

Curriculum Vitae

Yijun RUAN, PhD

Professor and Director of Genomic Sciences
The Jackson Laboratory for Genomic Medicine
The Department of Genetics and Developmental Biology
University of Connecticut
400 Farmington Avenue, Farmington, CT 06030
Office phone: 860.856.2474; Cell phone: 860.990.7382; Fax: 860.856.2398
Email: yijun.ruan@jax.org



AREA OF RESEARCH

My current research interest is to elucidate the topological structures of the human genome and the dynamic functions of all DNA regulatory elements. My strategy is to develop innovative genomic technologies and apply them to address fundamental questions pertinent to human disease. To this end, my main focus is on genome structural variations and their impact to genome regulatory functions in cancer and stem cells. I have also been interested in exploring metagenomic approaches to understand microbial populations involved in human health.

EDUCATION

1990-1994 PhD in Plant Molecular Biology, University of Maryland, College Park, Maryland, USA
1982-1985 MS in Microbiology, Huazhong Agricultural University, Wuhan, China
1978-1982 BS in Microbiology, Huazhong Agricultural University, Wuhan, China

PROFESSIONAL APPOINTMENTS:

2012- Professor and Director for Genomic Sciences, Jackson Lab, Farmington, CT06032
2012- Professor, Department of Genetics and Developmental Biology, University of Connecticut
2006-2012 Professor, National University of Singapore
2003-2012 Associate Director for Genome Technologies, Genome Institute of Singapore
2002-2012 Senior Group Leader, Genome Technology and Biology, Genome Institute of Singapore
1999-2002 Director, Core Genomics and Applications; Large Scale Biology Corporation, Vacaville, California, USA
1996-1999 Senior Scientist, Genome Technology, Monsanto Company, St. Louis, Missouri, USA
1995-1996 Post-doctoral Fellow, Gene Discovery and Gene Expression, Monsanto Company, St Louis, Missouri, USA
1990-1995 Graduate Research Assistant, Department of Plant Molecular Biology, University of Maryland, College Park, Maryland, USA

HONORS AND SERVICES

1. National Science Award, Singapore, 2006
2. Rockefeller Foundation Fellowship (1998-2001)
3. Carroll E. Cox Graduate Research Excellence Award, University of Maryland, 1995
4. China “One Thousand Talents” Award, 2012
5. Editorial board member, Cell Reports, 2012 – present

PUBLICATIONS

2013

1. Kieffer-Kwon KR, Tang Z, Mathe E, Qian J, Sung MH, Li G, Resch W, Baek S, Pruett N, Grøntved L, Vian L, Nelson S, Zare H, Hakim O, Reyon D, Yamane A, Nakahashi H, Kovalchuk AL, Zou J, Joung JK, Sartorelli V, Wei CL, Ruan X, Hager GL, **Ruan Y**, Casellas R. 2013. Interactome maps of mouse gene regulatory domains reveal basic principles of transcriptional regulation. *Cell*. 155(7):1507-20.
2. Chen D, Fu LY, Zhang Z, Li G, Zhang H, Jiang L, Harrison AP, Shanahan HP, Klukas C, Zhang HY, **Ruan Y**, Chen LL, Chen M. 2012. Dissecting the chromatin interactome of microRNA genes. *Nucleic Acids Res*. 2013 Dec 18.
3. Zhang Y, Wong CH, Birnbaum RY, Li G, Favaro R, Ngan CY, Lim J, Tai E, Poh HM, Wong E, Mulawadi FH, Sung WK, Nicolis S, Ahituv N, **Ruan Y**, Wei CL. 2013. Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. *Nature*. 504(7479):306-10. doi: 10.1038/nature12716.
4. Mercer TR, Edwards SL, Clark MB, Neph SJ, Wang H, Stergachis AB, John S, Sandstrom R, Li G, Sandhu KS, **Ruan Y**, Nielsen LK, Mattick JS, Stamatoyannopoulos JA. 2013. DNase I-hypersensitive exons colocalize with promoters and distal regulatory elements. *Nature Genetics*. 45(8):852-9. doi: 10.1038/ng.2677. Epub 2013 Jun 23.
5. Wang X, Zhao Z, Muller J, Iyu A, Khng AJ, Guccione E, **Ruan Y**, Ingham PW. (2013) Targeted inactivation and identification of targets of the Gli2a transcription factor in the zebrafish. *Biol Open*. 2(11):1203-13. doi: 10.1242/bio.20136262. eCollection 2013.

