Ning Li, Ph.D.

Phone: (301) 978-6176 • E-mail: liningsdu@gmail.com

EDUCATION

Ph. D. in Microbiology/Structural Biology
Shandong University (09/2007 – 12/2012), Jinan, Shandong Province, China

B.S. in Biotechnology
Shandong University (09/2003 – 07/2007), Jinan, Shandong Province, China

RESEARCH EXPERIENCE

Research associate at James R. Williamson lab, The Scripps Research Institute
La Jolla, CA, 07/26/2017-present

Visiting Fellow at Dr. Wei Yang's Lab, National Institutes of Health (NIH)
Bethesda, MD, 07/28/2013-07/26/2017

- Structural and functional study involving DNA mismatch repair protein MutSβ and MutLα. Goal of this research is to (1) capture signal state of MutSβ which engage ATP and mismatch DNA, (2) assemble the signal state of MutSβ with MutLα to obtain initial mismatch repair complex, and (3) solve the 3-D structure of signal state of MutSβ or MutSβ-MutLα by using X-ray chromatography and Cryo-EM method.
- MutSβ and MutLα protein purification from insect cells. Inspection of ATPase activity and DNA binding ability of MutSβ and MutLα using the purified protein. Identification of biological activity of MutSβ and MutLα.
- Assembling of MutSβ and MutLα complex which could initiate DNA mismatch repair progress; determination of the 3-D structure of this complex is in progress.

Ph.D. Student at Prof. Lichuan Gu's Lab, Shandong University
Jinan, Shandong Province, China, 09/2007-12/2012

- Participation of the project of structure biology involving bacterial siderophore metabolism.
- X-ray crystal structure determination of vibriobactin periplasm binding protein ViuP, clarification of the coordination modus for vibriobactin and Fe(III).
- X-ray crystal structure determination of enterobactin periplasm binding protein FepB; with the additional knockout and complement experiments, C-terminal domain of FepB is proved to play a pivotal role in recognizing downstream proteins.

PUBLICATIONS

- Bingqing Li*, **Ning Li*,** Yingying Yue, Lichuan Gu, Sujuan Xu. An unusual crystal structure of ferric-enterobactin bound FepB suggests novel functions of FepB in microbial iron uptake. **Biochem Biophys Res Commun.** (2016) (Vol 478, No. 3, pp 1049-1053, *Co-first author)
- **Ning Li**, Conggang Zhang, Bingqing Li, Lichuan Gu. Unique Iron Coordination in Iron-chelating Molecule Vibriobactin Helps *Vibrio cholerae* Evade Mammalian Siderocalin-mediated Immune Response. **The Journal of Biological Chemistry.** (2012) (Vol 287, No. 12, pp 8912-8919).
- Guijun Shang*, Deyu Zhu*, **Ning Li***, Junbing Zhang*, Chuanyuan Zhu, Lichuan Gu. Crystal structures of STING protein reveal basis for recognition of cyclic di-GMP. **Nature Structural & Molecular Biology.** (2012) (Vol 19, No. 7, pp 725-727, *Co-first author)

- Bingqing Li, **Ning Li**, Feng Wang, Yan Huang, Lichuan Gu. Structural insight of a concentration-dependent mechanism by which YdiV inhibits *Escherichia coli* flagellum biogenesis and motility. **Nucleic Acids Research.** (2012) (Vol 40, No. 21, pp 11073-85)
- Guijun Shang, Xiuhua Liu, Defen Lu, Junbing Zhang, **Ning Li**, Chunyuan Zhu, Lichuan Gu. Structural insight into how *Pseudomonas aeruginosa* peptidoglycan hydrolase Tse1 and its immunity protein Tsi1 function. **Biochemical Journal.** (2012) (Vol 448, No. 2, 201-211)
- Shiheng Liu, Conggang Zhang, **Ning Li**, Bei Niu, Lichuan Gu. Structural insight into the ISC domain of VibB from Vibrio cholerae at atomic resolution: a snapshot just before the enzymatic reaction. **Acta Crystallogr D Biol Crystallogr.** (2012) (D68, pp 1329-1338)
- Xiuhua Liu, Qian Du, Zhi Wang, Deyu Zhu, Yan Huang, **Ning Li**, Tiandi Wei, Lichuan Gu. Crystal structure and biochemical features of EfeB/YcdB from Escherichia coli O157: ASP235 plays divergent roles in different enzyme-catalyzed processes. **The Journal of Biological Chemistry.** (2011) (Vol 286, No. 17, pp 14922-14931)
- XiuHua Liu, Qian Du, Zhi Wang, Shiheng Liu, **Ning Li**, Ying Chen, Lichuan Gu. Crystal structure of periplasmic catecholate-siderophore binding protein VctP from Vibrio cholerae at 1.7 Å resolution. FEBS Letters. (2012) (Vol 586, No. 8, pp 1240-1244)

EXPERIMENTAL SKILLS

1) X-ray crystallography

- DNA cloning and mutagenesis
- Protein expression and purification from *E.coli*, insect cells and mammalian cells
- Protein crystallization
- Diffraction date collection and structure determination using HKL2000, CCP4i, Phenix, COOT, PyMOL

2) Electron Microscopy

- Negative stain and visualizing sample using T12 machine
- Cryo-EM sample preparation
- EM data processing using EMAN2 and Relion

3) Biochemical assay

- Isothermal calorimetry (ITC)
- EMSA, ATPase assay, Nuclease assay
- Several designed assays
- Genetic manipulation in *E.coli* such as gene knockout

AWARDS and MEETINGS

- Participated in Dynamic DNA Structures in Biology on July 10-15, 2016
- Participated in SCBA DC-Baltimore chapter annual scientific symposium on March 19, 2016
- Participated in SCBA DC-Baltimore chapter annual scientific symposium on February 22, 2015 and showed a poster named 'Study of DNA mismatch repair protein'.

  Abstract: DNA mismatch repair plays a pivotal role in correcting replication errors, which can reduce mutation rates and microsatellite instability. Previous studies indicate that genetic defects in this pathway cause Lynch syndrome and various cancers. Mismatched bases are recognized by MutS proteins, then mismatch bound MutS

could recruit downstream protein MutL in presence of ATP to initiate mismatch repair pathway. Although binding of a mispaired or unpaired base by bacterial MutS or eukaryotic MutSα and MutSβ have been well characterized, we lack the information about how signal state of MutS protein recruit downstream proteins in presence of ATP and mismatch DNA. MutSβ(MSH2/MSH3) is one of the homologue protein of MutS in eukaryotic cells, mainly recognizing larger insertion/deletion loops. To obtain the signal state structure of MutSβ, we constructed some mutation types relating to ATP binding or hydrolysis because ATP will induce mismatch DNA dissociating from MutSβ. For Msh2 subunit of MutSβ, the essential residue E749 participating in hydrolyzing ATP was mutated to glutamine, and for Msh3 subunit of MutSβ, a series of mutations have been constructed to occlude the binding site for ATP. Now I'm working on this part and will obtain clean mutation proteins, then crystals of MutSβ-ATP-mismatch DNA will be screened.

- Scholarship of Guanghua in December, 2012.
- Outstanding graduate student in 2012.
- Participated in the 3rd microbial genetics conference in 2008 and gave a talk named 'Structural-function basis research for siderophore binding protein of *Vibrio cholera*'.
- Participated in the microbial annual meeting of China in 2011.