
BIOGRAPHICAL SKETCH

NAME Xuan, Zhenyu	POSITION TITLE Assistant Professor		
eRA COMMONS USER NAME (credential, e.g., agency login) ZHENYUXUAN			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YY	FIELD OF STUDY
Nanjing University, Nanjing, China	B.S.	1995	Theoretical Physics
Institute of Biophysics, Chinese Academy of Science, Beijing, China	Ph.D.	2000	Bioinformatics

Personal Webpage: <http://www.utdallas.edu/biology/faculty/research/xuan.html>

A. Positions and Honors

Positions

July 2000-Sept 2005 Computational Postdoctoral Fellow, Cold Spring Harbor Laboratory (Lab of Dr. Michael Zhang), Cold Spring Harbor, NY
Oct 2005-Jan 2008 Research Investigator, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
Feb 2008-Dec 2009 Research Assistant Professor, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
Jan 2010- Present Assistant Professor, Department of Molecular Cell Biology, University of Texas at Dallas
Oct 2012- Present Adjunct Assistant Professor, Eugene McDermott Center for Human Growth & Development, Internal Medicine, UT Southwestern medical center

B. Selected Peer-reviewed Publications (Selected from 57 peer-reviewed publications)

Most relevant to the current application

- Smith AD*, **Xuan Z***, Zhang MQ (2008) Using quality scores and longer reads improves accuracy of Solexa read mapping. *BMC Bioinformatics* 9:128. (* Equally contributed first author with S.A.).
- Wang X*, **Xuan Z***, Zhao X, Li Y and Zhang MQ. (2008) High-resolution Human Core-promoter prediction with CoreBoost_HM. *Genome Res.* 19:266-275 (* Equally contributed first author with W.X.).
- Pang K, Cheng C, **Xuan Z**, Sheng H, Ma X. (2010) Understanding protein evolutionary rate by integrating gene co-expression with protein interactions. *BMC Syst Biol.* 4:179.
- Zhang B, Chen B, Wu T, **Xuan Z**, Zhu X, Chen R. (2011) Estimating developmental states of tumors and normal tissues using a linear time-ordered model. *BMC Bioinformatics.* 12:53.
- Renault VM, Thekkat PU, Hoang KL, White JL, Brady CA, Kenzelmann Broz D, Venturelli OS, Johnson TM, Oskoui PR, **Xuan Z**, Santo EE, Zhang MQ, Vogel H, Attardi LD, Brunet A. (2011) The pro-longevity gene FoxO3 is a direct target of the p53 tumor suppressor. *Oncogene.* 30:3207-21.
- Xie W., ..., **Xuan Z**, *et al.* (2013) Epigenomic analysis of multilineage differentiation of human embryonic stem cells. *Cell.* 153:1134-48.

Olive V, ..., **Xuan Z**, *et.al.*. (2013) A component of the mir-17-92 polycistronic oncomir promotes oncogene-dependent apoptosis. *Elife*. 2:e00822. doi: 10.7554/eLife.00822.

Additional recent publications of importance to the field (in chronological order)

- Xuan Z**, Zhao F, Wang JH, Chen GX and Zhang MQ (2005) Genome-wide promoter extraction and analysis in human, mouse, and Rat. *Genome Biol.* 6(8):R72.
- He L, He X, Lim LP, de Stanchina E, **Xuan Z**, Liang Y, Xue W, Zender L, Magnus J, Ridzon D, Jackson AL, Linsley PS, Chen C, Lowe SW, Cleary MA, Hannon GJ (2007) A microRNA component of the p53 tumor suppressor network. *Nature*. 447, 1130-4.
- Hodges E*, **Xuan Z***, Baliya V, Kärner M, Molla MN, Smith SW, Middle CM, Rodesch MJ, Albert TJ, Hannon GJ, McCombie WR (2007) Genome-wide in-situ exon capture for selective resequencing. *Nat. Genet.* 39:1522-7. (* Equally contributed first author with H.E.).
- Bric A, Miething C, Bialucha CU, Scuoppo C, Zender L, Krasnitz A, **Xuan Z**, Zuber J, Wigler M, Hicks J, McCombie RW, Hemann MT, Hannon GJ, Powers S, Lowe SW. (2009) Functional identification of tumor-suppressor genes through an in vivo RNA interference screen in a mouse lymphoma model. *Cancer Cell*. 16:324-35. PMID: PMC2829755.
- Ma X, Kulkarni A, Zhang Z, **Xuan Z**, Serfling R, Zhang MQ. (2012) A highly efficient and effective motif discovery method for ChIP-seq/ChIP-chip data using positional information. *Nucleic Acids Res.* 40:e50. Epub 2012 Jan 6.