2012

6. Nagarajan N, Bertrand D, Hillmer AM, Zang ZJ, Yao F, Jacques PE, Teo AS, Cutcutache I, Zhang Z, Lee WH, Sia YY, Gao S, Ariyaratne PN, Ho A, Woo XY, Veeravali L, Ong CK, Deng N, Desai KV, Khor CC, Hibberd ML, Shahab A, Rao J, Wu M, Teh M, Zhu F, Chin SY, Pang B, So JB, Bourque G, Soong R, Sung WK, Tean Teh B, Rozen S, Ruan X, Yeoh KG, Tan PB, Ruan Y. (2012) Whole-genome reconstruction and mutational signatures in gastric cancer. *Genome Biol*. 13(12):R115. [Epub ahead of print]
7. Xu Q, Chen LL, Ruan X, Chen D, Zhu A, Chen C, Bertrand D, Jiao WB, Hao BH, Lyon MP, Chen J, Gao S, Xing F, Lan H, Chang JW, Ge X, Lei Y, Hu Q, Miao Y, Wang L, Xiao S, Biswas MK, Zeng W, Guo F, Cao H, Yang X, Xu XW, Cheng YJ, Xu J, Liu JH, Luo OJ, Tang Z, Guo WW, Kuang H, Zhang HY, Roose ML, Nagarajan N, Deng XX, **Ruan Y*** (2012) The draft genome of sweet orange (*Citrus sinensis*). *Nature Genetics* 2012 Nov 25. doi: 10.1038/ng.2472. [Epub ahead of print]
8. Papanonis A, Kohro T, Baboo S, Larkin JD, Deng B, Short P, Tsutsumi S, Taylor S, Kanki Y, Kobayashi M, Li G, Poh HM, Ruan X, Aburatani H, Ruan Y, Kodama T, Wada Y, Cook PR. (2012) TNF α signals through specialized factories where responsive coding and miRNA genes are transcribed. *EMBO J*. 31(23):4404-14. doi: 10.1038/emboj.2012.288. Epub 2012 Oct 26.
9. Sandhu KS, Li G, Poh HM, Quek YL, Sia YY, Peh SQ, Mulawadi FH, Lim J, Sikic M, Menghi F, Thalamuthu A, Sung WK, Ruan X, Fullwood MJ, Liu E, Csermely P, **Ruan Y*** (2012) Large-Scale Functional Organization of Long-Range Chromatin Interaction Networks. *Cell Reports* 2012 Oct 24. pii: S2211-1247(12)00326-9. doi: 10.1016/j.celrep.2012.09.022. [Epub ahead of print]
10. Lim JQ, Tennakoon C, Li G, Wong E, Ruan Y, Wei CL, Sung WK. (2012) BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. *Genome Biol*. 13(10): R82.

11. Yao F, Ariyaratne PN, Hillmer AM, Lee WH, Li G, Teo AS, Woo XY, Zhang Z, Chen JP, Poh WT, Zawack KF, Chan CS, Leong ST, Neo SC, Choi PS, Gao S, Nagarajan N, Thoreau H, Shahab A, Ruan X, Cacheux-Rataboul V, Wei CL, Bourque G, Sung WK, Liu ET, **Ruan Y*** (2012) Long span DNA paired-end-tag (DNA-PET) sequencing strategy for the interrogation of genomic structural mutations and fusion-point-guided reconstruction of amplicons. *PLoS One*. 7(9): e46152. doi: 10.1371/journal.pone.0046152.
12. Ohta Y, Nishiyama A, Wada Y, Ruan Y, Kodama T, Tsuboi T, Tokihiro T, Ihara S. (2012) Path-preference cellular-automaton model for traffic flow through transit points and its application to the transcription process in human cells. *Phys Rev E Stat Nonlin Soft Matter Phys*. 86(2 Pt 1): 021918. Epub 2012 Aug 21.
13. Derrien T, Johnson R, Bussotti G, Tanzer A, Djebali S, Tilgner H, Guernec G, Martin D, Merkel A, Knowles DG, Lagarde J, Veeravalli L, Ruan X, Ruan Y, Lassmann T, Carninci P, Brown JB, Lipovich L, Gonzalez JM, Thomas M, Davis CA, Shiekhata R, Gingeras TR, Hubbard TJ, Notredame C, Harrow J, Guigó R. (2012) The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. *Genome Res*. 2012 Sep;22(9):1775-89. doi: 10.1101/gr.132159.111.
14. Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Cheng C, Alexander R, Min R, Leng J, Yip KY, Rozowsky J, Yan KK, Dong X, Djebali S, Ruan Y, Davis CA, Carninci P, Lassman T, Gingeras TR, Guigó R, Birney E, Weng Z, Snyder M, Gerstein M. *Genome Res*. 2012 Sep;22(9):1658-67. doi: 10.1101/gr.136838.111.
15. Djebali S, Davis CA, Merkel A, Dobin A, Lassmann T, Mortazavi A, Tanzer A, Lagarde J, Lin W, Schlesinger F, Xue C, Marinov GK, Khatun J, Williams BA, Zaleski C, Rozowsky J, Röder M, Kokocinski F, Abdelhamid RF, Alioto T, Antoshechkin I, Baer MT, Bar NS, Batut P, Bell K, Bell I, Chakraborty S, Chen X, Chrast J, Curado J, Derrien T, Drenkow J, Dumais E, Dumais J, Duttagupta R, Falconnet E, Fastuca M, Fejes-Toth K, Ferreira P, Foissac S, Fullwood MJ, Gao H, Gonzalez D, Gordon A, Gunawardena H, Howald C, Jha S, Johnson R, Kapranov P, King B, Kingswood C, Luo OJ, Park E, Persaud K, Preall JB, Ribeca P, Risk B, Robyr D, Sammeth M, Schaffer L, See LH, Shahab A, Skancke J, Suzuki AM, Takahashi H, Tilgner H, Trout D, Walters N, Wang H, Wrobel J, Yu Y, Ruan X, Hayashizaki Y, Harrow J, Gerstein M, Hubbard T, Reymond A, Antonarakis SE, Hannon G, Giddings MC, Ruan Y, Wold B, Carninci P, Guigó R, Gingeras TR. (2012) Landscape of transcription in human cells. *Nature*. 2012 Sep 6;489(7414):101-8. doi: 10.1038/nature11233.
16. ENCODE Project Consortium, Bernstein BE, Birney E, Dunham I, Green ED, Gunter C, Snyder M. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012 Sep 6;489(7414):57-74. doi: 10.1038/nature11247.
17. Zhang J, Poh HM, Peh SQ, Sia YY, Li G, Mulawadi FH, Goh Y, Fullwood MJ, Sung WK, Ruan X, **Ruan Y*** (2012). ChIA-PET analysis of transcriptional chromatin interactions. *Methods*. 2012 Nov;58(3):289-99. doi: 10.1016/j.ymeth.2012.08.009. Epub 2012 Aug 25.
18. Goh Y, Fullwood MJ, Poh HM, Peh SQ, Ong CT, Zhang J, Ruan X, **Ruan Y***. (2012) Chromatin Interaction Analysis with Paired-End Tag Sequencing (ChIA-PET) for mapping chromatin interactions and understanding transcription regulation. *J Vis Exp*. 2012 Apr 30;(62). pii: 3770. doi: 10.3791/3770.
19. Chen Y, Negre N, Li Q, Mieczkowska JO, Slattery M, Liu T, Zhang Y, Kim TK, He HH, Zieba J, Ruan Y, Bickel PJ, Myers RM, Wold BJ, White KP, Lieb JD, Liu XS. (2012) Systematic evaluation of factors influencing ChIP-seq fidelity. *Nature Methods*. 2012 Jun;9(6):609-14. doi: 10.1038/nmeth.1985. Epub 2012 Apr 22.

