

# Curriculum Vitae

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### *Education & Position*

- 09/2005 - 07/2009** B.S.E. in Bioinformatics,  
Huazhong University of Science and Technology, China;
- 09/2009 - 07/2014** Ph.D. in Genetics,  
Fudan University, China;  
Thesis: Mutation, function, and evolution of structural variation in human genome.  
Supervisor: Prof. Li Jin;
- 07/2014 - 10/2015** Research associate,  
Ministry of Education Key Laboratory of Contemporary Anthropology, Jin Lab,  
Fudan University, China;
- 11/2015 - present** Postdoctoral fellowship,  
Mills Lab, Department of Computational Medicine and Bioinformatics,  
University of Michigan, Ann Arbor, MI, USA.

### *Teaching Experience*

- 09/2010 - 01/2011** Teaching assistant,  
[Journal club of Human Evolution] for undergraduate & graduate students. School of Life Sciences, Fudan University;
- 02/2011 - 06/2011** Teaching assistant,

- [Human Evolutionary Genetics] for undergraduate & graduate students. School of Life Sciences, Fudan University;
- 02/2012 - 06/2012** Teaching assistant,  
[Human Evolutionary Genetics] for undergraduate & graduate students. School of Life Sciences, Fudan University;
- 09/2012 - 01/2013** Teaching assistant,  
[Human Evolution] for undergraduate students. School of Life Sciences, Fudan University;
- 02/2013 - 06/2013** Teaching assistant,  
[Human Evolutionary Genetics] for undergraduate & graduate students. School of Life Sciences, Fudan University;

### ***Fellowship & Awards***

- 2010** Academic Scholarships, 1<sup>st</sup> Class, Fudan University;
- 2011** Academic Scholarships, 2<sup>nd</sup> Class, Fudan University;
- 2012** Academic Scholarships, 2<sup>nd</sup> Class, Fudan University;
- 2013** **The 4th Research Funding of National Key Disciplines for Outstanding Ph.D. Students**; title: Formation, mutation, and evolution of copy number variations in human genome.
- 2013** **Outstanding Graduate Students**, Fudan University;
- 2013** **National Scholarship for Graduate Students**, Ministry of Education of the People's Republic of China;
- 2014** **Outstanding Graduates**, Shanghai Municipal Education Commission.
- 2016** **Outstanding Dissertation of Ph.D.**, Shanghai Municipal Education Commission

### ***Presentations & Posters***

1. POSTER. The 16th Annual Pathology Research Symposium, University of Michigan, 2017. Zhou W, Chapman M, Yeh G. Stress-Induced Alzheimer's Disease.
2. POSTER. The American Society of Human Genetics, 2017. **Reviewers' Choice Abstract**. Zhou W, Emery SB, Flasch DA, Wang Y, Kwan KY, Moran JV, Kidd JM, Mills RE. PALMER: A novel pre-masking method for detecting mobile element insertions using long-read sequencing technology.

3. SPEAKER. The Annual Meeting of Shanghai Genetics Society, 2013. Zhou W, Jin L. Whole genome functional traits and evolutionary clues between Copy Number Variations and Segmental Duplications in human genome.
4. POSTER. The Annual Meeting of Shanghai Genetics Society, 2012. **The 1st Poster Award.** Zhou W, Jin L, Zhang F. Increased genome instability in human DNA segments with closely spaced repeats.
5. POSTER. The 13th International Meeting on Human Genome Variation and Complex Genome Analysis, 2012. Zhou W, Zhang F, Jin L. Increased genome instability in human DNA segments with short low-copy repeats.

