

# Shaozhen Xing

Hebei Normal University, College of Science (050024)

Mobile: 13501141278

Tel: (010)66948407

E-mail: shaozhen0302@163.com

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- Education**
- Graduating University: **Hebei Normal University (2014. 9-2017. 6)**
  - Joint Cultivation Unit: **Beijing Institute of Microbiology and epidemiology (2014.12-2017.5)**
  - Major: Microbiology
  - Supervisor: Baohua Zhao and Yigang Tong
  - Degree: Master

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**Academic capacity** During the Master's degree of study, mastered:

- ① Identification and culture of bacteria and identification, culture and purification of phage
- ② Bacterial genomic DNA and plasmid extraction
- ③ PCR, qPCR
- ④ Molecular cloning
- ⑤ Protein expression, purification and Western Blotting

Proficient in high throughput sequencing:

- ① Pre-processing of various type of samples,
- ② DNA and RNA library preparation,
- ③ Sequencing with Ion Torrent or Illumina

Proficient in Office Automation: Microsoft Excel, PowerPoint and Bioinformatics software:

Newbler, MEGA, CLC Genomics, Cytoscape, Vector NTI, Github, Jupyter, Docker

Fluent in English: TOEFL, assist teacher translate part of the book of "Molecular" and also completed the proofreading of other translated books.

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- Paper**
- **The first author**
    - Genomic sequences of Banna orbivirus, a mosquito-borne reassortment Orbivirus from Xishuangbanna, China. *Virologica Sinica*
    - Complete genome of the first virulent bacteriophage infecting the opportunist pathogen *Serratia rubidaea*. *Archives of virology*
    - Complete Genome Sequence of a Novel Multi-drug-resistant *Klebsiella pneumoniae* Phage, vB\_Kpn\_IME260. *Genome Announcements*
    - Characterization and complete genome sequence analysis of *Enterococcus faecalis* bacteriophage vB\_E. faecalis\_IME196. *Microbiol. China*
    - Characterization and genome analysis of a novel bacteriophage vB\_EfaP\_IME195 infecting *Enterococcus faecalis*. *Microbiol. China*
  - **The Second author**
    - Complete Genome Sequence of a New *Enterococcus faecalis* Bacteriophage vB\_EfaS\_IME197. *Genome Announcements*
    - Characterization and complete genome sequence analysis of a novel virulent Siphoviridae phage against *Staphylococcus aureus* isolated from bovine mastitis in Xinjiang, China. *Virus Genes*