20. Zang ZJ, Cutcutache I, Poon SL, Zhang SL, McPherson JR, Tao J, Rajasegaran V, Heng HL, Deng N, Gan A, Lim KH, Ong CK, Huang D, Chin SY, Tan IB, Ng CC, Yu W, Wu Y, Lee M, Wu J, Poh D, Wan WK, Rha SY, So J, Salto-Tellez M, Yeoh KG, Wong WK, Zhu YJ, Futreal PA, Pang B, **Ruan Y**, Hillmer AM, Bertrand D, Nagarajan N, Rozen S, Teh BT, Tan P. (2012) Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. *Nature Genetics*. 2012 May;44(5):570-4. doi: 10.1038/ng.2246.
21. Ng KP, Hillmer AM, Chuah CT, Juan WC, Ko TK, Teo AS, Ariyaratne PN, Takahashi N, Sawada K, Fei Y, Soh S, Lee WH, Huang JW, Allen JC Jr, Woo XY, Nagarajan N, Kumar V, Thalamuthu A, Poh WT, Ang AL, Mya HT, How GF, Yang LY, Koh LP, Chowbay B, Chang CT, Nadarajan VS, Chng WJ, Than H, Lim LC, Goh YT, Zhang S, Poh D, Tan P, Seet JE, Ang MK, Chau NM, Ng QS, Tan DS, Soda M, Isobe K, Nöthen MM, Wong TY, Shahab A, Ruan X, Cacheux-Rataboul V, Sung WK, Tan EH, Yatabe Y, Mano H, Soo RA, Chin TM, Lim WT, **Ruan Y***, Ong ST*. (2012) A common BCL2L1 deletion polymorphism mediates intrinsic resistance and inferior responses to tyrosine kinase inhibitors in cancer. *Nature Medicine* 18(4): 521-528
22. Guoliang Li, Xiaohan Ruan, Raymond K. Auerbach, Kuljeet Singh Sandhu, Meizhen Zheng, Ping Wang, Huay Mei Poh, Yufen Goh, Joanne Lim, Jingyao Zhang, Hui Shan Sim, Su Qin Peh, Fabianus Hendriyan Mulawadi, Chin Thing Ong, Yuriy L. Orlov, Shuzhen Hong, Zhizhuo Zhang, Steve Landt, Debasish Raha, Ghia Euskirchen, Chia-Lin Wei, Weihong Ge, Huaien Wang, Carrie Davis, Katherine Fisher, Ali Mortazavi, Mark Gerstein, Thomas Gingeras, Barbara Wold, Yi Sun, Melissa J. Fullwood, Edwin Cheung, Edison Liu, Wing-Kin Sung, Michael Snyder, **Yijun Ruan*** (2012) Extensive Promoter-centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. *Cell* 148: 84-98
23. Ruan X, Ruan Y. (2012) Genome wide full-length transcript analysis using 5' and 3' paired-end-tag next generation sequencing (RNA-PET). *Methods Mol Biol*. 2012;809:535-62. doi: 10.1007/978-1-61779-376-9_35.

2011

24. Lusy Handoko, Han Xu, Guoliang Li, Chew Yee Ngan, Elaine Chew, Charlie Wah Heng Lee, Chaopeng Ye, Eleanor Wong, Yubo Zhang, Fabianus Mulawadi, Jianpeng Sheng, Thompson Poh, Chee Seng Chan, Galih Kunarso, Atif Shahab, Guillaume Bourque, Valere Cacheux-Rataboul, Wing-Kin Sung, **Yijun Ruan***, Chia-Lin Wei* (2011) Functional Genome Architecture Revealed by CTCF-Associated Chromatin Interactome in Pluripotent Cells. *Nature Genetics* 43: 630–638 (June 19, 2011)
25. Ng TF, Willner DL, Lim YW, Schmieder R, Chau B, Nilsson C, Anthony S, **Ruan Y**, Rohwer F, Breitbart M. (2011) Broad surveys of DNA viral diversity obtained through viral metagenomics of mosquitoes *PLoS One*. 6(6):e20579. doi: 10.1371/journal.pone.0020579. Epub 2011 Jun 6.
26. ENCODE Project Consortium. (2011) A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biol*. 9(4): e1001046. doi: 10.1371/journal.pbio.1001046. Epub 2011 Apr 19.
27. Kuljeet Singh Sandhu, Guoliang Li, Wing-Kin Sung, **Yijun Ruan*** (2011) Chromatin Interaction Networks and Higher Order Architectures of Eukaryotic Genomes (Prospects). *Journal of Cellular Biochemistry* 112, 2218-2221
28. Axel M. Hillmer, Yao Fei1, Koichiro Inaki, Wah Heng Lee, Pramila N. Ariyaratne, Audrey S.M. Teo, Xing Yi Woo, Zhenshui Zhang, Zhao Hao, Leena Ukil, Jieqi P. Chen, Zhu Feng, Jimmy B.Y. So, Manuel Salto-Tellez, Wan Ting Poh, Kelson F.B. Zawack, Hui Ping J. Lim, Yee Yen Sia, Chee Seng Chan, See Ting Leong, Say Chuan Neo, Poh Sum D. Choi, Hervé Thoreau, Patrick B.O. Tan, Atif Shahab, Xiaohan Ruan, Jonas Bergh, Per Hall, Valère Cacheux-Rataboul, Chia-Lin Wei, Khay

