Curriculum Vitae

Kuo-Ping CHIU, PhD

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EDUCATION

Ph.D. (9/1985-3/1991) Microbiology, University of California at Davis, CA, USA
B.S. (9/1980-6/1984) Biology, Fu-Jen University, Taiwan ROC

PROFESSIONAL APPOINTMENTS:

Asso. Research Fellow (08/2008-present)	GRC, Academia Sinica, Taiwan
Joint Asso. Professor (08/2007-present)	Natl. Central University, Taiwan
Joint Asso. Professor (02/2011-present)	Natl. Taiwan University, Taiwan
Associate Professor (2008-present)	Natl. Yang-Ming University, Taiwan
Research Scientist (8/2002-8/2008)	Genome Institute of Singapore, Singapore
Principal Investigator (3/1999-3/2000)	Dev. Ctr. for Biotechnology, Taipei Taiwan
R&D Scientist (5/1996-4/1998)	Bio-Rad Laboratories, Hercules, CA USA
Postdoctoral Associate (2/1993-6/1996)	Harvard Medical School, Boston, MA USA

PATENTS

1. 2014/09/09 US 8829172. Kuo Ping Chiu et al. **Novel multiplex barcoded Paired-End Ditag (mbPED) sequencing approach and its application in fusion gene identification**.
2. 2013/06/03 US 8481699. Kuo Ping Chiu. **Multiplex barcoded Paired-End ditag (mbPED) library construction for ultra high throughput sequencing.**
3. 2013/04/23 US 8428882, Kuo-Ping Chiu et al. **Methods of processing and/or genome mapping of diTag sequences**.
4. 2014/12/15 Patent application. Kuo Ping Chiu and Yu-Shin Nai. **Methods for full-length amplification of double-stranded linear nucleic acids of unknown sequences**.

BOOK

Chiu, Kuo Ping. *Next-Generation Sequencing and Sequence Data Analysis.* Saif Zone, Sharjah, United Arab Emirates: Bentham Science Publishers, 2015.

BOOk CHAPTER

Chiu, Kuo Ping. Applications of Single Cell Sequencing in Cancer. In Fan-Gang Tseng and Tuhin Subhra Santra, *Essentials of Single Cell Analysis*. Heidelberg, Germany: Springer-Verlag GmbH, 2015.

PUBLICATIONS

1. Hong-Sen Chen, Shin-Chen Hou, Jhih-Wei Jian, King-Siang Goh, San-Tai Shen, Yu-Ching Lee, Jhong-Jhe You, Hung-Pin Peng, Wen-Chih Kuo, Shui-Tsung Chen, Ming-Chi Peng, Hwei-Jiung Wang, Chung-Ming Yu, Ing-Chien Chen, Chao-Ping Tung, Tzu-Han Chen, Kuo Ping Chiu, Che Ma, Chih Yuan Wu, Sheng-Wei Lin, and An-Suei Yang. **Predominant structural configuration of natural antibody repertoires enables potent antibody responses against protein antigens.** *Scientific Reports 2015 accepted.*

2. Yu-Feng Huang, Yu-Shin Nai, Mohit K. Midha, Tan-Chi Fan, Nai-Chuan Chang, Tzu-Han Chen, Ming-Ren Yeh, Chen-Yang Shen, Chien-Jen Chen, Alice L. Yu, and Kuo Ping Chiu. **Efficient amplification of trace amount of plasma DNA samples by T Oligo-Primed Polymerase Chain Reaction (TOP-PCR).** *In preparation*.

3. Yu-Feng Huang, Tzu-Han Chen, Yu-Tai Wong, David Glenn Smith, Kurtis Jai-Chyi Pei, and Kuo Ping Chiu. **Complete Taiwanese macaque (*Macaca cyclopis*) mitochondrial genome: reference-assisted *de novo* assembly with multiple-kmer strategy.** *PLoS One. 2015, Jun 30;10(6):e0130673. doi: 10.1371.*

4. Chiu, Kuo Ping. ***Next-Generation Sequencing and Sequence Data Analysis*.** Saif Zone, Sharjah, United Arab Emirates: Bentham Science Publishers, 2015.

5. Chiu, Kuo Ping. **Applications of Single Cell Sequencing in Cancer.** In Fan-Gang Tseng and Tuhin Subhra Santra, *Essentials of Single Cell Analysis*. Heidelberg, Germany: Springer-Verlag GmbH, 2015.

