

## CURRICULUM VITAE

Feb 2017

### Chaolin Zhang



Center for Motor Neuron Biology and Disease  
Columbia University Medical Center  
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#### ACADEMIC APPOINTMENTS

- 11/2012-present    **Assistant Professor**  
Department of Systems Biology  
Department of Biochemistry and Molecular Biology  
Center for Motor Neuron Biology and Disease  
Columbia University Medical Center
- 07/2011-10/2012    **Research Assistant Professor**  
Laboratory of Molecular Neuro-Oncology  
Howard Hughes Medical Institute, The Rockefeller University  
Mentor: Robert B. Darnell

#### EDUCATION

- 07/2008-07/2011    **Postdoctoral Associate**  
Laboratory of Molecular Neuro-Oncology  
Howard Hughes Medical Institute, The Rockefeller University  
Mentor: Robert B. Darnell
- 08/2004-07/2008    **Ph.D.**, Department of Biomedical Engineering  
Cold Spring Harbor Laboratory & SUNY at Stony Brook  
Mentors: Profs. Michael Q. Zhang and Adrian R. Krainer
- 09/1998-07/2002    **B.E.** Department of Automation (with honor)  
Tsinghua University, Beijing, China

## CURRENT AND PAST FUNDING

- 07/2016-06/2018 NIH (NINDS) R21. Systematic functional dissection of neuronal transcriptome diversity. (PI)
- 07/2015-04/2020 NIH (NINDS) R01. RNA regulatory networks in motor neuron development and function. (PI, co-I: Wichterle)
- 09/2014-08/2017 Simons Foundation Autism Research Initiative Research Award. Elucidating pathogenic mutations disrupting RNA regulation in autism. (PI, co-I: Yazawa/Krainer)
- 10/2013-09/2014 Simons Foundation Autism Research Initiative Explorer Award. Modeling alteration of RBFOX1 (A2BP1) target network in autism. (PI)
- 02/2011-12/2015 NIH (NIGMS) K99/R00 Pathway to Independence Award. An integrative genomic strategy to infer global RNA regulatory networks. (PI) (NCE: 11/2016)

## ACADEMIC AWARDS

- 2011 NIH (NIGMS) K99/R00 Pathway to Independence Award.
- 2010 Poster Award, Gordon Research Conference: Biology of Post-transcriptional Gene Regulation
- 2004-2008 Scholarship, Cold Spring Harbor Laboratory & SUNY at Stony Brook
- 2006 Sigma Xi Award
- 2006 Travel Fellowship to Sequence Analysis Towards Systems Biology Workshop, IPAM, UCLA
- 2004 Travel Fellowship to GenePattern Workshop, MIT
- 2002 Best Proposal, Seed Fund for Extracurricular Scientific Activities, Tsinghua University
- 2002 Rank 6th, SCILAB Programming Contest (national wide)
- 2001 Tsinghua University Outstanding Student Scholarship (General Electric)
- 2000 Tsinghua Outstanding Student Scholarship

## PEER-REVIEWED PUBLICATIONS

(• co-first authors; † co-corresponding authors)