- Guan Yeoh, Wing-Kin Sung, Guillaume Bourque, Edison T. Liu, **Yijun Ruan*** (2011) Comprehensive Long Span Paired-End-Tag Mapping Reveals Characteristic Patterns of Structural Variations in Epithelial Cancer Genomes. *Genome Research* 21 (5): 665-675 (May 01, 2011)
29. Koichiro Inaki, Axel Hillmer, Leena Ukil, Fei Yao, Xing Yi Woo, Leah Vardy, Kelson Folkvard Braaten Zawack, Charlie Wah Heng Lee, Pramila Nuwantha Ariyaratne, Yang Sun Chan, Kartiki Vasant Desai, Jonas Bergh, Per Hall, Thomas Choudary Putti, Wai Loon Ong, Atif Shahab, Valere Cacheux-Rataboul, Radha Krishna Murthy Karuturi, Wing-Kin Sung, Xiaoan Ruan, Guillaume Bourque, **Yijun Ruan**, Edison T. Liu. (2011) Transcriptional Consequences of Genomic Structural Aberrations in Breast Cancer. *Genome Research* 21 (5): 676-687 (May 01, 2011)
30. **Yijun Ruan** (2011) Genome-sequencing anniversary. Presenting the human genome: now in 3D! *Science* 2011 Feb 25; 331(6020): 1025-6. doi: 10.1126/science.1203602.
31. Edwin Cheung and **Yijun Ruan*** (2011) Determination of transcription factor binding. *Nature Genetics* 43: 11-12 (January 2011)

2010

32. Joseph R, Orlov YL, Huss M, Sun W, Kong SL, Ukil L, Pan YF, Li G, Lim M, Thomsen JS, Ruan Y, Clarke ND, Prabhakar S, Cheung E, Liu ET. (2010) Integrative model of genomic factors for determining binding site selection by estrogen receptor- α . *Mol Syst Biol*. 2010 Dec 21;6:456. doi: 10.1038/msb.2010.109.
33. Phillips Yao Hui Huang, Yuyuan Han, Lusy Handoko, Stoyan Velkov, Eleanor Wong, Edwin Cheung, Xiaoan Ruan, Chia-Lin Wei, Melissa Jane Fullwood*, **Yijun Ruan***. (2011) Protocol: Sonication-based Circular Chromosome Conformation Capture with nextgeneration sequencing analysis for the detection of chromatin interactions. *Nature Protocol* (December 14, 2010) doi:10.1038/protex.2010.207
34. Hao Wu, Jifang Tao, Pauline J. Chen , Atif Shahab, Weihong Ge, Ronald P. Hart, Xiaoan Ruan, **Yijun Ruan**, Yi E. Sun (2010) Systematic screening identifies microRNAs dys-regulated in a mouse model of Rett syndrome. *PNAS* 107 (42) 18161-18166 (ahead of print October 4, 2010, doi:10.1073/pnas.1005595107)
35. **Ruan Y**, Wei CL. (2010) Multiplex parallel pair-end-ditag sequencing approaches in system biology. *Wiley Interdiscip Rev Syst Biol Med*. 2010 Mar-Apr;2(2):224-34. doi: 10.1002/wsbm.40. Review.
36. The International Cancer Genome Consortium (2010). International network of cancer genome projects. *Nature* 464, 993-998.
37. Nandi T, Ong C, Singh AP, Boddey J, Atkins T, Sarkar-Tyson M, Essex-Lopresti AE, Chua HH, Pearson T, Kreisberg JF, Nilsson C, Ariyaratne P, Ronning C, Losada L, **Ruan Y**, Sung WK, Woods D, Titball RW, Beacham I, Peak I, Keim P, Nierman WC, Tan P. (2010). A genomic survey of positive selection in *Burkholderia pseudomallei* provides insights into the evolution of accidental virulence. *PLoS Pathog*. 6(4): e1000845.
38. Guoliang Li, Melissa J. Fullwood, Han Xu, Fabianus Hendriyan Mulawadi, Stoyan Velkov, Vinsensius B Vega S N, Pramila Nuwantha Ariyaratne, Yusoff Bin Mohamed, Hong-Sain Ooi, Chandana Tennakoon, Chia-Lin Wei1, **Yijun Ruan***, Wing-Kin Sung* (2010). ChIA-PET Tool: A comprehensive software for chromatin interaction analysis with paired-end-tag sequencing. *Genome Biology* 11:R22
39. Melissa J. Fullwood, Yuyuan Han, Chia-Lin Wei, Xiaoan Ruan, **Yijun Ruan*** (2010). Chromatin Interaction Analysis using Paired-End Tag Sequencing. *Current Protocols in Molecular Biology*: Chapter 21: Unit 21.15.1-25.

40. Stefan Schoenfelder, Tom Sexton, Lyubomira Chakalova, Nathan F. Cope, Alice Horton, Simon Andrews, Sreenivasulu Kurukuti, Jennifer A. Mitchell, David Umlauf, Daniela S. Dimitrova, Christopher H. Eskiw, Yanquan Luo, Chia-Lin Wei, **Yijun Ruan**, James J. Bieker, and Peter Fraser (2010). Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. Nature Genetics 42: 53-62.