### ***Publications (Peer-Reviewed Journals and Publications)***

1. **Zhou W\***, Wang Y\*, Fujino M, Shi L, Jin L, Li X, Wang J. 2017. A standardized fold change (SFC) method for microarray differential expression analysis used to reveal genes involved in acute rejection in murine allograft models. *FEBS Open Bio*. doi:10.1002/2211-5463.12343. (\*Co-first authors)
2. McConnell MJ, Moran JV, et al. Brain Somatic Mosaicism Network. 2017. Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. *Science*. doi:10.1126/science.aal1641
3. **Zhou W\***, Ma Y\*, Zhang J, Hu J, Zhang M, Wang Y, Li Y, Wu L, Pan Y, Zhang Y, Zhang X, Zhang X, Zhang Z, Zhang J, Li H, Lu L, Jin L, Wang J, Yuan Z, Liu J. 2017. Predictive model for inflammation grades of chronic hepatitis B: Large-scale analysis of clinical parameters and gene expressions. *Liver International*. doi:10.1111/liv.13427. (\*Co-first authors)
4. Zhang L, Wang J, Zhang C, Li D, Carvalho C, Ji H, Xiao J, Wu Y, **Zhou W**, Wang H, Jin L, Luo Y, Wu X, Lupski JR, Zhang F, Jiang Y. 2017. Efficient CNV breakpoint analysis reveals unexpected structural complexity and correlation of dosage-sensitive genes with clinical severity in genomic disorders. *Human Molecular Genetics*. doi:10.1093/hmg/ddx102.
5. Co-author. 2015. TBX6 Null Variants and a Common Hypomorphic Allele in Congenital Scoliosis. *New England Journal of Medicine*. doi:10.1056/NEJMoa1406829.
6. Chen L, **Zhou W**, Zhang L, Zhang F. 2014. Genome architecture and its roles in human copy number variation. *Genomics & Informatics*. doi:10.5808/GI.2014.12.4.136
7. Chen L\*, **Zhou W\***, Zhang C, Lupski JR, Jin L, Zhang F. 2014. CNV instability associated with DNA replication dynamics: evidence for replicative mechanisms in CNV mutagenesis. *Human Molecular Genetics*. doi:10.1093/hmg/ddu572. (\*Co-first authors)

8. Peng Z, **Zhou W**, Fu W, Du R, Jin L, Zhang F. 2014. Correlation between frequency of non-allelic homologous recombination and homology properties: evidence from homology-mediated CNV mutations in the human genome. *Human Molecular Genetics*. doi:10.1093/hmg/ddu533.
9. Chen Y, Guo L, Chen J, Zhao X, **Zhou W**, Zhang C, Wang J, Jin L, Pei D, Zhang F. 2014. Genome-wide CNV analysis in mouse induced pluripotent stem cells reveals dosage effect of pluripotent factors on genome integrity. *BMC Genomics*. doi:10.1186/1471-2164-15-79
10. **Zhou W\***, Zhang F\*, Chen X, Shen Y, Lupski JR, Jin L. 2013. Increased genome instability in human DNA segments with self-chains: homology-induced structural variations via replicative mechanisms. *Human Molecular Genetics*. doi:10.1093/hmg/ddt113. (\*Co-first authors)
11. Lin R, Wang X, **Zhou W**, Fu W, Wang Y, Huang W, Jin L. 2011. Association of Polymorphisms in the Solute Carrier Organic Anion Transporter Family Member 1B1 Gene with Essential Hypertension in the Uyghur Population. *Annals of human Genetics*. doi:10.1111/j.1469-1809.2010.00622.x.
12. Lin R, Fu W, **Zhou W**, Wang Y, Wang X, Huang W, Jin L. 2011. Association of Heme Oxygenase-1 Gene Polymorphisms with Essential Hypertension and Blood Pressure in the Chinese Han Population. *Genetic Testing and Molecular Biomarkers*. doi:10.1089/gtmb.2010.0103.
13. Lin R, Wang X, **Zhou W**, Fu W, Wang Y, Huang W, Jin L. 2011. Association of a BLVRA Common Polymorphism with Essential Hypertension and Blood Pressure in Kazaks. *Clinical and Experimental Hypertension*. doi:10.3109/10641963.2010.531854.
14. **Zhou W**, Tan J. 2010. Dental Anthropology Suggests Southeast Asian Origins amongst the Jomon People of Japan. *COM. on C.A.* doi:10.4236/coca.2010.41012.
15. **Zhou W**. 2010. Genetic and environmental factors of pathogeny: a population genetics view. *COM. on C.A.* doi:10.4236/coca.2010.41021.