1. Ustianenko, D., Weyn-Vanhentenryck, S.M., Zhang, C. 2017. Microexons: discovery, regulation, and function. *WIREs RNA*. e1418. doi: 10.1002/wrna.1418 (review).
2. Zhang, C.\*, †, Shen, Y. \*† 2016. A cell type-specific expression signature predicts haploinsufficient autism-susceptibility genes. *Hum Mut.* DOI: 10.1002/humu.23147.
3. Shah, A., Qian, Y., Weyn-Vanhentenryck, S.M., Zhang, C. 2016. CLIP Tool Kit (CTK): a flexible and robust pipeline to analyze CLIP sequencing data. *Bioinformatics*. in press. DOI: 10.1093/bioinformatics/btw653.
4. Goodwin, M., Mohan, A. Batra, R., Lee, K.-Y., Charizanis, K., Francisco Jose Fernandez-Gomez, F.J., Eddarkaoui, S., Sergeant, N., Buee, L., Kimura, T., Clark, H.B., Dalton, J., Takamura, K., Weyn-Vanhentenryck, S.M., Zhang, C., Reid, T., Ranum, L.P.W., Day, J.W., Swanson, M.S. 2015. MBNL sequestration by toxic RNAs and RNA misprocessing in the myotonic dystrophy brain. *Cell Rep.* <http://dx.doi.org/10.1016/j.celrep.2015.07.029>.
5. Feng, H., Zhang, X., Zhang, C., 2015. mRIN for direct assessment of genome-wide and gene-specific mRNA integrity from large-scale RNA-sequencing data. *Nat Comm.* **6**:7816.  
- Research highlights, “How good are those RNA-seq data?”, *Nature Methods*, 12:910 (2015).
6. Yan, Q.\*, Weyn-Vanhentenryck, S.M.\*, Wu, J., Sloan, S.A., Zhang, Y., Chen, K., Wu, J.-Q., Barres, B.A.†, Zhang, C.† 2015. Systematic discovery of regulated and conserved alternative exons in the mammalian brain reveals NMD modulating chromatin regulators. *Proc. Nat. Acad. Sci. USA.* **112**:3445-3450.

