Zeng, **Yuan Shang**, Yoichi Araki, Tingfeng Guo, et al. (2016). Phase transition in postsynaptic densities underlies formation of synaptic complexes and synaptic plasticity. *Cell 166*,1163-1175.
12. Menglong Zeng*, **Yuan Shang***, Tingfeng Guo, Qinghai He*, et al.* (2016). A binding site outside the canonical PDZ domain determines the specific interaction between Shank and SAPAP and their function. *Proc Natl Acad Sci USA 113*, E3081-3090.
13. Jinwei Zhu, **Yuan Shang**, and Mingjie Zhang (2016). Mechanistic basis of MAGUK-organized complexes in synaptic development and signalling. *Nat Rev Neurosci 17*, 209-223.
14. Fei Ye, Wei Liu, **Yuan Shang**, and Mingjie Zhang (2016). An Exquisitely Specific PDZ/Target Recognition Revealed by the Structure of INAD PDZ3 in Complex with TRP Channel Tail. *Structure 24*, 383-391.
15. Jinwei Zhu*, **Yuan Shang***, Qingwen Wan, Yitian Xia*, et al.* (2014). Phosphorylation-dependent interaction between tumor suppressors Dlg and Lgl. *Cell Res 24*, 451-463.
16. Zhu Pan*, Jinwei Zhu*, **Yuan Shang***, Zhiyi Wei*, et al.* (2013). An Autoinhibited Conformation of LGN Reveals a Distinct Interaction Mode between GoLoco Motifs and TPR Motifs. *Structure 21*, 1007-1017.
17. Zhu Pan, **Yuan Shang**, Min Jia, Lu Zhang*, et al.* (2013). Structural and Biochemical Characterization of the Interaction between LGN and Frmpd1. *J Mol Biol 425*, 1039-1049.
18. Jinwei Zhu, **Yuan Shang**, Jia Chen, and Mingjie Zhang (2012). Structure and function of the guanylate kinase-like domain of the MAGUK family scaffold proteins. *Front Biol 7*, 379-396.
19. Chihao Wang*, **Yuan Shang***, Jiang Yu, and Mingjie Zhang (2012). Substrate Recognition Mechanism of Atypical Protein Kinase Cs Revealed by the Structure of PKC$^{\iota}$ in Complex with a Substrate Peptide from Par-3. *Structure 20*, 791-801.
20. Jinwei Zhu*, **Yuan Shang***, Caihao Xia, Wenning Wang*, et al.* (2011). Guanylate kinase domains of the MAGUK family scaffold proteins as specific phospho‐protein‐binding modules. *EMBO J 30*, 4986-4997.
21. Jinwei Zhu, Wenyu Wen, Zhen Zheng, **Yuan Shang**, *et al.* (2011). LGN/mInsc and LGN/NuMA Complex Structures Suggest Distinct Functions in Asymmetric Cell Division for the Par3/mInsc/LGN and Gαi/LGN/NuMA Pathways. *Mol Cell 43*, 418-431.
22. Wenfu Ma, **Yuan Shang**, Zhiyi Wei, Wenyu Wen*, et al.* (2010). Phosphorylation of DCC by ERK2 Is Facilitated by Direct Docking of the Receptor P1 Domain to the Kinase. *Structure 18*, 1502-1511.

*:Co-first authors