

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:

02/2008-present Research Assistant Professor, Cold Spring Harbor Laboratory

- Develop bioinformatics tools to analyze next-generation sequencing data
- Detect genome variation from high-throughput data
- Refine promoter prediction with histone modification signal

10/2005-02/2008 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 re-sequencing.

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 (2007) *Bioinformatics Study in next-Generation Sequencing*, CSHL Bush-In-House lecture.

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

- 02/2008-present Manage CSHL bioinformatics shared resource of cancer center
- 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

Zhan L, Rosenberg A, Bergami KC, Yu M, **Xuan Z**, Jaffe AB, Allred C, Muthuswamy SK. (2008) Deregulation of scribble promotes mammary tumorigenesis and reveals a role for cell polarity in carcinoma. *Cell*. **135**:865-78.

Wang X*, **Xuan Z***, Zhao X, Li Y and Zhang MQ. (2008) High-resolution Human Core-promoter prediction with CoreBoost_HM. *Genome Res.* (In press) (* Equally contributed first author with W.X.).

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.).

Chen J, Kim YC, Jung YC, **Xuan Z**, Dworkin G, Zhang Y, Zhang MQ, Wang SM. (2008) Scanning the human genome at kilobase resolution. *Genome Res.***18**:751-762.

Murchison EP, Kheradpour P, Sachidanandam R, Smith C, Hodges E, **Xuan Z**, Kellis M, Grützner F, Stark A, Hannon GJ. (2008) Conservation of small RNA pathways in platypus. *Genome Res.* **18**(6):995-1004.

Wu Q, Kim YC, Lu J, **Xuan Z**, Chen J, Zheng Y, Zhou T, Zhang MQ, Wu CI, Wang SM. (2008) Poly A- transcripts expressed in HeLa cells. *PLoS ONE*. **3**(7):e2803.

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.).

Karginov FV, Conaco C, **Xuan Z**, Schmidt BH, Parker JS, Mandel G, Hannon GJ. (2007) A biochemical approach to identifying microRNA targets. *Proc Natl Acad Sci U S A*. **104**:19291-6.

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.