

Education and Professional Profile

<i>Year(s)</i>	<i>Field of study</i>	<i>Position</i>	<i>Institution and Location</i>
2011.3. -	Bioinformatics and Genomics	PI	Tsinghua University, Beijing, China
2008.7-2011.1	Bioinformatics	Postdoc	Yale University, New Haven, CT, US
2003.9-2008.6	Biophysics	Ph.D.	University of Rochester, Rochester, NY, US
1998.9-2003.6	Life Sciences	B.S.	University of Science and Technology of China

Research and Teaching Experience

- **Principal Investigator (Mar. 2011 -)** **Tsinghua University**
Research:
 - Development of bioinformatics methods for **RNA structure** prediction and **protein-RNA interaction**
 - Characterization of **novel long noncoding RNAs** in model genomes
 - Development of databases and analysis methods for **personal genomics** data
 - Identification of novel bio-markers in **cancer genomes**Teaching:
 - *Introduction to Bioinformatics* (for Undergraduate Students)
 - *Bioinformatics and Systems Biology* (for Graduate Students)
 - *Genomics and Bioinformatics* (for Ph.D. students from Peking-Tsinghua-NIBS program)

- **Postdoctoral Research (Jul. 2008 – Jan. 2011)** **Yale University**
Advisor: Dr. Mark B. Gerstein (PH.D., Albert L Williams Professor)
 - Core researcher in **modENCODE/ENCODE** pilot projects
 - Structured novel **non-coding RNA** prediction and characterization in Human/Worm Genome
 - **SNP** and **SV** analysis among non-coding regions (1000 Genomes Pilot Project)

- **Graduate Research (Sep. 2003 – Jun. 2008)** **University of Rochester**
Advisor: Dr. David Mathews (Ph.D., M.D)
 - **siRNA design** using hybridization thermodynamics in RNA interference with Support Vector Machine
 - **RNA secondary structure** prediction using Nearest Neighbor Model and Dynamic Programming
 - Replica Exchange of RNA hairpin's tertiary structure using Molecular Dynamics with AMBER

Funding

- Development of ncRNA database and identification technology
Core member, National High-tech Research and Development Program of China (863) (2014-2016: 2014AA021103)
- Tumor genesis and cell differentiation study using next generation sequencing technology
Core member, National Key Basic Research Program of China (973) (2012-2016: 2012CB316503)
- Characterization of protein-RNA interactions in yeast genome
PI, National Natural Science Foundation of China (2013-2016: 31271402)
- Prediction and characterization of novel ncRNAs in fly genome
PI, National Natural Science Foundation of China (2012-2014: 31100601)
- Uncovering stimulus-induced novel long non-coding RNAs in plants/crops
PI, Bayer CropScience (2013-2014: No.20133000137)
- Characterizing RNAs associated with Fragile X syndrome
PI, Roche (2012-2013)

Selected Publications

- ★ Long Hu, Chao Di, Mingxuan Kai, Yu-Cheng T. Yang, Yang Li, Yunjiang Qiu, Xihao Hu, Kevin Y. Yip, Michael Q. Zhang and **Zhi John Lu** (2015) A common set of distinct features that characterize noncoding RNAs across multiple species. *Nucleic Acids Research* 43(1): 104-114.
- ★ Yu-Cheng T. Yang*, Chao Di*, Boqin Hu*, Meifeng Zhou, Yifang Liu, Nanxi Song, Yang Li, Jumpei Umetsu and **Zhi John Lu** (2015) CLIPdb: a CLIP-seq database for protein-RNA interactions. *BMC Genomics* In press. (*contributed equally)
- ★ Chao Di*, Jiawei Yuan*, Yue Wu, Jingrui Li, Huixin Lin, Long Hu, Ting Zhang, Yijun Qi, Mark B. Gerstein, Yan Guo and **Zhi John Lu** (2014) Characterization of Stress-responsive lncRNAs in *Arabidopsis thaliana* by Integrating Expression, Epigenetic and Structural Features. *The Plant Journal* 80:848–861
- ★ **Lu ZJ***, Yip KY*, Wang G, Shou C, Hillier LW, et al. (2011) Predicting and characterizing non-coding RNA in *C. elegans* by integrating conservation, secondary structure and high-throughput sequencing and array data. *Genome Research* 21: 276-2857 (*contributed equally) [modENCODE special issue – Cover Story]
- ★ Gerstein MB [#], **Lu ZJ***, Van Nostrand EL*, Cheng C*, Arshinoff BI*, et al. (2010) Integrative analysis of the *Caenorhabditis elegans* genome by the modENCODE project. *Science* 330(6012): 1775-1787 (*co-first authors, [#]corresponding authors) [Cover Story]

