**Yuan SHANG**

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**EDUCATION**

2017-, **Center for Biomedical Informatics and Biostatistics;Center for Innovation in Brain Science, the University of Arizona,** Arizona**, Research Specialist,Principal**

2014-2016, **Division of Life Science, Hong Kong University of Science and Technology,** Hong Kong

**Research Associate**

2009-2014, **Division of Life Science, Hong Kong University of Science and Technology,** Hong Kong

**Ph.D. student**, **Biochemistry**

2007-2009, **Department of Bioinformatics,** **Shanghai Jiao Tong University**, Shanghai, China

**B.Sc**., **Bioinformatics**

2005-2007, **Teaching Reformed Class, Shanghai Jiao Tong University**, Shanghai, China

**HONORS**

**Best Thesis Award** (1 awardee/per year), **Division of Life Science, School of Science,** HKUST, 2014

**Annual Research Award for Postgraduate Students** (1-2 award/year), **Division of Life Science, School of Science,** HKUST, 2011

**Best Poster Award, 17th International Biophysics Congress,** 2011

**National Scholarship** (top 5%), 2008

**First Prize, Undergraduate Mathematical Modeling Competition** (top 5% of ~12000 teams nationwide), 2007

**Barclays’ Scholarship,** 2007

**Secondary Prize, Undergraduate Mathematical Modeling Competition** (top 10% of ~12000 teams nationwide), 2006

**First Prize, National Chemistry Competition for Senior High School Students, twice in** 2003&2004

**Second Prize, National Mathematics Competition for Senior High School Students,** 2004

**PUBLICATIONS**

1. Jinwei Zhu, **Yuan Shang**\*, Yitian Xia, Rongguang Zhu, et al. (2016). An unexpected MAGUK GK target recognition mode revealed by the interaction between DLG and KIF13B. *Structure 24*,1-10.

2. 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.

3. 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.

4. 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.

5. 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.

6. 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.

7. 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.

8. 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.

9. 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.

10. Chihao Wang\*, **Yuan Shang**\*, Jiang Yu, and Mingjie Zhang (2012). Substrate Recognition Mechanism of Atypical Protein Kinase Cs Revealed by the Structure of PKC¹ in Complex with a Substrate Peptide from Par-3. *Structure 20*, 791-801.

11. 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.

12. 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.

13. 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