

# Xuebing Wu, Ph.D.

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## EMPLOYMENT

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- 11/1/2018- **Assistant Professor**  
Departments of Medicine and Systems Biology  
Columbia University Irving Medical Center
- 2014-2018 **Helen Hay Whitney Postdoctoral Fellow**  
Whitehead Institute for Biomedical Research  
Advisor: **David P. Bartel, Ph.D.**  
Research: Widespread influence of RNA structures on mRNA processing and stability

## EDUCATION

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- 2009-2014 **Ph.D.** in Computational and Systems Biology  
Massachusetts Institute of Technology (MIT)  
Advisor: **Phillip A. Sharp, Ph.D.** (co-advisor: **Christopher B. Burge, Ph.D.**)  
Thesis: Mechanism and function of pervasive noncoding transcription in mammalian genomes
- 2007-2009 **M.S.** in Control Science and Engineering (Area: Bioinformatics)  
Department of Automation, Tsinghua University, China  
Advisor: **Rui Jiang, Ph.D.**  
Thesis: Disease gene and pathway identification using network alignment approaches
- 2003-2007 **B.S.** in Control Science and Engineering  
Department of Automation, Tsinghua University, China  
Advisor: **Shao Li, M.D.** (co-advisor: **Michael Q. Zhang, Ph.D.**)  
Thesis: Network-based global inference of human disease genes

## PUBLICATIONS

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\* co-first authors; # co-corresponding authors

1. Zhang C\*, Konermann S\*, Brideau NJ, Lotfy P, Wu X, Novick SJ, Strutzenberg T, Griffin PR, Hsu PD, Lyumkis D.  
Structural basis for the RNA-guided ribonuclease activity of CRISPR-Cas13d.  
**Cell**. 2018, 175:212-223
2. Tycko J, Barrera LA, Huston N, Friedland AE, Wu X, Gootenberg JS, Abudayyeh OO, Myer VE, Wilson CJ, Hsu PD.  
Pairwise library screen systematically interrogates *Staphylococcus aureus* Cas9 specificity in human cells.  
**Nature Communications**. 2018, 9:2962
3. Jiang W\*, Wei Y\*, Long Y\*, Owen A, Wang B, Wu X, Luo S, Dang Y, Ma DK.  
A cold-warming genetic program promotes *C. elegans* organismic death.  
**eLife**. 2018, 7:e35037

4. Liu XS, Wu H, Krzisch M, Wu X, Greaf J, Muffat J, Hnisz D, Li C, Yuan B, Xu C, Li Y, Vershkov D, Cacace A, Young RA, Jaenisch R.  
Rescue of fragile X syndrome by DNA methylation editing of the *FMR1* gene.  
**Cell**. 2018, 172:979–992
5. Chiu AC\*, Suzuki HI\*, Wu X, Mahat DB, Kriz AJ, Sharp PA.  
U1 snRNP suppresses premature polyadenylation at transcriptional pause sites associated with stable nucleosomes.  
**Molecular Cell**. 2018, 69:648–663
6. Wu X, Bartel DP.  
Widespread influence of 3'-end structures on mammalian mRNA processing and stability.  
**Cell**. 2017, 169:905–917
7. Wu X<sup>#</sup>, Bartel DP<sup>#</sup>.  
kpLogo: positional *k*-mer analysis reveals hidden specificity in biological sequences.  
**Nucleic Acids Research**. 2017, W1:gkx323
8. Liu XS\*, Wu H\*, Ji X, Stelzer Y, Wu X, Czauderna S, Shu J, Shivalila CS, Dadon D, Young RA, Jaenisch R.  
Editing DNA methylation in the mammalian genome.  
**Cell**. 2016, 167:233-247
9. Zhang X, Chen MH, Wu X, Kodani A, Fan J, Doan R, Ozawa M, Ma J, Yoshida N, Reiter J, Black DL, Kharchenko PV, Sharp PA, Walsh CA.  
Cell type-specific alternative splicing governs cell fate in the developing cerebral cortex.  
**Cell**. 2016, 166:1147-1162 (cover story)
10. Ran FA\*, Cong L\*, Yan WX\*, Scott DA, Gootenberg JS, Kriz AJ, Zetsche B, Shalem O, Wu X, Makarova KS, Koonin EV, Sharp PA, Zhang F.  
In vivo genome editing using *Staphylococcus aureus* Cas9.  
**Nature**. 2015, 520:186-191
11. Wu X, Scott DA, Kriz AJ, Chiu AC, Hsu PD, Dadon DB, Cheng AW, Trevino AE, Konermann S, Chen S, Jaenisch R, Zhang F<sup>#</sup>, Sharp PA<sup>#</sup>.  
Genome-wide binding of CRISPR-Cas9 in mammalian cells.  
**Nature Biotechnology**. 2014, 32:670-676
12. Wu X, Kriz AJ, Sharp PA.  
Target specificity of the CRISPR-Cas9 system.  
**Quantitative Biology**. 2014, 2:59-70 (review & cover, peer reviewed)
13. Chen S\*, Xue Y\*, Wu X, Cong L, Bhutkar A, Bell E, Zhang F, Langer R, Sharp PA.  
Global microRNA depletion suppresses tumor angiogenesis.  
**Genes & Development**. 2014, 28:1054-1067
14. Wu X, Sharp PA.  
Divergent transcription: a driving force for new gene origination?  
**Cell**. 2013, 155:990-996 (perspective/theory, peer reviewed)
15. Almada AA\*, Wu X\*, Kriz AJ, Burge CB, Sharp PA.  
Promoter directionality is controlled by U1 snRNP and polyadenylation signals.  
**Nature**. 2013, 499:360-363
16. Cong L\*, Ran FA\*, Cox D, Lin S, Barretto R, Habib R, Hsu PD, Wu X, Jiang W, Marraffini LA, Zhang F.  
Multiplex genome engineering using CRISPR/Cas systems.  
**Science**. 2013, 339 (6121):819-823
17. Hsu PD\*, Scott DA\*, Weinstein JA, Ran FA, Konermann S, Agarwala V, Li Y, Fine EJ, Wu X, Shalem O, Cradick TJ, Marraffini LA, Bao G, Zhang F.

