

## CURRICULUM VITAE

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# Xiao-Ou Zhang

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### POSITIONS AND EMPLOYMENT:

11/2020-present **Principal Investigator and Group Leader**, School of Life Sciences and Technology, Tongji University, Shanghai, P.R. China  
09/2016-09/2020 **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 honors)  
CAS-MPG Partner Institute for Computational Biology,  
Shanghai Institutes for Biological Sciences,  
Chinese Academy of Sciences, P.R. China  
• Supervisor: Prof. Li Yang  
• Thesis: Identification of Long Noncoding RNAs with Special Structure and Characterization of Underlying Mechanisms of Their Biogenesis  
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 honors)  
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, CAS
2014	First-author Award, CAS-MPG Partner Institute for Computational Biology, SIBS, CAS
2013	First-author Award, CAS-MPG Partner Institute for Computational Biology, SIBS, CAS

## PUBLICATIONS:

Google Scholar: <https://scholar.google.com/citations?user=KpX6MewAAAAJ>

(\* co-first authors; † corresponding authors)

### Selected peer-reviewed publications:

1. Sun S\*, Zhao Q\*, Zhao Y, Geng M, Wang Q, Gao Q, **Zhang XO**†, Zhang W†, Suai L†. BCL2 is a major regulator of haploidy maintenance in murine embryonic stem cells. *Cell Prolif.* 2023, e13498.
2. **Zhang XO**, Pratt HE, Weng Z†. Investigating the potential roles of SINEs in the human genome. *Annu Rev Genomics Hum Genet.* 2021. 22:199-218. (Review)
3. Zhang P\*, **Zhang XO**\*, Jiang T, Cai L, Huang X, Liu Q, Li D, Lu A, Liu Y, Xue W, Zhang P†, Weng Z†. Comprehensive identification of alternative back-splicing in human tissue transcriptomes. *Nucleic Acids Res.* 2020, 48:1779-1789.
4. **Zhang XO**, Gingeras TR, Weng Z†. Genome-wide analysis of polymerase III-transcribed *Alu* elements suggests cell-type-specific enhancer function. *Genome Res.* 2019, 29:1402-1414.
5. **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, 14:e1007579.
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. (ESI top 1%)
7. **Zhang XO**\*, Wang HB\*, Zhang Y, Lu X, Chen LL†, Yang L†. Complementary sequence-mediated exon circularization. *Cell.* 2014, 159:134-147. (Issue

### Highlight and ESI top 1%)

- Editorial by: Vicens Q and Westhof E. *Cell*. 2014, 159:13-14.
  - Research Highlight by: Burgess DJ. *Nat Rev Genet*. 2014, 15:707.
  - Recommended by **F1000**.
8. **Zhang XO**, Yin QF, Chen LL, Yang L†. Gene expression profiling of non-polyadenylated RNA-seq across species. *Genomics Data*. 2014, 2:237-241.
  9. **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.
  10. 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 and ESI top 1%)
    - 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 2<sup>nd</sup> (doi:10.1038/nchina.2013.95).

### Peer-reviewed publications:

11. Cao J\*, Yu T\*, Xu B, Hu Z, **Zhang XO**, Theurkauf WE, Weng Z†. Epigenetic and chromosomal features drive transposon insertion in *Drosophila melanogaster*. *Nucleic Acids Res*. 2023, 51:2066-2086.
12. Lv B, **Zhang XO**, Pazour GJ†. Aih2 regulates Hedgehog signaling through smoothened ubiquitylation and ER-associated degradation. *J Cell Sci*. 2022, 135:jcs260299.
13. Huang L, **Zhang XO**, Rozen EJ, Sun X, Sallis B, Verdejo-Torres O, Wigglesworth K, Moon D, Huang T, Cavaretta JP, Wang G, Zhang L, Shohet JM, Lee MM†, Wu Q†. PRMT5 activates AKT via methylation to promote tumor metastasis. *Nat Commun*. 2022, 13:3955.
14. Moore JE, **Zhang XO**, Elhajjajy SI, Fan K, Pratt HE, Reese F, Mortazavi A, Weng Z†. Integration of high-resolution promoter profiling assays reveals novel, cell type-specific transcription start sites across 115 human cell and tissue types. *Genome Res*. 2022, 32:389-402.
15. Jiang T, **Zhang XO**, Weng Z, Xue W†. Deletion and replacement of long genomic sequences using prime editing. *Nat Biotechnol*. 2022, 40:227-234.
16. Ghanta KS\*, Chen Z\*, Mir A, Dokshin GA, Krishnamurthy PM, Yoon Y, Gallant J, Xu P, **Zhang XO**, Ozturk AR, Shin M, Idrizi F, Liu P, Gneid H, Edraki A, Lawson ND, Rivera-Pérez JA, Sontheimer E†, Watts JK†, Mello CC†. 5'-Modifications improve potency and efficacy of DNA donors for precision genome editing. *Elife*. 2021, 10:e72216.
17. Wang EY, Kuzmanov U, Smith JB, Dou W, Rafatian N, Lai BFL, Lu RXZ, Wu Q, Yazbeck J, **Zhang XO**, Sun Y, Gramolini A, Radisic M†. An organ-on-a-chip