2009

41. Melissa J. Fullwood, Mei Hui Liu, You Fu Pan, Jun Liu, Xu Han, Yusoff Bin Mohamed, Yuriy L. Orlov, Stoyan Velkov, Andrea Ho, Poh Huay Mei, Elaine G. Y. Chew, Phillips Yao Hui Huang, Willem-Jan Welboren, Yuyuan Han, Hong-Sain Ooi, Pramila N. Ariyaratne, Vinsensius B. Vega, Yanquan Luo, Peck Yean Tan, Pei Ye Choy, K. D. Senali Abayratna Wansa, Bing Zhao, Kar Sian Lim, Shi Chi Leow, Jit Sin Yow, Roy Joseph, Haixia Li, Kartiki V. Desai, Jane S. Thomsen, Yew Kok Lee, R. Krishna Murthy Karuturi, Thoreau Herve, Guillaume Bourque, Hendrik G. Stunnenberg, Xiaoran Ruan, Valere Cacheux-Rataboul, Wing-Kin Sung, Edison T. Liu, Chia-Lin Wei, Edwin Cheung, and **Yijun Ruan*** (2009). An oestrogen-receptor- α -bound human chromatin interactome. Nature 462: 58-64.
42. The Schistosoma japonicum Genome Sequencing and Functional Analysis Consortium, Yan Zhou, Huajun Zheng, Yangyi Chen, Lei Zhang, Kai Wang, Jing Guo, Zhen Huang, Bo Zhang, Wei Huang, Ke Jin, Tonghai Dou, Masami Hasegawa, Li Wang, Yuan Zhang, Jie Zhou, Lin Tao, Zhiwei Cao, Yixue Li, Tomas Vinar, Brona Brejova, Dan Brown, Ming Li, David J. Miller, David Blair, Yang Zhong, Zhu Chen, Feng Liu, Wei H7, Zhi-Qin Wang, Qin-Hua Zhang, Huai-Dong Song, Saijuan Chen, Xuenian Xu, Bin Xu, Chuan Ju, Yucheng Huang, Paul J. Brindley, Donald P. McManus, Zheng Feng, Ze-Guang Han, Gang Lu, Shuangxi Ren, Yuezhu Wang, Wenyi Gu, Hui Kang, Jie Chen, Xiaoyun Chen, Shuting Chen, Lijun Wang, Jie Yan, Biyun Wang, Xinyan Lv, Lei Jin, Bofei Wang, Shiyin Pu, Xianglin Zhang, Wei Zhang, Qiuping Hu, Genfeng Zhu, Jun Wang, Jun Yu1, Jian Wang, Huanming Yang, Zemin Ning, Matthew Beriman, Chia-Lin Wei, **Yijun Ruan**, Guoping Zhao, Shengyue Wang (2009) The Schistosoma japonicum genome reveals features of host–parasite interplay. Nature 460: 345-351.
43. Rosario K, Nilsson C, Lim YW, **Ruan Y**, Breitbart M. (2009) Metagenomic analysis of viruses in reclaimed water. Environmental Microbiology 11: 2806–2820.
44. Hillmer AM, Freudenberg J, Myles S, Herms S, Tang K, Hughes DA, Brockschmidt FF, **Ruan Y**, Stoneking M, Nöthen MM (2009). Recent positive selection of a human androgen receptor/ectodysplasin A2 receptor haplotype and its relationship to male pattern baldness. Hum Genet. 2009 Aug; 126(2):255-64.
45. Melissa J. Fullwood, Chia Lin Wei, Edison T. Liu, and **Yijun Ruan*** (2009) Next-Generation DNA Sequencing of Paired End diTags for Transcriptome and Genome Analysis (Review) Genome Research 19: 521-532.
46. Hamza MS, Pott S, Vega VB, Thomsen JS, Kandhadayar GS, Ng PW, Chiu KP, Pettersson S, Wei CL, **Ruan Y**, Liu ET (2009). De-novo identification of PPAR γ /RXR binding sites and direct targets during adipogenesis. PLoS One. 4(3):e4907.
47. Melissa Fullwood and **Yijun Ruan*** (2009) ChIP-based methods for the identification of long-range chromatin interactions. J. Cellular Biochemistry 107: 30-39.
48. Chia-Lin Wei and **Yijun Ruan** (2009). Transcriptome and Genome Characterization Using Massively Parallel Paired End Tag (PET) Sequencing Analysis, Cap-Analysis Gene Expression (CAGE): The Science of Decoding Gene Transcription 978-981-4241-34-2