7. Batra, R., Charizanis, K., Manchanda, M., Mohan, A., Li, M., Finn, D.J., Goodwin, Zhang, C., Sobczak, K., Thornton, C.A., Swanson, M.S. 2014. Loss of MBNL function leads to disruption of developmentally regulated alternative polyadenylation in RNA-mediated disease. *Mol Cell*. **56**: 311-322.
8. Zhang, Y., Chen, K., Sloan, S., Bennett, M.L., Scholze, A.R., O'Keefe, S., Phatnani, H.P., Guarnieri, P., Caneda, C., Ruderisch, N., Deng, S., Liddelow, S.A., Zhang, C., Daneman, R., Maniatis, T., Barres, B.A., Wu, J.-Q. 2014. An RNA-sequencing transcriptome and splicing database of glia, neurons, and vascular cells of the cerebral cortex. *J Neurosci*. **34**:11929-11947.
9. Weyn-Vanhenhenryck, S., M.\*, Mele, A.\* , Yan, Q.\*, Sun, S., Farny, N., Zhang, Z., Xue, C., Herre, M., Silver, P.A., Zhang, M.Q., Krainer, A.R., Darnell, R.B. †, Zhang, C. † 2014. HITS-CLIP and integrative modeling define the Rbfox splicing-regulatory network linked to brain development and autism. *Cell Rep*. **6**:1139-1152.
10. Moore, M.\* , Zhang, C.\*, Gantman, E.C., Mele, A., Darnell, J.C., Darnell, R.B. 2014. Mapping Argonaute and conventional RNA-binding protein interactions with RNA at single-nucleotide resolution using HITS-CLIP and CIMS analysis. *Nat Protocols*. **9**:263-293.
11. Poulos, M.G., Batra, R., Li, M., Yuan, Y., Zhang, C., Darnell, R.B., Swanson, M.S. 2013. Progressive impairment of muscle regeneration in Muscleblind-like 3 isoform knockout mice. *Hum Mol Genet*. **22**:3547-3558.
12. Zhang, C. †, Lee, K.-Y., Swanson, M.S., Darnell, R.B. † 2013. Prediction of clustered RNA-binding protein motif sites in the mammalian genome. *Nucleic Acids Res*. **41**:6793-6807.
13. Wu, J., Anczukow, O., Krainer, A.R., Zhang, M.Q. †, Zhang, C. †, 2013. OLego: Fast and sensitive mapping of spliced mRNA-Seq reads using small seeds. *Nucleic Acids Res*. **41**:5149-5163.
14. Eom, T., Zhang, C., Wang, H., Lay, K., Fak, J., Noebels, J.L., Darnell, R.B. 2012. NOVA-dependent regulation of cryptic NMD exons controls synaptic protein levels after seizure. *eLife*, **2**:e00178.
15. Ince-Dunn, G., Okano, H.J., Jensen, K.B., Park, W.Y., Zhong, R., Ule, J., Mele, A., Fak, J.J., Yang, C., Zhang, C., Yoo, J., Herre, M., Okano, H., Noebels, J.L., Darnell, R.B., 2012. Neuronal Elav-like (Hu) proteins regulate RNA splicing and abundance to control glutamate levels and neuronal excitability. *Neuron*, **75**:1067-1080.
16. Zhang, B., Arun, G., Mao, Y.S., Lazar, Z., Hung, G., Bhattacharjee, G., Xiao, X., Booth, C.J., Wu, J., Zhang, C., Spector, D.L., 2012. The lncRNA Malat1 is dispensable for mouse development but its transcription plays a cis-regulatory role in the adult. *Cell Reports*, **2**:111-123.
17. Charizanis, K., Lee, K.-Y., Batra, R., Goodwin, M., Zhang, C., Yuan, Y., Shuie, L., Cline, M., Scotti, M.M., Xia, G., Kumar, A., Ashizawa, T., Clark, H.B., Kimura, T., Takahashi, M.P., Fujimura, H., Jinnai, K., Yoshikawa, H., Pereira, M.G., Gourdon, G., Sakai, N., Nishino, S., Foster, T.C., Ares, M. Jr, Darnell, R.B. Swanson, M.S., 2012. Muscleblind-like 2 mediated alternative splicing in the developing brain and dysregulation in myotonic dystrophy. *Neuron*, **75**:437-450.
18. Licatalosi, D.D., Yano, M., Fak, J.J., Mele, A., Grabinski, S.E., Zhang, C., Darnell, R.B., 2012. Ptbp2 represses adult-specific splicing to regulate the generation of neuronal precursors in the embryonic brain. *Genes Dev.*, **26**:1626-1642.
19. Rajan P., Dalgliesh, C., Carling, P., Buist, T., Zhang, C., Grellscheid, S., Armstrong, K., Stockley, J., Simillion, C., Gaughan, L., Kalna, G., Zhang, M.Q., Robson, C., Leung, H., Elliott, D. 2011. Identification of novel androgen-regulated pathways and mRNA isoforms through genome-wide exon-specific profiling of the LNCaP transcriptome. *PLoS One*, **6**: e29088.
20. Watts, J.A., Zhang, C., Klein-Szanto, A.J., Kormish, J.D., Fu, J., Zhang, M.Q., Zaret, K.S. 2011. Study of FoxA pioneer factor at silent genes reveals Rfx-repressed enhancer at Cdx2 and a potential indicator of esophageal adenocarcinoma development. *PLoS Genet*, **7**: e1002277.