- model for pre-clinical drug evaluation in progressive non-genetic cardiomyopathy. *J Mol Cell Cardiol*. 2021, 160:97-110.
18. Fan K, Moore JE, **Zhang XO**, Weng Z†. Genetic and epigenetic features of promoters with ubiquitous chromatin accessibility support ubiquitous transcription of cell-essential genes. *Nucleic Acids Res*. 2021, 49:5705-5725.
  19. Zhang Y, Nguyen TM, **Zhang XO**, Wang L, Phan T, Clohessy JG†, Pandolfi PP†. Optimized RNA-targeting CRISPR/Cas13d technology outperforms shRNA in identifying functional circRNAs. *Genome Biol*. 2021, 22:41.
  20. Smith JL, Rodríguez TC, Mou H, Kwan SY, Pratt HE, **Zhang XO**, Cao Y, Liang S, Ozata DM, Yu T, Yin Q, Hazeltine M, Weng Z, Sontheimer EJ, Xue W†. YAP1 withdrawal in hepatoblastoma drives therapeutic differentiation of tumor cells to functional hepatocyte-like cells. *Hepatology*. 2021, 73:1011-1027.
  21. **The ENCODE Project Consortium**. Perspectives on ENCODE. *Nature*. 2020, 583:693-698. (**Zhang XO** is one co-author of **The ENCODE Project Consortium**)
  22. **The ENCODE Project Consortium**. Expanded encyclopedias of DNA elements in the human and mouse genomes. *Nature*. 2020, 583:699-710. (**Zhang XO** is one co-author of **The ENCODE Project Consortium**)
  23. Jiang T, Henderson JM, Coote K, Cheng Y, Valley HC, **Zhang XO**, Wang Q, Rhym LH, Cao Y, Newby GA, Bihler H, Mense M, Weng Z, Anderson DG, McCaffrey AP, Liu DR, Xue W†. Chemical modifications of adenine base editor mRNA and guide RNA expand its application scope. *Nat Commun*. 2020, 11:1979.
  24. Kwan SY\*, Sheel A\*, Song CQ, **Zhang XO**, Dang H, Cao Y, Mou H, Yin H, Weng Z, Wang XW, Xue W†. Depletion of TRRAP/KAT5 induces p53-independent senescence in liver cancer by regulating G2/M genes. *Hepatology*. 2020, 71:275-290.
  25. Wu Z, Oeck S, West AP, Mangalhara KC, Sainz AG, Newman LE, **Zhang XO**, Wu L, Yan Q, Bosenberg M, Liu Y, Sulkowski PL, Tripple V, Kaech SM, Glazer PM, Shadel GS†. Mitochondrial DNA stress signaling protects the nuclear genome. *Nat Metab*. 2019, 1:1209-1218. (Recommended by **F1000**)
  26. 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, 24:3413-3422.e4.
  27. 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. (**Zhang XO** is one co-author of **The Bioconda Team**)
  28. 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. (Recommended by **F1000**)

29. Mou H\*, Smith JL\*, Peng L, Yin H, Moore JE, **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.
30. Dong R, **Zhang XO**, Zhang Y, Ma XK, Chen LL, Yang L†. CircRNA-derived pseudogenes. *Cell Res.* 2016, 26:747-750.
31. 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.
32. 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. (Recommended by **F1000**)
33. 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, Issue Highlight and ESI top 1%)
34. 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 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

#### **INVITED TALKS & CONFERENCE PRESENTATIONS:**

2019. ENCODE Consortium Meeting 2019. December 8-11. Monterey, United States. (Poster)

2019. The 84<sup>th</sup> Cold Spring Harbor Symposium: RNA Regulation and Control. May 29-June 3. Cold Spring Harbor, United States. (Poster)

2015. The 6<sup>th</sup> Ray Wu Symposium. October 24-25. Wuhan, China. (Invited Talk)

2015. The 12<sup>th</sup> International Bioinformatics Workshop. July 9-10. Harbin, China. (Selected Talk)

2015. The 20<sup>th</sup> Annual Meeting of the RNA Society. May 26-31. Madison, United States. (Poster)

2014. Cold Spring Harbor Asia RNA Biology. November 10-14. Suzhou, China. (Poster)

2014. The 8<sup>th</sup> Biennial Meeting of the Chinese RNA Society. April 12-13. Hefei,

China. (Poster Award)

2013. Otto Warburg International Summer School and Research Symposium 2013.  
August 19-26. Berlin, Germany. (Poster)

**JOURNAL REVIEWER**

Reviewer for Bioinformatics, Molecular Genetics and Genomics, Cancer Management and Research, Biomedicine & Pharmacotherapy, International Journal of Genomics, Disease Markers, Pathology - Research and Practice, Oncotarget