2008

49. Bourque G, Leong B, Vega VB, Chen X, Lee YL, Srinivasan KG, Chew JL, **Ruan Y**, Wei CL, Ng HH, Liu ET (2008). Evolution of the mammalian transcription factor binding repertoire via transposable elements. Genome Research 18(11):1752-62.
50. Zhao X, **Ruan Y**, Wei CL (2008). Tackling the epigenome in the pluripotent stem cells. J Genet Genomics. 35(7): 403-12. Review
51. Xi Chen, Han Xu, Ping Yuan, Fang Fang, Mikael Huss, Vinsensius B. Vega, Eleanor Wong, Yuriy L. Orlov, Weiwei Zhang, Jianming Jiang, Yuin-Han Loh, Hock Chuan Yeo, Zhen Xuan Yeo, Vipin Narang, Kunde Ramamoorthy Govindarajan, Bernard Leong, Atif Shahab, **Yijun Ruan**, Guillaume Bourque, Wing-Kin Sung, Neil D. Clarke, Chia-Lin Wei, and Huck-Hui Ng (2008) Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. Cell 133: 1106-1117.
52. Susannah G. Tringe, Tao Zhang, Xuguo Liu, Yiting Yu, Wah Heng Lee, Jennifer Yap, Fei Yao, Sim Tiow Suan, Seah Keng Ing, Matthew Haynes, Forest Rohwer, Chia Lin Wei, Patrick Tan, James Bristow, Edward M. Rubin, **Yijun Ruan*** (2008) The Airborne Metagenome in an Indoor Urban Environment. PLoS One 3(4): e1862
53. Melissa J. Fullwood, Jack J. S. Tan, Patrick W. P. Ng, Kuo Ping Chiu, Liu Jun, Chia Lin Wei, and **Yijun Ruan*** (2008). The use of multiple displacement amplification to amplify complex DNA libraries. Nucleic Acid Research (doi:10.1093/nar/gkn074).
54. Elizabeth A. Dinsdale, Robert A. Edwards, Dana Hall1, Florent Angly, Mya Breitbart, Jennifer M. Brulc, Mike Furlan, Christelle Desnues, Matthew Haynes1, Linlin Li1, Lauren McDanie, Mary Ann Moran, Karen E. Nelson, Christina Nilsson, Robert Olson, John Paul, Beltran Rodriguez Brito, **Yijun Ruan**, Brandon K. Swan, Rick Stevens, David L. Valentine, Rebecca Vega Thurber, Linda Wegley, Bryan A. White, Forest Rohwer (2008) Functional metagenomic profiling of nine biomes Nature 452: 629-632.
55. Christelle Desnues, Beltran Rodriguez-Brito, Steve Rayhawk, Scott Kelley, Tuong Tran, Matthew Haynes, Hong Liu, Mike Furlan, Linda Wegley, Betty Chau, **Yijun Ruan**, Dana Hall, Florent E. Angly, Robert A. Edwards, Linlin Li, Rebecca Vega Thurber, R. Pamela Reid, Janet Siefert, Valeria Souza, David L. Valentine, Brandon K. Swan, Mya Breitbart, Forest Rohwer (2008) Biodiversity and biogeography of phages in modern stromatolites and thrombolites. Nature 452: 340-343.

2007

56. Kuznetsov VA, Orlov YL, Wei CL, **Ruan Y** (2007). Computational analysis and modeling of genome-scale avidity distribution of transcription factor binding sites in chip-pet experiments. Genome Inform. 19: 83-94.
57. Ng P, Wei CL, **Ruan Y*** (2007). Paired-end diTagging for transcriptome and genome analysis. Curr Protoc Mol Biol. Chapter 21: Unit 21.12.
58. 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 (2007) Whole-Genome Mapping of Histone H3 Lys4 and 27 Trimethylations Reveals Distinct Genomic Compartments in Human Embryonic Stem Cells. Cell Stem Cell 1 (3): 286-298.
59. Lim CA, Yao F, Wong JJ, George J, Xu H, Chiu KP, Sung WK, Lipovich L, Vega VB, Chen J, Shahab A, Zhao XD, Hibberd M, Wei CL, Lim B, Ng HH, **Ruan Y***, Chin KC*. (2007) Genome-wide Mapping of RELA (p65) Binding Identifies E2F1 as a Transcriptional Activator Recruited by NF-kappaB upon TLR4 Activation. Mol Cell 27(4): 622-35.

60. Chiu KP, Ariyaratne P, Xu H, Tan A, Ng P, Liu ET, **Ruan Y**, Wei CL, Sung WK. (2007) Pathway aberrations of murine melanoma cells observed in Paired-End diTag transcriptomes. *BMC Cancer* 7: 109 (doi: 10.1186/1471-2407-7-109).
61. ENCODE (2007) Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature* 447 (7146): 799-816.
62. Euskirchen GM, Rozowsky JS, Wei CL, Lee WH, Zhang ZD, Hartman S, Emanuelsson O, Stolc V, Weissman S, Gerstein MB, **Ruan Y**, Snyder M. (2007) Mapping of transcription factor binding regions in mammalian cells by ChIP: comparison of array- and sequencing-based technologies. *Genome Research* 17(6): 898-909.
63. Zheng D, Frankish A, Baertsch R, Kapranov P, Reymond A, Choo SW, Lu Y, Denoeud F, Antonarakis SE, Snyder M, **Ruan Y**, Wei CL, Gingeras TR, Guigo R, Harrow J, Gerstein MB. (2007) Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. *Genome Research* 17(6): 839-851.
64. **Ruan Y***, Ooi HS, Choo SW, Chiu KP, Zhao XD, Srinivasan KG, Yao F, Choo CY, Liu J, Ariyaratne P, Bin WG, Kuznetsov VA, Shahab A, Sung WK, Bourque G, Palanisamy N, Wei CL. (2007) Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). *Genome Research* 17(6): 828-838.
65. Lin CY, Vega VB, Thomsen JS, Zhang T, Kong SL, Xie M, Chiu KP, Lipovich L, Barnett DH, Stossi F, Yeo A, George J, Kuznetsov VA, Lee YK, Charn TH, Palanisamy N, Miller LD, Cheung E, Katzenellenbogen BS, **Ruan Y**, Bourque G, Wei CL, Liu ET. (2007) Whole-genome cartography of estrogen receptor alpha binding sites. *PLoS Genet.* 3(6): e87