6. Chang, H.-J., J.-W. Jian, H.-J. Hsu, Y.-C. Lee, H.-S. Chen, J.-J. You, S.-C. Hou, C.-Y. Shao, Y.-J. Chen, K.-P. Chiu, H.-P. Peng, K. H. Lee and A.-S. Yang. **Loop sequence features and stability determinants in antibody variable domains by high throughput experiments.** *Structure 2014, 22:1-13.*

7. Hsu, H.-J., K. H. Lee, J.-W. Jian, H.-J. Chang, C.-M. Yu, Y.-C. Lee, I.-C. Chen, H.-P. Peng, C. Y. Wu, Y.-F. Huang, C.-Y. Shao, K. P. Chiu and A.-S. Yang. **Antibody variable domain interface and framework sequence requirements for stability and function by high throughput experiments.** *Structure 2014, 22:1-13*.

8. Yen-Ju Chen, Mike W.C. Thang, Yu-Tzu Chan, Yu-Feng Huang, Nianhan Ma, Alice L. Yu, Chung-Yi Wu, Miao-Lin Hu, and Kuo-Ping Chiu. **Global assessment of *Antrodia cinnamomea*-induced microRNA alterations in hepatocarcinoma cells.** *PLoS ONE 2013, 8(12):e82751.*

9. Yu-Tzu Chan, You-Chin Lin, Ruey-Jen Lin, Huan-Hsien Kuo, Wai-Cheng Thang, Kuo-Ping Chiu, and Alice Yu. **Concordant and discordant regulation of target genes by miR-31 and its isoforms.** *PLoS ONE* 2013, 83(3), e58169.

10. Yu-Feng Huang, Sheng-Chung Chen, Yih-Shien Chiang, Tzu-Han Chen, and Kuo Ping Chiu. **Palindromic sequence impedes sequencing-by-ligation mechanism.** *BMC Systems Biology* 2012, **6**(Suppl 2):S10.

11. Mohamed Sabry Hamza, Sebastian Pott, Vinsensius B. Vega, Jane S. Thomsen, Gopalan Srinivasan Kandhadayar, Patrick Ng, Kuo Ping Chiu, Sven Pettersson, Chia Lin Wei, Yijun Ruan, and Edison T. Liu. ***De-Novo* identification of PPARγ/RXR binding sites and direct targets during adipogenesis.** PLoS ONE 2009, 4(3): e4907. doi:10.1371/ journal.pone.0004907.

12. Melissa Fullwood, Jack Tan, Patrick Ng, Kuo Ping Chiu, Jun Liu, Chia Lin Wei, and Yijun Ruan. **The Use of Multiple Displacement Amplification to Amplify Complex DNA libraries.** *Nucleic Acid Research* 2008, doi:10.1093/nar/gkn074.

13. Kuo Ping Chiu. Review: **Novel Applications of the Paired-End diTag (PET) Technology in Pharmacogenomics.** *Current Pharmacogenomics and Personalized Medicine* 2008, 6:23-32.

14. Ching-Aeng Lim, Fei Yao, Joyce Jing-Yi Wong, Joshy George, Han Xu, Kuo Ping Chiu, Wing-Kin Sung, Leonard Lipovich, Vinsensius B. Vega, Joanne Chen, Atif Shahab, Xiao Dong Zhao, Martin Hibberd, Chia-Lin Wei, Bing Lim, Huck-Hui Ng, Yijun Ruan, and Keh-Chuang Chin. **Genome-wide Mapping of RELA(p65) Binding Identifies E2F1 as a Transcriptional Activator Recruited by NF-kB upon TLR4 Activation.** *Molecular Cell* 2007, 27(4):622-635.

15. Xiao Dong Zhao, Xu Han, Joon Lin Chew, Jun Liu, Kuo Ping Chiu, Andre Choo, Yuriy L. Orlov, Wing-Kin Sung, Atif Shahab, Vladimir A. Kuznetsov, Guillaume Bourque, Steve Oh, Yijun Ruan, Huck-Hui Ng, and Chia-Lin Wei. **Whole genome mapping of histone H3 Lys4 and 27 trimethylations reveals distinct genomic compartments in human embryonic stem cells.** *Cell Stem Cell* 2007, 1:286-298.

16. The ENCODE Project Consortium. **Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project.** *Nature* 2007, 447:799-816.

17. Chin-Yo Lin, Vinsensius B Vega, Jane S Thomsen, Tao Zhang, Say Li Kong, Min Xie, Kuo Ping Chiu, Leonard Lipovich, Daniel H Barnett, Fabio Stossi, Ailing Yeo, Joshy George, Vladimir A Kuznetsov, Yew Kok Lee, Tze Howe Charn, Nallasivam Palanisamy, Lance D Miller, Edwin Cheung, Benita S Katzenellenbogen, Yijun Ruan, Guillaume Bourque, Chia-Lin Wei, and Edison T Liu. **Whole-Genome Cartography of Estrogen Receptor alpha Binding Sites.** *PLoS Genet.* 2007, Jun 1;3(6):e87

18. Kuo Ping Chiu, Pramila Ariyaratne, Han Xu, Adrian Tan, Patrick Ng, Edison Tak-Bun Liu, Yijun Ruan, Chia-Lin Wei, and Wing-Kin Ken Sung. **Pathway**

aberrations of murine melanoma cells observed in Paired-End diTag transcriptomes. *BMC Cancer* 2007, 7:109.

