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CURRICULUM VITAE

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EDUCATION:

09/1995-06/2000 Institute of Biophysics, Chinese Academy of Sciences Ph.D.

09/1991-07/1995 Department for Intensive Instruction B.S.
Nanjing University, Nanjing, Jiangsu, China.

RESEARCH EXPERIENCES:

10/2005-present Research Investigator, Cold Spring Harbor Laboratory

- Identify *cis*-regulatory modules to control tissue-specific gene expression.
- Characterize non-coding RNA functions during development and disease.
- Develop a method for *in situ* exon capture and selective resequencing.

07/2000-10/2005 Postdoctoral fellow with Dr. Michael Q Zhang, Cold Spring Harbor Laboratory

- Predict novel genes using protein sequence motifs and genome sequences.
- Compare human and mouse genomes and estimate human gene number.
- Promoter prediction using cross-species conservation and promoter database construction (CSHLmpd).

09/1995-06/2000 Ph.D. thesis with Dr. Runsheng Chen, Institute of Biophysics,
Chinese Academy of Sciences.

- Identify protein structural domains from 3D structure.
- Join the Bacteria genome sequencing and the human genome project.

FELLOWSHIP AND AWARD

- Di Ao Fellowship 2000
- Yi Li Da Fellowship 1996

PRESENTATIONS:

Xuan Z (2006) *MicroRNA and cancer*, invited lecture in Peking University, Beijing, China.

Xuan Z (2005) *CSHL Mammalian Promoter Database*, CSHL Bush-In-House lecture.

Xuan Z, Zhang MQ (2005) *Predict non-CpG promoters by using Genetic Algorithm (GA) and Support Vector Machine (SVM)*, poster in *Biology of Genome Meeting* in Cold Spring Harbor, NY, USA.

Xuan Z, An H, Zhang MQ (2001) *Genomic DNA motif search for gene-region finding*, poster in *Genome Sequencing & Biology Meeting* in Cold Spring Harbor, NY, USA.

TEACHING AND MENTORING EXPERIENCES

- 07/2002-08/2007 Lecturer for “*Bioinformatics Workshop*” in CSHL Undergraduate Research Program (URP) (2005, 2007); Co-mentor for five students in URP.
- 09/2006-05/2007 Supervisor of graduate student Journal Club in CSHL.
- 03/1999-02/2000 Founded and directed Bioinformatics section in Beijing Genome Institute.

PUBLICATIONS

- Hodges E*, **Xuan Z***, Balija V, Karmar 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.* (In press) (* Equally contributed first author with H.E.).
- 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.
- Murchison EP, Stein P, **Xuan Z**, Pan H, Zhang MQ, Schultz RM, and Hannon GJ (2007) Critical roles for Dicer in the female germline. *Gene & Dev*. **21**, 682-93.
- Zhao X, **Xuan Z**, Zhang MQ. (2007) Boosting with stumps for predicting transcription start sites. *Genome Biol*. **8**, R17
- Jiang C, **Xuan Z**, Zhao F, Zhang MQ. (2007) TRED: a transcriptional regulatory element database, new entries and other development. *Nucleic Acids Res*. **35**(Database issue):D137-40.
- Wang X, Bandyopadhyay S, **Xuan Z**, Zhao X, Zhang MQ, Zhang X. (2007) Prediction of Transcription Start Sites Based on Feature Selection Using AMOSA. *Comput. Syst. Bioinformatics Conf*. **6**:183-93.
- Kim YC*, Jung YC*, **Xuan Z***, Dong H, Zhang MQ, Wang SM. (2006) Pan-genome isolation of low abundance transcripts using SAGE tag. *FEBS Lett*. **580**, 6721-9 (* Equally contributed first author).
- Das R, Dimitrova N, **Xuan Z**, Rollins RA, Haghghi FG, Edwards JR, Ju J, Bestor TH and Zhang MQ, (2006) Computational prediction of DNA methylation landscape in the human genome. *Proc. Natl. Acad. Sci. USA*. **103**, 10713-10716
- Smith AD, Sumazin P, **Xuan Z**, Zhang MQ (2006) DNA motifs in human and mouse proximal promoters predict tissue-specific expression. *Proc. Natl. Acad. Sci. USA*. **103**, 6275-6280.
- Zhang C, **Xuan Z**, Mandel G, Zhang MQ (2006) A Clustering Property of Highly-degenerate Transcription Factor Binding Sites in the Mammalian Genome. *Nucl. Acid. Res*. **34**, 238-2246
- Prasanth KV, Prasanth SG, **Xuan Z**, Sachidandam R, Hearn S, Frier SM, Bennett CF, Zhang MQ and Spector DL (2005) Regulating Gene Expression Through RNA Nuclear Retention. *Cell* **123**, 249-63.
- Xuan Z**, Zhao F, Wang J, Chen G, Zhang MQ (2005), Improving Promoter Prediction by Incorporating Sequence Conservation. *Genome Biology*. **6**, R72.
- Zhao F, **Xuan Z**, Liu L, Zhang MQ (2005) TRED: A Transcription Regulatory Element Database and a Platform for *in silico* Gene Regulation Studies. *Nucl Acid Res* **33**, D103-107.