2006

66. Hibberd ML, Ling L, Tolfvenstam T, Mitchell W, Wong C, Kuznetsov VA, George J, Ong SH, **Ruan Y**, Wei CL, Gu F, Fink J, Yip A, Liu W, Schreiber M, Vasudevan SG. (2006). A genomics approach to understanding host response during dengue infection. *Novartis Found Symp.* 277: 206-214.
67. 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 (2006) Global Mapping of c-Myc Binding Sites and Target Gene Networks in Human B Cells. *Proc Natl Acad Sci USA.* 103: 17834-17839.
68. Kuo Ping Chiu, Chee-Hong Wong, Qiong Yu Chen, Chia Lin Wei, Wing-Kin Sung, and **Yijun Ruan*** (2006) PET-Tool: A Software Suite for Comprehensive Processing and Managing of Paired-End diTag Sequence Data. *BMC Bioinformatics* 7: 390 (doi:10.1186/1471-2105-7-390).
69. Patrick Ng, Jack J.S. Tan, K.-P. Chiu, H.S. Ooi, Y.L. Lee, Melissa J. Fullwoods, Lie Du, W.-K. Sung, Chia Lin Wei, **Yijun Ruan*** (2006) Multiplex Sequencing of Paired-End diTag for Human Transcriptome and Genome Characterization. *Nucleic Acid Research* 34: No. 12, e84.
70. Patrick Ng, Chia Lin Wei, **Yijun Ruan*** (2006) Paired-End diTagging for Transcriptome and Genome Analysis. *Current Protocols in Molecular Biology* UNIT 21.12.
71. Yui-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, Leonard Lipovich, Vladimir A. Kuznetsov, Paul Robson, Lawrence W. Stanton, Chia-Lin Wei, **Yijun Ruan***, Bing Lim, Huck-Hui Ng*, (2006) The Oct4 and Nanog transcription network that regulates pluripotency in mouse embryonic stem cells. *Nature Genetics* 38: 431-440.
72. Chia Lin Wei, Qiang Wu, Vinsensius Vega, Kuo Ping Chiu, Patrick Ng, Tao Zhang, Atif Shahab, How Choong Yong, YuTao Fu, Zhiping Weng, Jian Jun Liu, XiaoDong Zhao, Yen Ling Lee,

Vladimir A. Kuznetsov, Ken Sung, Bing Lim, Edison T. Liu, Qiang Yu, Huck Hui Ng, and **Yijun Ruan*** (2006) A Global Map of p53 Transcription Factor Binding Sites in the Human Genome. Cell 124: 207-219.

73. Tao Zhang, Mya Breitbart, Wah Heng Lee, Jin-Quan Run, Chia Lin Wei, Shirlena Wee Ling Soh, Martin L. Hibberd1, Edison T. Liu, Forest Rohwer, and **Yijun Ruan*** (2006) RNA Viral Community in the Human Gut: Prevalence of plant pathogenic viruses. PLoS Biology 4: Issue 1, e3.

2005

74. FANTOM Consortium (2005) The Transcriptional Landscape of the Mammalian Genome. Science 309: 1559-1563.
75. Sinnakaruppan Mathavan, Serene G. P. Lee, Alicia Mak, Lance D. Miller, Karuturi Radha Krishna Murthy, Kunde R. Govindarajan, Yan Tong, Yi Lian Wu, Siew Hong Lam, Henry Yang, **Yijun Ruan**, Vladimir Korzh, Zhiyuan Gong, Edison T. Liu, and Thomas Lufkin (2005) Transcriptome Analysis of Zebrafish Embryogenesis Using Microarrays. PLoS Genetics 1: Issue 2, e29. (IF 8.883)
76. Patrick Ng, Chia-Lin Wei, Wing-Kin Sung, Kuo Ping Chiu, Leonard Lipovich, Chin Chin Ang, Sanjay Gupta, Atif Shahab, Azmi Ridwan, Chee Hong Wong, Edison T. Liu, and **Yijun Ruan*** (2005) Gene Identification Signature (GIS) Analysis for Transcriptome Characterization and Genome Annotation. Nature Methods 2: 105-111.
77. Wei Chia Lin, Takumi Miura, Robson Paul, Lim Sai-Kiang, Xiu-qin Xu, Mathia Yu-Chuan Lee, Gupta Sanjay, Stanton W Lawrence, Yongquan Luo, Jacqui Schmitt, Scott Thies, Wei Wang, Irina Khrebtukova, Daixing Zhou, Liu Tak-Bun Edison, **Ruan Yijun**, Mahendra Rao, and Lim Bing (2005) Transcriptome Profiling of Murine and Human ES Cells Identifies Divergent Paths Required to Maintain the Stem Cell State. Stem Cells 23: 166-185.
78. The FANTOM Consortium, P. Carninci, ..., Kuo Ping CHIU, Edison Tak-Bun LIU, **Yijun RUAN**, Chia Lin WEI, Leonard LIPOVICH, et al, RIKEN Genome Exploration Research Group, Genome Science Group - Genome Network Project Core Group (2005) "The Transcriptional Landscape of the Mammalian Genome" Science 309 1559-1563
79. Jianjun LIU, SL Lim, **Yijun RUAN**, Ling AE, Ng LF, C Drostein, Edison Tak-Bun LIU, Lawrence STANTON, Martin Lloyd HIBBERD (2005) "SARS Transmission Pattern in Singapore Reassessed by Viral Sequence Variation Analysis" PLoS Med 2(2) 162-168

2004

80. Liu Jianjun, Lam L.S., **Ruan Yijun**, Ling A.E., Dorsten C., Liu Tak-Bun Edison, Stanton W Lawrence, and Hibberd Lloyd Martin (2004) SARS-CoV transmission epidemiology revealed by MALDI-TOF mass spectrometry-based viral genotyping. PLoS Medicine 2: e43.
81. MGC Project Team (2004) The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). Genome Research 14: 2121-2127
82. Wei Chia Lin, Ng Patrick Wei Pern, Chiu Kuo Ping, Chee Hong Wong, Chin Chin Ang, Lipovich Leonard, Liu Edison Tak-Bun, and **Ruan Yijun*** (2004) 5' Long serial analysis of gene expression (LongSAGE) and 3' LongSAGE for transcriptome characterization and genome annotation. Proc Natl Acad Sci U S A. 101:11701-11706
83. Lim P.L., Kurup A., Gopalakrishna G., Chan K.P., Wong Wing-Cheong Christopher, Ng L.C., Su Yun S.T., Oon L., Bai X., Stanton W Lawrence, **Ruan Yijun**, Miller D Lance, Vinsensius B Vega S, James L., Ooi P.L., Kai C.S., Olsen S.J., Ang B., Leo Y.S. (2004) Laboratory-acquired SARS-Singapore 2003. New Eng J Med 350: 1740-1745