19. Yijun Ruan, Hong Sain Ooi, Siew Woh Choo, Kuo Ping Chiu, Xiao Dong Zhao, K.G. Srinivasan, Fei Yao, Chiou Yu Choo, Jun Liu, Pramila Nuwantha, Wilson G. W. Bin, Vladimir A. Kuznetsov, Atif Shahab, Wing-Kin Sung, Guillaume Bourque, Nallasivam Palanisamy, and Chia-Lin Wei. **Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTag (PETs).** *Genome Research* 2007, 17:828-838.

20. Kuo Ping Chiu, Chee-Hong Wong, Qiongyu Chen, Pramila Ariyaratne, Hong Sain Ooi, Chia-Lin Wei, Wing-Kin Ken Sung, and Yijun Ruan. **PET-Tool: a software suite for comprehensive processing and managing of Paired-End diTag (PET) sequence data.** *BMC Bioinformatics* 2006, 7:390.

21. Patrick Ng, Jack J.S. Tan, Hong Sain Ooi, Yen Ling Lee, Kuo Ping Chiu, Melissa J. Fullwood, Clotilde Perbost, Lei Du, Wing-Kin Sung, Chia-Lin Wei, and Yijun Ruan. **Multiplex sequencing of Paired-End Ditag (MS-PET): a strategy for the ultra-high-throughput analysis of transcriptome and genomes.** *Nucleic Acid Research* 2006, 34(12):e84.

22. Karen I. Zeller, XiaoDong Zhao, Charlie W. H. Lee, Kuo Ping Chiu, Hong Sain Ooi, Fei Yao, Atif Shahab, How Choong Yong, YuTao Fu, Zhiping Weng, Vladimir A. Kuznetsov, Wing-Kin Sung, Yijun Ruan, Chi V. Dang, and Chia-Lin Wei. **Global mapping of c-Myc binding sites and target gene networks in human B cells.** *PNAS* 2006, 103:17834-17839.

23. Yuin-Han Loh, Qiang Wu, Joon-Lin Chew, Vinsensius B. Vega, Weiwei Zhang, Xi Chen, Guillaume Bourque, Joshy George, Bernard Leong, Jun Liu, Kee-Yew Wong, Ken W. Sung, Charlie W.H. Lee, Xiao-Dong Zhao, Kuo-Ping Chiu, Leonard Lipovich, Vladimir A. Kuznetsov, Paul Robson, Lawrence W. Stanton, Chia-Lin Wei, Yijun Ruan, Bing Lim, and Huck-Hui Ng. **The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells.** *Nature Genetics* 2006, 38:431-440.

24. Chia Lin Wei, Qiang Wu, Vinsensius B. Vega, Kuo Ping Chiu, Patrick Ng, Tao Zhang, Atif Shahab, Azmi Ridwan, YuTao Fu, Zhiping Weng, Jian Jun Liu, Vladimir A. Kuznetsov, Ken Sung, Bing Lim, Edison Liu, Qiang Yu, Huck Hui Ng, and Yijun Ruan. **A global mapping of p53 transcription factor binding sites in the human genome.** *Cell* 2006, 124:207-219.

25. The FANTOM3 Consortium. **The transcriptional landscape of the mammalian genome.** *Science* 2005, 309:1559-1563.

26. Patrick Ng, Chia Lin Wei, Wing-Kin Ken Sung, Kuo Ping Chiu, Leonard Lipovich, Chin Chin Ang, Sanjay Gupta, Atif Shahab, Chee Hong Wong, Azmi Ridwan, Edison T. Liu, and Yijun Ruan. **Gene identification signature (GIS)**

analysis for transcriptome characterization and genome annotation. *Nature Methods* 2005, 2: 105-111.

27. Chia Lin Wei, Patrick Ng, Kuo Ping Chiu, Chee Hong Wong, Chin Chin Ang, Leonard Lipovich, Edison T. Liu, and Yijun Ruan. **5' long serial analysis of gene expression (LongSAGE) and 3' LongSAGE for transcriptome characterization and genome annotation.** *PNAS USA* 2004, 101:11701-11706.