21. Darnell, J.C., Van Driesche, S.J., Zhang, C., Hung, K.Y.S., Mele, A., Fraser, C.E., Stone, E.F., Chen, C., Fak, J.J., Chi, S.W., Licatalosi, D.D., Richter, J.D., Darnell, R.B., 2011. FMRP stalls ribosomal translocation on mRNAs linked to synaptic function and autism. *Cell*, **146**:247-261.
22. Zhang, C. †, Darnell, R.B. † 2011. Mapping in vivo protein-RNA interactions at single-nucleotide resolution from HITS-CLIP data. *Nat. Biotech.* **29**:607-614.
23. Zhang, C. †, Frias, M.A., Mele, A., Ruggiu, M., Eom, T., Marney, C.B., Wang, H., Licatalosi, D.D., Fak, J.J., Darnell, R.B. † 2010. Integrative modeling defines the Nova splicing-regulatory network and its combinatorial controls. *Science*. **329**: 439-443.  
 - Editor's choice, Pickersgill, H. 2010. Making the Final Cut. *Sci. Signal.* **3**:ec234;  
 - Nominated by leading researchers as one of the 33 papers that represent breakthroughs in computational biology in 2010. Mak H.C., 2011. Trends in computational biology-2010. *Nat Biotech.* **29**, doi:10.1038/nbt.1747.
24. Chicas, A., Wang, X., Zhang, C., McCurrach, M., Zhao Z., Mert, O., Dickins, R., Narita, M., Zhang, M.Q., Lowe, S.W. 2010. Dissecting the unique role of the retinoblastoma tumor suppressor during cellular senescence. *Cancer Cell*, **17**: 376-387.  
 -Comment in Burd, C.E., Sharpless, N.E. 2010. What's so special about RB. *Cancer Cell*. **17**:313-314.
25. Castle, J.C., Zhang, C., Shah, J.K., Kulkarni, A.V., Kalsotra, A., Cooper, T.A., Johnson, J.M. 2008. Expression of 24,426 human alternative splicing events and predicted cis regulation in 48 tissues and cell lines. *Nat. Genet.* **40**:1416-1425.
26. Zhang, C. \*, Zhang, Z. \*, Castle, J., Sun, S., Johnson, J., Krainer, A.R., Zhang, M.Q. 2008. Defining the regulatory network of the tissue-specific splicing factors Fox-1 and Fox-2. *Genes Dev.* **22**:2550-2563.
27. Zhang, C., Li, W.-H., Krainer, A.R., Zhang, M.Q. 2008. RNA landscape of evolution for optimal exon and intron discrimination. *Proc. Nat. Acad. Sci. USA.* **105**:5797-5802.
28. Zhang, C., Hasting, M.L., Krainer, A.R., Zhang, M.Q. 2007. Dual-specificity splice sites function alternatively as 5' and 3' splice sites. *Proc. Nat. Acad. Sci. USA* **104**: 15028-15033.
29. Zhang, C., Krainer, A.R., and Zhang, M.Q. 2007. Evolutionary impact of limited splicing fidelity in mammalian genes. *Trends Genet.* **23**(10): 484-488.
30. Zhang, C., Zhang, X., Zhang, M.Q., Li, Y. 2007. Neighbor number, valley seeking and clustering. *Pattern Recogn. Lett.* **28**:173-180.
31. Smith P.J., Zhang, C., Wang, J., Chew, S.L., Zhang, M.Q., Krainer, A.R. 2006. An increased specificity score matrix for the prediction of SF2/ASF-specific exonic splicing enhancers. *Hum. Mol. Genet.* **15**: 2490-2508.
32. Zhang, C., Xuan, Z., Otto, S., Hover, J.R., McCorkle, S.R., Mandel, G., Zhang, M.Q. 2006. A clustering property of highly-degenerate transcription factor binding sites in the mammalian genome. *Nucleic Acids Res.* **34**: 2238-2246.
33. Zhang, C., Li, H.-R., Fan, J.-B., Wang-Rodriguez, J., Downs, T., Fu, X.-D., Zhang, M.Q. 2006. Profiling alternatively spliced mRNA isoforms for prostate cancer classification. *BMC Bioinfo.* **7**: 202. (highly accessed paper)
34. Zhang, C. \*, Lu, X. \*, Zhang, X. 2006. Significance of gene ranking for classification of microarray Samples. *IEEE ACM T Comput Biol Bioinfo.* **3**(3): 312-320.

## BOOK CHAPTERS

Weyn-Vanhentenryck,S.M., Zhang,C. 2016. mCarts: genome-wide prediction of clustered sequence motifs as binding sites for RNA-binding proteins. *Methods Mol Biol.*1421:215-226.

Zhang, C., Zhang, M.Q. 2012. Identification of Splicing Factor Target Genes by High-Throughput Sequencing. Chapter 51 in *Alternative pre-mRNA Splicing: Theory and Protocols*. (S. Stamm, C.W. J. Smith, R. Lührmann, ed) Wiley-VCH Verlag GmbH & Co.

