

CURRICULUM VITAE

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POSITIONS AND EMPLOYMENT:

09/2016-present Post Doctoral Associate with Prof. Zhiping Weng, University of Massachusetts Medical School, Worcester, MA, USA

EDUCATION:

- 09/2011-06/2016 **Ph.D.**, Computational Biology (with honor)
CAS-MPG Partner Institute for Computational Biology,
Shanghai Institutes for Biological Sciences,
Chinese Academy of Sciences, P.R. China
- Supervisor: Prof. Li Yang
 - Non-polyadenylated long noncoding RNAs (e.g. circular RNAs) and their regulatory network
- 02/2009-06/2011 **B.S.**, Computer Science and Technology
School of Computer Science and Technology,
Huazhong University of Science and Technology, P.R. China
- 09/2007-06/2011 **B.S.**, Bioengineering (with honor)
College of Life Science and Technology,
Huazhong Agricultural University, P.R. China

AWARDS & HONORS:

- 2017 Excellent Doctoral Thesis Prize of Chinese Academy of Sciences, Chinese Academy of Sciences
- 2015 Ray Wu Prize, Ray Wu Memorial Fund
- 2015 CAS President Scholarship (Special Prize), Chinese Academy of Sciences
- 2015 UCAS-BHPB Scholarship, University of Chinese Academy of Sciences & BHP Billiton

2014	National Scholarship for Outstanding Graduate Student, Ministry of Education of the People's Republic of China
2014	Pacemaker to Merit Student, University of Chinese Academy of Sciences
2014	First-author Award, Shanghai Institutes for Biological Sciences
2014	First-author Award, CAS-MPG Partner Institute for Computational Biology
2013	First-author Award, CAS-MPG Partner Institute for Computational Biology

PEER-REVIEWED PUBLICATIONS:

(* co-first authors; † corresponding authors)

1. **Zhang XO**, Fu Y, Mou H, Xue W, Weng Z†. The temporal landscape of recursive splicing during Pol II transcription elongation in human cells. *PLoS Genet*, 2018, *accepted*.
2. Zhang G*, Tu S*, Yu T, **Zhang XO**, Parhad SS, Weng Z†, Theurkauf WE†. Co-dependent assembly of Drosophila piRNA precursor complexes and piRNA cluster heterochromatin. *Cell Rep*, 2018, *accepted*.
3. Grüning B*, Dale R*, Sjödin A, Chapman BA, Rowe J, Tomkins-Tinch CH, Valieris R, Köster J†, **The Bioconda Team**. Bioconda: sustainable and comprehensive software distribution for the life sciences. *Nat Methods*, 2018, 15:475-476.
4. Huang L, Liu J, **Zhang XO**, Sibley K, Najjar SM, Lee MM, Wu JQ†. Inhibition of protein arginine methyltransferase 5 enhances hepatic mitochondrial biogenesis. *J Biol Chem*, 2018, 17:jbc-RA118.
5. Mou H*, Smith JL*, Peng L, Yin H, Moore J, **Zhang XO**, Song CQ, Sheel A, Wu Q, Ozata DM, Li Y, Anderson DG, Emerson CP, Sontheimer EJ, Moore MJ†, Weng Z†, Xue W†. CRISPR/Cas9-mediated genome editing induces exon skipping by alternative splicing or exon deletion. *Genome Biol*, 2017, 18:108.
6. **Zhang XO***, Dong R*, Zhang Y*, Zhang JL, Luo Z, Zhang J, Chen LL†, Yang L†. Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. *Genome Res*, 2016, 26:1277-1287. (**Highly Accessed**)
7. Dong R, **Zhang XO**, Zhang Y, Ma XK, Chen LL, Yang L†. CircRNA-derived pseudogenes. *Cell Res*. 2016, 26:747-750.
8. Chen T*, Xiang JF*, Zhu S*, Chen S, Yin QF, **Zhang XO**, Zhang J, Feng H, Dong R, Li XJ, Yang L†, Chen LL†. ADAR1 is required for differentiation and neural induction by regulating microRNA processing in a catalytically independent manner. *Cell Res*. 2015, 25:459-476.
9. Wang D*, Cai C*, Dong X, Yu QC, **Zhang XO**, Yang L, Zeng YA†. Identification of multipotent mammary stem cells by protein C receptor expression. *Nature*. 2015, 517:81-84.