28. Yijun Ruan, Chia Lin Wei, Ai Ee Ling, Vinsensius B. Vega, Herve Thoreau, Yun Se Thoe Su, Jer-Ming Chia, Wei Pern Patrick Ng, Kuo Ping Chiu, Landri Lim, Tao Zhang, Kwai Peng Chan, Oon Lin Ean Lynette, Mah Lee Ng, Yee Sin Leo, Fong Poh Lisa Ng, Chee Ee Ren, W. Lawerence Stanton, M. Philip Long, and Tak Bun Edison Liu. **Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection.** *Lancet* 2003, 361:1779-1785.

29. Karen Duca, Kuo Ping Chiu, Thomas Sullivan, Steve A. Berman, and Sherry Bursztajn. **Nuclear clustering in myotubes: A proposed role in acetylcholine receptor mRNA expression.** *Biochimica et Biophysica Acta* 1998, 140:1-20.

30. Kuo Ping Chiu, Diana Davis, and Craig Hixson. **Antimicrobial susceptibility testing using flow cytometry.** Special ISAC edition. Purdue University Cytometry Laboratories. *The Purdue Cytometry CD-ROM* 1998, vol. 4.

31. Kuo Ping Chiu, Diana Davis, Fabio Frezzini, and Dwight Kirkpatrick. **Rapid assessment of cellular viability using flow cytometric assay.** Purdue University Cytometry Laboratories. *The Purdue Cytometry CD-ROM* 1996, vol. 2.

32. Kuo Ping Chiu, Thomas Sullivan, and Sherry Bursztajn. **Improved *in situ* hybridization: Color intensity enhancement procedure for the alkaline phosphatase/Fast Red system.** *BioTechniques* 1996, 20:964-968.

33. Kuo Ping Chiu, Karen Duca, Steve A. Berman, Thomas Sullivan, and Sherry Bursztajn. **A novel *in situ* double labeling method for simultaneous detection of mRNA and expressed protein or two different mRNAs.** *J. Neuroscience Methods* 1996, 66:69-79.

34. Kuo Ping Chiu, Steve H. Cohen, David W. Morris, and George W. Jordan. **Intracellular amplification of proviral DNA in tissue sections using the polymerase chain reaction.** *J. Histochemistry and Cytochemistry* 1992, 40:333-341.

PRESENTATIONS (2008 – 2013)

1. Invited speaker (2013/10/08): **Multiplex barcoded Paired-End Ditag (mbPED) for ultra high throughput sequencing**. In 3rd Annual Next Generation Sequencing Asia Congress, 8th & 9th October 2013, Singapore.

2. Selected oral presentation (2013/06/21): **Multiplex barcoded Paired-End Ditag (mbPED) for ultra high throughput NGS sequencing**. In Nucleic Acid Summit, June 19-21, 2013, San Francisco, California.

3. Invited speaker (2012/12/21): **What we have learned from the study of *Antrodia cinnamomea***. At Department of Food Science and Biotechnology, National Chung-Hsing University, Taichung, Taiwan.

4. Invited speaker (2012/12/13): **Palindromic sequence impedes sequencing-by-ligation mechanism**. In 23rd International Conference on Genome Informatics (GIW2012), to be held at National Cheng Kung University, Tainan, Taiwan.

5. Invited speaker (2012/09/20): **Multiplex barcoded Paired-End Ditag (mbPED) for ultra high throughput sequence data analysis**. In International Symposium of Root Systems Biology, held at Academia Sinica, Taipei, Taiwan.

6. Colloquium lecture (2011/03): **Single cell transcriptome analysis of MCF-7 breast cancer cell population**. At National Central University, ChungLi, Taiwan.

7. Oral presentation (2010/11): **Single cell transcriptome analysis of MCF7 breast cancer cell population using Next-Generation Sequencing. In Systems Biology and Bioinformatics Symposium**. At Tsing-Hua University, Taiwan.

8. Poster presentation (2010/10): **Single cell transcriptome analysis of MCF7 breast cancer cell population**. In 'Beyond the Genome' International Conference, held at Harvard Medical School, USA.

9. Oral presentation (2009/10): **Unraveling the mystery of gene expression and regulation/dysregulation by sequencing**. In 2nd Symposium on Molecular Medicine in Post-genomic Era, held in Taipei Taiwan.

10. Oral presentation (2009/10): **Applications of Next-Generation Sequencing technology on systems biology**. At National Chang Gung University, Taoyuan Taiwan.

11. Poster presentation (2008): **Analysis of the MCF-7 breast cancer transcriptome and effects of estrogen using an ultra-high-throughput Multiplex Sequencing-coupled Paired-End diTag (MS-PET) approach**. In Keystone Symposia, held in Keystone, Colorado USA.