Zhang, C., Zhang, M.Q. 2008. Biomedical literature mining. Chapter 10 in *Bioinformatics: A Concept-Based Introduction*. (Mathura, V. & Kanguane, P., ed) Springer. 115-127.

Zhang, C., Zhao, X., Zhang, M.Q. 2006. Functional *in silico* analysis of gene regulatory polymorphism. Chapter 12 in *Bioinformatics for Geneticists 2nd Edition - A Bioinformatics primer for the analysis of genetic data*. 2nd edition (M.R. Barnes, ed) John Wiley & Sons, LTD.

## INVITED TALKS

10/2016. An integrative approach to dissecting neuronal transcriptome diversity. Graduate Student Seminar Series, Department of Systems Biology, Columbia University.

09/2016. Dynamic regulation of alternative splicing during neural development. Department Retreat, Department of Systems Biology, Columbia University.

08/2016. Dissecting neuronal transcriptome diversity using an *in vitro* ES model. Summer Research Bootcamp, Doctoral Program of Neurobiology and Behavior, Columbia University.

07/2016. The splicing code: how far are we off? Bioinformatics Division, TNLIST, Tsinghua University, Beijing, China.

04/2016. A high-resolution view of neuronal RNA regulatory networks. Department of Biological Sciences Seminar Series, St John's University. Queens, NY.

02/2016. Temporal regulation of transcriptome diversity during neural development. Penn State University Neuroscience Seminar. University Park, PA.

02/2016. A high-resolution view of RNA regulatory networks. Amgen Inc. Boston, MA.

01/2016. A high-resolution view of RNA regulatory networks. Robert H Lurie Comprehensive Cancer Center, Northwestern University. Chicago, IL.

09/2015. A high-resolution view of neural RNA regulatory networks. Center for RNA Biology, Ohio State University. Columbus, OH.

05/2014. Dissecting a modular RNA-splicing program in neurodevelopment. Columbia University MAGNet Retreat.

12/2013. Integrative Analysis of the Transcriptome & Protein-RNA Interactome to Elucidate RNA Regulation. RNA-seq in Biomedical Research Workshop, Columbia University Genome Center.

10/2013. From RNA regulatory networks to rare mutations in neurological disorders. Department of Biochemistry and Molecular Biophysics, Columbia University retreat.

05/2013. RNA regulatory networks in the mammalian nervous system. Columbia University MAGNet Retreat.

02/2013. RNA regulation, neuronal cell fate, and brain tumor: A systems perspective. Columbia University Graduate Admission Talk.

10/2012. Global RNA regulatory networks in the mammalian brain: insights from an integrative systems biology

approach. Bioinformatics Division, TNLIST, Tsinghua University, Beijing, China.

10/2012. Searching for the specificity of RNA-binding proteins. Tsinghua Symposium on Genomics and Epigenomics. Beijing, China.

10/2012. Searching for the specificity of RNA-binding proteins. CSHA RNA Biology. Suzhou, China.

09/2012. Global RNA regulatory networks in the mammalian brain: insights from an integrative systems biology approach. CAS-MPG Partner Institute for Computational Biology. Shanghai, China.

## EARLIER CONFERENCE PRESENTATIONS

Zhang, C., Darnell, R.B. 2012. Searching for the specificity of non-specific RNA-binding proteins. *2012 Annual Meeting of the RNA Society. May 29-June 3. Ann Arbor, MI* (selected talk).

Zhang, C. 2011. Mapping microRNA target networks: HITS-CLIP and beyond. *ASN Annual meeting Advances in Research Conference: MicroRNA. Nov 8-9. Philadelphia, PA* (invited talk).

Zhang, C. 2011. HITS-CLIP analysis of protein-RNA interactions: four computational challenges & two applications. *Rockefeller Bioinformatics/Biostatistics Collaborative Group meeting. Oct 21. Rockefeller University* (invited talk).

