

## 【Info】

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## 【Education】

2010.08 - 2015.07      PhD. Academy of Military Medical Sciences. *Bioinformatics*  
2006.08 - 2010.07      BSc. Tsinghua University. *Computer Science and Technology*

## 【Experience】

2015.08 - Present      Assistant Researcher. Academy of Military Medical Sciences

## 【Awards】

2011 - 2014      Postgraduate Scholarships in Academy of Military Medical Sciences  
2015      Excellent Doctor Degree Dissertation in Academy of Military Medical Sciences

## 【Research Area】

Integrated analysis of multi-omics, big data and biological network models.

Focus on the variation and conservation of genetic information from DNA sequences (1D, linear) to genome architecture (3D, multiplex) during the cell cycle (spatial, temporal) and evolution.

## 【Skills】

1. Excellent understanding of bioinformatics, human genomics and different genome sequencing platforms. More than 5 years' experience with omics data generated from next generation sequencing. Familiar with common databases and tools.
2. Good knowledge of C++, Java, scripting languages (Perl, Python) and mathematics tools (R,

Matlab). Basic knowledge of MySQL. Experience in system management in a Linux environment.

3. Fluent in reading, writing and speaking Chinese and English.
4. Excellent communication and interpersonal skills, team working and self-driven.

## 【Publications】

1. **Shen W**<sup>1</sup>, Wang D, Ye B, Shi M, Ma L, Zhang Y<sup>\*</sup>, Zhao Z<sup>\*</sup>. GC3-biased gene domains in mammalian genomes. *Bioinformatics*. 2015, 31(19):3081-3084.
2. **Shen W**<sup>1</sup>, Wang D, Ye B, Shi M, Zhang Y<sup>\*</sup>, Zhao Z<sup>\*</sup>. A possible role of Drosophila CTCF in mitotic bookmarking and maintaining chromatin domains during the cell cycle. *Biological Res*. 2015, 48:27.
3. Zhang Y<sup>1</sup>, **Shen W**<sup>1</sup>, Shi M<sup>1</sup>, Zhang L, Zhang Z, Li P, Xing L, Luo F, Sun Q<sup>\*</sup>, Zheng X, Yang X<sup>\*</sup>, Zhao Z<sup>\*</sup>. Involvement of aberrant miR-139/Jun feedback loop in human gastric cancer. *Biochim Biophys Acta - Mol Cell Res*. 2015, 1853(2):481-488.
4. Li P<sup>1</sup>, Shi M, **Shen W**, Zhang Z, Xie D, Zhang X, He C, Zhang Y<sup>\*</sup>, Zhao Z<sup>\*</sup>. Coordinated regulation of IFITM1, 2 and 3 genes by an IFN-responsive enhancer through long-range chromatin interactions. *Biochim Biophys Acta – Gene Regul Mech*. 2017.
5. Ye B<sup>1</sup>, **Shen W**, Wang D, Li P, Zhang Z, Shi M, Zhang Y, Zhang F<sup>\*</sup>, Zhao Z<sup>\*</sup>. ZNF143 is involved in CTCF-mediated chromatin interactions by cooperation with cohesin and other partners. *Mol Biol*. 2016, 50(3):496-503.
6. Zhang Z<sup>1</sup>, Zhang Y, Shi M, Ye B, **Shen W**, Li P, Xing L, Zhang X, Hou L, Xu J<sup>\*</sup>, Zhao Z<sup>\*</sup>, Chen W<sup>\*</sup>. Anthrax Susceptibility: Human Genetic Polymorphisms Modulating ANTXR2 Expression. *Toxins*. 2016, 8(1).
7. Zhang Y<sup>1</sup>, Fan K<sup>1</sup>, Sun Q<sup>1,\*</sup>, Chen A, **Shen W**, Zhao Z, Zheng X<sup>\*</sup>, Yang X<sup>\*</sup>. Functional screening for miRNAs targeting Smad4 identified miR-199a as a negative regulator of TGF- $\beta$  signalling pathway. *Nucleic Acids Res*. 2012, 40(18):9286-9297.