10. **Zhang XO***, Wang HB*, Zhang Y, Lu X, Chen LL†, Yang L†. Complementary sequence-mediated exon circularization. *Cell*. 2014, 159:134-147. (**Issue Highlight**)
 - Editorial by: Vicens Q and Westhof E. *Cell*. 2014, 159:13-14.
 - Research Highlight by: Burgess DJ. *Nat Rev Genet*. 2014, 15:707.
11. **Zhang XO**, Yin QF, Chen LL, Yang L†. Gene expression profiling of non-polyadenylated RNA-seq across species. *Genomics Data*. 2014, 2:237-241.
12. **Zhang XO***, Yin QF*, Wang HB, Zhang Y, Chen T, Zheng P, Lu X, Chen LL†, Yang L†. Species-specific alternative splicing leads to unique expression of sno-lncRNAs. *BMC Genomics*. 2014, 15:287. (**Highly Accessed**)
13. Xiang JF, Yin QF, Chen T, Zhang Y, **Zhang XO**, Wu Z, Zhang S, Wang HB, Ge J, Lu X, Yang L, Chen LL†. Human colorectal cancer-specific CCAT1-L lncRNA regulates long-range chromatin interactions at the MYC locus. *Cell Res*. 2014, 24:513-531. (**Cover Article and Issue Highlight**)
14. Zhang Y*, **Zhang XO***, Chen T, Xiang JF, Yin QF, Xing YH, Zhu S, Yang L†, Chen LL†. Circular intronic long noncoding RNAs. *Mol Cell*. 2013, 51:792-806. (**Issue Highlight**)
 - Editorial by: Bolisetty MT and Graveley BR. *Mol Cell*. 2013, 51:705-706.
 - Research Highlight by: *Nature*. 2013, 501:464.
 - Research Highlight by: Reid T. *Nature China*. 2013, Epub. on October 2nd (doi:10.1038/nchina.2013.95).
15. Zhu S, **Zhang XO**, Yang L†. Panning for long noncoding RNAs. *Biomolecules*. 2013, 3:226-241. (Review)

PATENTS:

2015. Li Yang, Ling-Ling Chen, **Xiao-Ou Zhang**, Yang Zhang. *The construction and application of vectors for circular RNA expression*. Patent Application Number: 201510100793.9

2013. Ling-Ling Chen, Li Yang, Yang Zhang, **Xiao-Ou Zhang**. *Identification and application of circular intronic long noncoding RNAs and their essential sequences*. Patent Number: 201310398809.X

PROFESSIONAL EXPERIENCES:

- 09/2016-present **University of Massachusetts Medical School**
- Research Assistant with Prof. Zhiping Weng
- 09/2011-06/2016 **CAS-MPG Partner Institute for Computational Biology**
- Research Assistant with Prof. Li Yang
 - Genome-wide identification and characterization of human circular intronic RNAs

- Evolutionary analysis of sno-lncRNAs
- Biogenesis mechanism of exon circularization and alternative circularization in human
- Alternative splicing characterization of circRNAs
- Identification of circRNA-derived pseudogenes in human
- Collaborative projects: 4C and ChIP-seq analysis to study the chromatin interaction between CCAT1-L locus and cMYC locus, iCLIP analysis to characterize the RNA binding sites of ADAR1 (with Prof. Ling-Ling Chen Lab at SIBCB, SIBS, CAS); Differential gene expression analysis using RNA-seq and microarray to find the key biomarker of multipotent mammary stem cell population (with Prof. Yi Ariel Zeng Lab at SIBCB, SIBS, CAS)

09/2010-06/2011 **Center for Bioinformatics, Huazhong Agricultural University**

- Research Assistant with Prof. Hong-Yu Zhang
- Chemoinformatic analysis of C-H \cdots π interactions in protein-ligand complexes

INVITED TALKS & CONFERENCE PRESENTATIONS:

2015. *Complementary sequence-mediated exon circularization*. the 6th Ray Wu Symposium. October 24-25. Wuhan, China. (Invited Talk)
2015. *Complementary sequence-mediated exon circularization*. IBW 2015. July 9-10. Harbin, China. (Selected Talk)
2015. *Complementary sequence-mediated exon circularization*. RNA 2015. May 26-31. Madison, United States. (Poster)
2014. *Species-specific alternative splicing leads to unique expression of sno-lncRNAs*. 2014 CSHA RNA Biology. November 10-14. Suzhou, China. (Poster)
2014. *Complementary sequence-mediated exon circularization*. CAS-MPG Partner Institute for Computational Biology Institute Seminar. September 24. Shanghai, China. (Selected Talk)
2014. *Species-specific alternative splicing leads to unique expression of sno-lncRNAs*. 2014 CAS-MPG Partner Institute for Computational Biology Scientific Exchange Meeting. June 5-6. Shanghai, China. (Selected Talk)
2014. *Species-specific alternative splicing leads to unique expression of sno-lncRNAs*. The 8th Biennial Meeting of Chinese RNA Society. April 12-13. Hefei, China. (Poster Award)
2013. *Circular intronic long noncoding RNAs*. Otto Warburg International Summer School and Research Symposium 2013. August 19-26. Berlin, Germany. (Poster)
2013. *Pan for intron-derived long noncoding RNAs from non-polyadenylated RNA-seq*. 2013 CAS-MPG Partner Institute for Computational Biology Scientific

Exchange Meeting. June 6-7. Shanghai, China. (Poster Award)