Zhang, C., Mele, A., Yano, M., Darnell, R.B., 2011. Single-nucleotide-resolution mapping of protein-RNA interactions using cross-linking induced mutation site (CIMS) analysis of HITS-CLIP data and its applications. *Eukaryotic mRNA Processing. Aug 23-27. Cold Spring Harbor, NY* (poster).

Zhang, C. 2011. Mapping the exact base of in vivo protein-RNA interactions. *Rockefeller University Postdoctoral Retreat. August 03-04* (selected talk).

Zhang, C. 2011. Elucidating global mammalian RNA-regulatory networks—an integrative systems biology approach. *Rockefeller University. May 31* (special seminar).

Zhang, C., Frias, M.A., Mele, A., Ruggiu, M., Eom, T., Marney, C.B., Wang, H., Licatalosi, D.D., Fak, J.J., Darnell, R.B. 2010. Integrative modeling defines the Nova splicing-regulatory network and its combinatorial controls. *Gordon Research Conference: Biology of Post-transcriptional Gene Regulation. Newport, RI* (RNA Society Poster Award).

Zhang, C. 2010. Elucidating RNA-regulatory networks in the brain. *FASEB Posttranscriptional Control of Gene Expression: Mechanisms of mRNA Decay. July 11-16. Carefree, AZ* (invited talk).

Zhang, C., Frias, M.A., Ruggiu, M., Eom, T., Marney, C.B., Wang, H., Licatalosi, D.D., Mele, A., Fak, J.J., Darnell, R.B., 2010. Integrative discovery and analysis of a global splicing-regulatory network in mouse brain. *Systems Biology: Global Regulation of Gene Expression. Mar 23-27. Cold Spring Harbor, NY* (poster).

Zhang, C. 2009. HITS-CLIP defines in vivo protein-RNA interactions in mouse brain. *New York Illumina Genome Analyzer User Group Meeting. Nov. 18* (invited talk).

Zhang, C. 2009. Integrative discovery and analysis of a global splicing-regulatory network in mouse brain. *Rockefeller University Postdoctoral Retreat. Sep. 21-22* (selected talk).

Zhang, C., Ruggiu, M., Frias, M.A., Eom, T., Marney, C.B., Wang, H., Licatalosi, D.D., Mele, A., Fak, J.J., Darnell, J., Darnell, R.B., 2009. Integrative discovery and analysis of a global splicing-regulatory network in mouse brain. *Eukaryotic mRNA Processing. Aug 18-22. Cold Spring Harbor, NY* (selected talk).

Zhang, C. 2009. From Bayesian network to gene regulatory network: a strategy of information fusion. *Integrative Statistical Analysis of Genome Scale Data. Cold Spring Harbor. June 20.* (invited lecture, with R.B. Darnell).

Zhang, C., Li, W.-H., Krainer, A.R., Zhang, M.Q. 2008. RNA landscape of evolution for optimal exon and intron discrimination. *Systems Biology: Global Regulation of Gene Expression. Mar27-30. Cold Spring Harbor, NY* (poster).

Zhang, C. 2007. Genome evolution and signals for fidelity and regulation of pre-mRNA splicing. *Cold Spring Harbor Laboratory In-House Seminar. Oct. 26. CSHL* (selected talk).

Zhang, C., Zhang, Z., Castle, J., Sun, S., Johnson, J., Krainer, A.R., Zhang, M.Q. 2007. Comprehensive prediction and characterization of pre-mRNA targets of the tissue-specific alternative splicing factors Fox-1/2. *RECOMB Regulatory Genomics 2007. Oct 11-13. MIT/Broad Institute, Boston, NY* (selected talk).

Zhang, C., Zhang, Z., Castle, J., Sun, S., Johnson, J., Krainer, A.R., Zhang, M.Q. 2007. Comprehensive prediction and characterization of pre-mRNA targets of the tissue-specific alternative splicing factors Fox-1/2. *Eukaryotic mRNA Processing. Aug 22-26. Cold Spring Harbor, NY* (selected talk).