DNA targeting specificity of the RNA-guided Cas9 nuclease.

**Nature Biotechnology**. 2013, 31:827-832 (cover story)

18. Lyubimova A, Itzkovitz S, Junker JP, Fan ZP, Wu X, van Oudenaarden A.  
Single-molecule mRNA detection and counting in mammalian tissue.  
**Nature Protocols**. 2013, 8:1743–1758
19. Chen Y, Wu X, Jiang R.  
Integrating human omics data to prioritize candidate genes.  
**BMC Medical Genomics**. 2013, 6:57
20. Wu X, Li S.  
Cancer gene prediction using a network approach.  
**Cancer Systems Biology** (Edited by Wang E). CRC Press, 2010, Chapter 11:191-212 (book chapter)
21. Wu X, Liu Q, Jiang R.  
Align human interactome with phenome to identify causative genes and networks underlying disease families.  
**Bioinformatics**. 2009, 25:98-104
22. Tang W, Wu X, Jiang R, Li Y.  
Epistatic module detection for case-control studies: A Bayesian model with a Gibbs sampling strategy.  
**PLOS Genetics**. 2009, 5(5):e1000464
23. Jiang R, Tang W, Wu X, Fu W.  
A random forest approach to the detection of epistatic interactions in case-control studies.  
**BMC Bioinformatics**. 2009, 10(Suppl 1):S65
24. Zhang W, Zeng F, Wu X, Zhang X, Jiang R.  
A comparative study of ensemble learning approaches in the classification of breast cancer metastasis.  
**International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing**. 2009, 242-245
25. Jiang R, Zeng F, Zhang W, Wu X, Yu Z.  
Accelerating genome-wide association studies using CUDA compatible graphics processing units.  
**International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing**. 2009, 70-76
26. Wu X, Jiang R, Zhang MQ, Li S.  
Network-based global inference of human disease genes.  
**Molecular Systems Biology**. 2008, 4:189