- Gerstein MB, Joel Rozowsky, Koon-Kiu Yan, ..., **Lu Z**, ..., Thomas Gingeras and Robert Waterston (2014) Comparative Analysis of the Transcriptome across Distant Species. *Nature* 512(7515):445-448.
- Yang YC, Umetsu J, **Lu ZJ** (2014) Global signatures of protein binding on structured RNAs in *Saccharomyces cerevisiae*. *Science China Life Sciences* (Tsinghua Special Issue) 57:1, 22-35
- Hu X, Wong TKF, **Lu ZJ**, Chan TF, Lau TCK, Yiu SM and Yip KY. (2014) Computational Identification of Protein Binding Sites on RNAs using High-Throughput RNA Structure-Probing Data. *Bioinformatics* vol. 30, no. 8, pp. 1049-1055.
- Freeberg MA, Han T, Moresco JJ, Kong A, Yang YC², **Lu ZJ**², Yates JR, Kim JK. (2013) Pervasive and dynamic protein binding sites of the mRNA transcriptome in *Saccharomyces cerevisiae*. *Genome Biology* 14 (2), R13. (²Lu Lab, School of Life Sciences, Tsinghua University)
- Kudron M, Niu W, **Lu ZJ**, Wang GL, Gerstein MB, Snyder M, Reinke V. (2013) Tissue-specific direct targets of *Caenorhabditis elegans* Rb/E2F dictate distinct somatic and germline programs. *Genome Biology*. 14 (1), R5.
- ENCODE Project Consortium[#]. (2012) An Integrated Encyclopedia of DNA Elements in the Human Genome. *Nature* 489, 57–74. ([#]**Lu Z** is part of ENCODE Consortium) [Cover Story]
- Tan X, Hu L², Luquette LJ, Gao G, Liu YF², Qu HJ, Xi RB, **Lu ZJ**², Park PJ & Elledge SJ. (2012) Systematic Identification of Synergistic Drug Pairs Targeting HIV. *Nature Biotech.* 30:1125-1130 (²Lu Lab, School of Life Sciences, Tsinghua University)
- Tan X, **Lu ZJ**², Gao G, Xu QK, Hu L², Fellmann C, Li MZ, Qu HJ, Lowe SW, Hannon GJ & Elledge SJ. (2012) Tiling genomes of pathogenic viruses identifies potent antiviral shRNAs and reveals a role for secondary structure in shRNA efficacy. *Proc. Natl. Acad. Sci. U. S. A.*, 109(3): 869-74 (²Lu Lab, School of Life Sciences, Tsinghua University)
- He CF, Li YX, Zhang GX, Gu ZG, Yang R, Li J, **Lu ZJ**, Zhou ZH, Zhang CY, Wang J. (2012) MiRmat: Mature microRNA Sequence Prediction. *PLoS ONE* 7(12):e51673.
- Niu W, **Lu ZJ**, Zhong M, Sarov M, Murray JI, et al. (2011) Diverse transcription factor binding features revealed by genome-wide ChIP-seq in *C. elegans*. *Genome Research* 21: 245-254.
- Mu XJ, **Lu ZJ**, Kong Y, Lam HYK, Gerstein MB (2011) Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. *Nucleic Acids Research*, 39 (16): 7058-7076.
- Li Y, Du X, **Lu ZJ**, Wu D, Zhao Y, et al. (2011) Regulatory Feedback Loop of Two *phz* Gene Clusters through 5'-Untranslated Regions in *Pseudomonas* sp. M18. *PLoS ONE* 6(4): e19413
- ENCODE Project Consortium[#] (2011) A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biology* 9: e1001046. ([#]**Lu Z** is part of ENCODE Consortium)

Zhi J. Lu – CV
Principal Investigator @Tsinghua University

- Cheng C, Yan KK, Hwang W, Qian J, Bhardwaj N, Rozowsky J, **Lu ZJ**, Niu W, Alves P, Kato M, Gerstein MB. (2011) Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data. *PLoS Comput Biol* 7: e1002190
- Zhong M, Niu W, **Lu ZJ**, Sarov M, Murray JI, et al. (2010) Genome-wide identification of binding sites defines distinct functions for *Caenorhabditis elegans* PHA-4/FOXA in development and environmental response. *PLoS Genetics* 6(2): e1000848.
- **Lu ZJ**, Gloor JW, Mathews DH (2009) Improved RNA secondary structure prediction by maximizing expected pair accuracy. *RNA* 15: 1805-1813.
- **Lu ZJ**, Mathews DH (2008) OligoWalk: an online siRNA design tool utilizing hybridization thermodynamics. *Nucleic Acids Research* 36:W104-W108.
- **Lu ZJ** and Mathews DH (2008) Efficient siRNA selection using hybridization thermodynamics. *Nucleic Acids Research* 36:640-647.
- **Lu ZJ**, Mathews DH. (2008) Fundamental differences in the equilibrium considerations for siRNA and antisense oligodeoxynucleotide design. *Nucleic Acids Research* 36:3738-3745.
- **Lu ZJ**, Turner DH, Mathews DH (2006) A set of nearest neighbor parameters for predicting the enthalpy change of RNA secondary structure formation. *Nucleic Acids Research* 34:4912-4924.

Awards

- Janssen Investigator Fellowship (2014, Janssen-Tsinghua Joint Research Center)
- Bayer Investigator Fellowship (2014, Bayer-Tsinghua Research Center for Crop Science)
- New Century Excellent Talents (2011, Ministry of Education of China)
- Junior Faculty Award (2011, Tsinghua University)
- Bayer Investigator Fellowship (2011, Bayer-Tsinghua Research Center for Innovative Drug Discovery)
- Wallace O. Fenn Award (2009, School of Medicine and Dentistry, U. of Rochester)
- George V. Metzger Award (2009, Program in Biophysics, Univ. of Rochester)
- Award for Excellent Student (2001, Top 10% students, Univ. of Sci. & Tech. of China)

Associations

- American Association for the Advancement of Science (AAAS) (Since 2010)
- International Society for Computational Biology (ISCB) (Since 2009)
- The RNA Society (U.S.) (Since 2009)
- New York Academy of Sciences (Since 2009)
- ENCODE/modENCODE Consortium (Since 2008)

Journals Reviewed

- *Bioinformatics, PLoS Comput Biol, RNA, BMC Genomics, BMC Bioinformatics, Molecular Therapy, Silence*