Zhang, C., Hasting, M.L., Krainer, A.R., Zhang, M.Q. 2007. Dual-specificity splice sites function alternatively as 5' and 3' splice sites. *Eukaryotic mRNA Processing. Aug 22-26. Cold Spring Harbor, NY* (poster).

Zhang, C., Hasting, M.L., Krainer, A.R., Zhang, M.Q. 2007. Dual-specificity splice sites are used as 3' and 5' splice sites. *Bioinformatics Divesion, TNLIST, Tsinghua University. July 25,2007* (invited talk).

Zhang, C., Hasting, M.L.\*, Krainer, A.R., Zhang, M.Q. 2007. Dual-specificity splice sites are used as 3' and 5' splice sites. *RNA 2007 Annual Meeting. May 29-June3. Madison WI* (\*presenter, selected talk).

Zhang, C., 2006. Profiling alternatively spliced mRNA isoforms for prostate cancer classification. Cambridge Healthtech Institute 6<sup>th</sup> Annual Workshop: Microarray Data and Interpretation. Aug23-25. Washington, DC (invited talk).

Zhang, C., Krainer, A.R., Zhang, M.Q. 2006. Comparative genomics evidence for frequent splicing errors in mammals. *RNA 2006 Annual Meeting. June 20-25. Seattle, WA* (poster).

Zhang, C., Xuan, Z. and Zhang, M.Q. 2005. Weak transcription factor binding sites enrich the genomes. *Mechanisms of Eukaryotic Transcription. Aug 31-Sep4. Cold Spring Harbor Laboratory. NY 11724* (poster).

Zhang, C., Li, Y., Zhang, X. 2004. gMap: extracting and interactively visualizing nonlinear relationships of genes from expression. *Proc. RECOMB 2004, March 2004, pp.228-229* (poster).

## **MENTORING**

01/2015-	Dmytro Ustianenko, Postdoc, Columbia University
08/2013-	Martin Jacko, Graduate Student (Joint with Hynek Wichterle lab), Columbia University
08/2013-	Sebastien Weyn-Vanhentenryck, Graduate Student, Columbia University
2015	Huijuan Feng, Visiting Graduate Student, Tsinghua University
2013-2014	Yong Zhang, Postdoc, Columbia University
2013-2015	Qinghong Yan, Postdoc, Columbia University
2011-2013	Jie Wu, Visiting Graduate Student, CSHL & SUNY at Stony Brook

## **PROFESSIONAL MEMBERSHIP**

2006-present	Member, RNA society
2015-present	Member, AAAS
2010-2011	Associate Faculty Member, Faculty 1000

## **ACADEMIC SERVICES**

- Reviewer for journals including *Anal. of Applied Statistics, BMC Bioinformatics, BMC Genomics, Bioinformatics, Cell, Cell Reports, Cell Systems, Genes and Development, Genome Biology, Genome Research, JoVE, Neuron, Nature Biotechnology, Nature Communications, Nucleic Acids Research, RNA, PLoS Biology, PLoS One, Quantitative Biology, WIRES RNA*, etc.
- Ad hoc reviewer, NIH Molecular Neurogenetics (MNG) study section (10/2016, 02/2017).

- Ad hoc reviewer, NIH Genomics, Computational Biology and Technology (GCAT) study section (02/2016).
- Ad hoc reviewer, MRF Competition for Research Grants (2014).
- Ad hoc reviewer, Columbia University internal grant competition: Edward Mallinckrodt, Jr. Foundation Research Grants (2016), Columbia RISE Competition (2015)
- 
- Thesis committee: Helena Lehrer (Maniatis), Forest Roy (Califano), Angela Xie (Allikmets), Nicholas Hornstein (Sims), Jose Martinez (Hengst), Erik Ladewig (Rabadan), and Kristin Politi (Przedborski).
- Interviewer of Ph.D. or M.D./Ph.D. applicants, Columbia University 2013-current
- K99 Panelist, NIH Career Development & Training Award Workshops. Tri-Institutional Collaboration Network. March 10, 2011.