## HONORS AND AWARDS

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2019	<b>The RNA Society/Scaringe Award</b>
2018	Finalist, The Regeneron Prize for Creative Innovation in a Postdoc
2017	<b>Margaret and Herman Sokol Postdoctoral Award</b> , Whitehead Institute
2017	<b>Oral Presenter Award</b> , RNA Symposium, University at Albany, SUNY
2016-2019	<b>Helen Hay Whitney Postdoctoral Fellowship</b> , Helen Hay Whitney Foundation
2014	Honorable Mention, The Regeneron Prize for Creative Innovation in a Graduate Student
2014	<b>AAAS/Science Program for Excellence in Science</b> , AAAS/Science
2011-2014	<b>International Student Research Fellowship</b> , Howard Hughes Medical Institute
2011	<b>Integrative Cancer Biology Program (ICBP) Graduate Student Fellowship</b> , NCI/MIT
2009	<b>Rising Stars of Research</b> , Tsinghua University, China
2008	<b>Top-grade Scholarship</b> (the highest honor), Tsinghua University, China
2008	<b>Outstanding Graduate Student</b> , Tsinghua University, China
2007	<b>Graduate with Great Honor</b> , Tsinghua University, China
2006	<b>National Scholarship</b> , Ministry of Education of China

## PRESENTATIONS

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2018 Jun **Talk**, RNA Therapeutics Conference at UMass Med School  
2018 Jun **Scaringe Award Talk**, RNA Society Annual Meeting in Krakow, Poland  
2017 Aug **Talk**, Cold Spring Harbor meeting on Eukaryotic mRNA Processing  
2017 Jun Poster, Gordon Research Conference on Nucleic Acids  
2017 Apr **Invited inaugural speaker**, Postdoc Work In Progress Seminar (WIPS), MIT  
2017 Mar **Talk**, RNA Symposium, University at Albany, SUNY  
2017 Feb **Talk**, Whitehead Forum  
2015 May **Invited panelist**, Genome Engineering 3.0 Workshop, Broad Institute  
2014 Jun **Invited talk**, Phillip Sharp 70th Birthday Symposium, MIT  
2014 Apr **Invited talk**, Computational and Systems Biology Student Seminar, MIT  
2014 Mar **Talk**, Cold Spring Harbor meeting on Systems Biology: Global Regulation of Gene Expression  
2014 Mar **Talk**, MIT Koch Institute Friday Focus Seminar Series  
2013 Nov **Invited talk**, RNA Genomics Symposium, Harvard Medical School  
2013 Oct **Talk**, MIT Koch Institute Retreat  
2013 Oct **Talk**, MIT Computational and Systems Biology Retreat  
2013 Aug Poster, Cold Spring Harbor meeting on Eukaryotic mRNA Processing  
2013 May Poster, HHMI Science Meeting  
2013 Jan **Invited talk**, Key Laboratory of Bioinformatics, Ministry of Education, China  
2011 Jul Poster, MIT Integrative Cancer Biology Program (ICBP) Retreat  
2008 Dec **Plenary talk**, Tsinghua Forum for Doctoral Candidates, Tsinghua University

## TEACHING EXPERIENCE

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2011 **Teaching assistant** (student rating 6.7/7), MIT  
Evolutionary Biology (Lecturers: Robert Berwick, Ph.D. & David Bartel, Ph.D.)  
2008 **Teaching assistant**, Tsinghua University, China  
Probability & Statistics for Computational Biology (Lecturer: Michael Waterman, Ph.D.)  
2007 **Teaching assistant**, Tsinghua University, China  
Proteins: Structure, Function, and Evolution (Lecturer: Zhirong Sun, Ph.D.)

## MENTORING EXPERIENCE

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- Rotation graduate student (MIT Biology)

Nima Jaber-Lashkari (04/2017)  
Byron Lee (02/2017)  
Kendall Condon (02/2016)

Charles Li (05/2015)  
Gina Mawla (05/2013)

- Undergraduate thesis or research training

Elizabeth Martin (06-09/2015)  
Andrea Kriz (2011-2014)  
Wenhui Fu (2009)  
Ming Yin (2009)  
Zheng Ke (2008)

MIT Computer Science & Molecular Biology  
MIT Biology (now graduate student at Harvard BBS)  
Tsinghua Electrical Engineering  
Tsinghua Software (now faculty at Purdue University)  
Tsinghua Physics (now faculty at the University of Chicago)

## OTHER PROFESSIONAL ACTIVITIES

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- Invited ad hoc reviewer for: *GigaScience*, *Bioinformatics*, *Scientific Reports*, *Genetics*, *PLOS Computational Biology*, *Genes*, *PLOS ONE*, *Molecular and Cellular Biochemistry*, *OMICS*, *BMC Bioinformatics*, *BMC Systems Biology*, *Journal of Theoretical Biology*, *Quantitative Biology*