84. Vinsensius B Vega S, **Ruan Yijun**, Liu Jianjun, Lee W.H., Wei Chia Lin, Su Yun S.T., Tang K.F., Zhang Tao, Lin S., Kolatkar R Prasanna, Eong O.E., Ling A.E., Stanton W Lawrence, Long P.M., Liu Tak-Bun Edison (2004) Mutational dynamics of the SARS corona virus in cell culture and human population. BMC Infectious Diseases 4(1): 32-40
85. **Ruan Y**, Le Ber P, Ng HH, and Liu ET. (2004) Interrogating the transcriptome. Trends in Biotechnology 22(1): 23-30
- 2003
86. **Ruan Yijun**, Wei Chia Lin, Ling Ai Ee, Vinsensius Vega S B, Thoreau Herve, Su Yun Se Thoe, Chia Jer-Ming, Ng Wei Pern Patrick, Chiu Kuo Ping, Lim Landri, Zhang Tao, Chan Kwai Peng, Lynette Oon Lin Ean, Ng Mah Lee, Leo Yee Sin, Ng Fong-Poh Lisa, Ren Chee Ee, Stanton W Lawrence, Long M. Philip, Liu Tak-Bun Edison (2003) Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection. Lancet 361 (9371): 1779-1785
- 87.
88. **Ruan, Y.**, Gilmore, J., and Conner, T.W. (2001) Plant Genome Analysis Using cDNA Microarrays. In Biochip Technology (edit by Jing Cheng and Larry Kricka, published in April 2001 by Gordon and Breach Publishing).
89. **Ruan, Y.**, Gilmore, J., and Conner, T.W. (1998) Towards Arabidopsis genome analysis: monitoring expression profiles of 1400 genes using cDNA microarrays. The Plant Journal 15: 821-833.
90. **Ruan, Y.** and Straney, D.C. (1995) Identification of elements in the PDA1 promoter of *Nectria haematococca* necessary for a high level of transcription in vitro. Molecular and General Genetics 250: 29-38.
91. He, J., **Ruan, Y.** and Straney, D.C. 1995. Analysis of determinants of binding and transcriptional activation of the pisatin-responsive DNA binding factor of *Nectria Haematococca*. Molecular Plant-Microbe Interaction 9: 171-179.
92. **Ruan, Y.** and Straney, D.C. (1995) Flavonoids stimulate spore germination in *Fusarium solani* pathogenic on legumes in a manner sensitive to inhibitors of cAMP-dependent protein kinase. Molecular Plant-Microbe Interaction 8: 929-938.
93. **Ruan, Y.** and Straney, D.C. (1994) In vitro transcription from *Nectria haematococca* PDA1 promoter in homo-logous extract reflects in vivo pisatin-responsive regulation. Current Genetics 27: 46-53.
94. **Ruan, Y.** and Straney, D.C. (1994) PCR-based construction of G-free template/promoter fusions for in vitro transcription analysis allows selection of plasmids with optimal template activity. Gene 146: 227-232.
95. Straney, D.C.; **Ruan, Y.** and He, J. (1994) In vitro transcription and binding analysis of promoter regulation by a host specific signal in a phytopathogenic fungus. Antonie van Leeuwenhoek 65: 183-189.

LECTURES

2013

Nov 21, NYC, NY

Memorial Sloan-Kettering Cancer Center

Invited lecturer for “Multi-level long-range and spatial regulation of gene transcription in cancer cells”

Nov 14, Farmington, CT

UCHC Dental Dean’s Seminar Series

Invited lecturer for “Multi-dimensional Gene Regulation in Cancer Cells”

Nov 04, Heidelberg Germany

EMBL conference, Cancer Genomics

Invited speaker for “Multi-Dimensional Gene Regulation in Cancer Cells”

Oct 30, College Park, MD

University of Maryland, Department of Molecular and Cell Biology seminar serial

Invited speaker for “Multi-Dimensional Gene Regulation in Cancer Cells”

Oct 05, Farmington, CT

JAX clinic genomics conference

Invited speaker for “Human Genome Structure and Function in Cancer Cells”

Aug 19, Provence, RI

CHI conference: NGX Applying Next Generation Sequencing, Short course Mapping Genome in 3D.

Invited lecturer for “From 1-Dimensional Mapping to 3-Dimensional Genome Structure and Function”

Aug 20, Provence, RI

CHI conference: NGX, Applying Next Generation Sequencing

Invited speaker for “From Genome Technology to Genome Biology”

June 5, Bethesda, Maryland

NIH/NIAMS RETREAT

Invited speaker for “Topological Basis of Higher-Order Chromatin Folding and Gene Transcription Regulation in Human Cells”

May 8, Bar Harbor, ME

High Throughput DNA sequencing Workshop

Invited lecture for “Genome structural variations”

April 15, Singapore

Joint conference of HGM 2013 & 21st International Congress of Genetics

Invited speaker for “3D Chromatin Interaction Architecture for Gene Transcription regulation and Disease”

March 26, Farmington, CT

UCHC Reproductive Biology Group Seminar

Invited speaker for “Topological basis for Gene transcription Regulation”

March 19, San Diego, CA

CHI’s 7th DNA-Seq: Advancing Clinic Applications

Session chair and invited speaker for “ChIA-PET Analysis for 3D Chromatin Interactions, Transcription Regulation, and Diseases”

Jan 23, Worcester, MA

UMass Medical School, Program of Biochemistry & Molecular Pharmacology Seminar

Invited speaker for “The Topological Basis of Chromatin Interactions for Transcription Regulation and Diseases”

CURRENT SUPPORT