- Xuan Z**, Zhang MQ (2005) From Worm to Human: Bioinformatics Approaches to Identify FOXO Target Genes. *Mech Ageing Dev* **126**, 209-215.
- Sujit Dike, Vivekanand S. Balija, Lidia U. Nascimento, **Xuan Z**, Jacqueline Ou, Theresa Zutavern, Lance E. Palmer, Greg Hannon, Michael Q. Zhang and W. Richard McCombie (2004) The Mouse Genome: Experimental Examination of Gene Predictions and Transcriptional Start Sites. *Genome Res* **14**, 2424-2429.
- Lo WS, Lau CF, **Xuan Z**, Chan CF, Feng GY, He L, Cao ZC, Liu H, Luan QM, Xue H (2004) Association of SNPs and haplotypes in GABAA receptor beta2 gene with schizophrenia. *Mol Psychiatry*. **9**, 603-8.
- Xuan Z**, Wang J, Zhang MQ (2003) Computational comparison of two mouse draft genomes and the human goldenpath. *Genome Biology*. **4**, R1.
- Carmell MA*, **Xuan Z***, Zhang MQ and Hannon G (2002) Argonaute proteins: tentacles that reach into RNAi, stem cell maintenance and tumorigenesis. *Gene & Dev*. **16**, 2733-2742 (* Equally contributed first author)
- Xuan Z**, McCombie R, Zhang MQ (2002) GFScan: a gene family search tool at genomic DNA level. *Genome Res*. **12**, 1142-1149.
- Bao Q, **Xuan Z et. al.** (2002) A complete sequence of the T. tengcongensis genome. *Genome Res*. **12**, 689-700.
- Li W, Fang W, Ling L, Wang J, **Xuan Z**, Chen R (2002) Phylogeny Based on Whole Genome as inferred from Complete Information Set Analysis. *J. Biological Physics*. **28**, 439-447.
- International Human Genome Sequencing Consortium (2001) Initial sequencing and analysis of the human genome. *Nature* **409**, 860-921
- Xu H, Huang K, Qu X, Gao Z, Liu Q, Chen R, and **Xuan Z** (2001) Identification of selenocysteine insertion sequence (SECIS) element in eukaryotic selenoproteins by RNA Draw program, *Chinese Science Bulletin*, **46**, 1159-60.
- Xuan Z**, Chen R (2000) A new method for protein domain recognition, *Eur. Biophys. J.* **29**, 7-16.
- Yang C, Ling L, **Xuan Z**, Chen R (1999) EST contig assembly by computer. *Progress in Natural Science*, **9**, 812-817.
- Shen L, **Xuan Z**, Chen R (1999) The molecular modeling and electron density calculation of PrP^C and PrP^{SC}. *ACTA Biophysica SINICA*, **15**, 766-774.