

**Chaolin Zhang, Ph.D.**

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**Date of Preparation:** Nov 3, 2021

**Academic Appointments:**

- 07/2019- Associate Professor (in Systems Biology; with tenure), Department of Systems Biology, Department of Biochemistry and Molecular Biology, Columbia University College of Physicians and Surgeons, New York, NY.
- 11/2012- Assistant Professor (in Systems Biology), Department of Systems Biology, Department of Biochemistry and Molecular Biology, Columbia University College of Physicians and Surgeons, New York, NY.
- 07/2011- Research Assistant Professor, The Rockefeller University, New York, NY.
- 10/2012

**Education:**

- 08/2004- Ph.D., Cold Spring Harbor Laboratory & Department of Biomedical Engineering, SUNY at Stony Brook, New York, NY.  
07/2008  
Advisors: Michael Q. Zhang and Adrian R. Krainer.  
Thesis: Genome evolution and signals for fidelity and regulation of pre-mRNA splicing.
- 08/2002- PhD program, TNILS, Department of Automation, Tsinghua University, Beijing, China. Advisors: Yanda Li, Xuegong Zhang.
- 06/2004
- 09/1998- B.E., Department of Automation (with honor), Tsinghua University, Beijing, China.  
07/2002

**Postdoctoral Training:**

- 07/2008- Laboratory of Molecular Neuro-Oncology, Howard Hughes Medical Institute, The Rockefeller University, New York, NY.  
07/2011  
Mentor: Robert B. Darnell.

**Other Training:**

- 2013 Cold Spring Harbor Laboratory Summer Course: Mouse Development, Stem Cells & Cancer.
- 2012 Cold Spring Harbor Laboratory Summer Course: Advanced Techniques in Molecular Neuroscience.
- 2011 Short Course: Statistical Learning and Data Mining (taught by Hastie & Tibshirani).
- 2006 Workshop: Sequence Analysis Toward System Biology, Institute for Pure & Applied Mathematics (IPAM), UCLA.

**Honors and Awards:**

- 2011 NIH Earl Stadtman Scholar, semi-finalist.
- 2011 NIH (NIGMS) K99/R00 Pathway to Independence Award.
- 2010 Best Poster Award, Gordon Research Conference: Biology of Post-transcriptional Gene Regulation.
- 2006 Sigma Xi Award.
- 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.

**Professional Activities and Services:**

- 2020-present Co-Organizer, CSHA Conference on Computational Biology of the Genome.
- 2019-present Editorial Board Member, *Quantitative Biology* (Springer)
- 2018 Associate Editor, *Quantitative Biology* (Springer), special issue on RNA Processing and Regulation
- 2017-2021 Scientific Advisory Board. Stoke Therapeutics, Bedford, MA
- 2018 Panelist, PI Crash Course - Skills for Future or New Lab Leaders, Columbia Mailman School of Public Health.
- 2011 Panelist, NIH Career Development & Training Award Workshops. Tri-Institutional Collaboration Network.

### Grant Review Services

Ad hoc reviewer, NSF CAREER Award (BIO/Genetic Mechanisms, 2021)

Ad hoc reviewer, NIH MNG, NCF, GCAT, and GGG (Fellowship) Study Sections (2016-present)

Ad hoc reviewer, Azrieli Science Grants Program, RNA & the Brain (10/2020)

Ad hoc reviewer, Czech Science Foundation grant (08/2018).

Ad hoc reviewer, Columbia University internal competition for Revson Postdoctoral Fellowship (2018).

Ad hoc reviewer, Columbia University RISE award competition (Research Initiative in Science and Engineering) (2015, 2018).

Ad hoc reviewer, Columbia University internal competition for Edward Mallinckrodt, Jr. Foundation Research Grants (2016).

Ad hoc reviewer, MRF Competition for Research Grants (2014).

K99 Panelist, NIH Career Development & Training Award Workshops. Tri-Institutional Collaboration Network (2011).

### Ad-hoc Journal Reviewer

Science, Nature, Cell, PNAS, Neuron, Molecular Cell, Cell Stem Cell, Nature Genetics, Nature Biotechnology, Nature Methods, Nature Neuroscience, Nature Structural and Molecular Biology, Nature Communications, Genes and Development, Genome Research, PLoS Biology, PLoS Genetics, American Journal of Human Genetics, eLife, Cell Reports, Cell Systems, Genome Biology, J Neurosci, Nucleic Acids Research, RNA, Bioinformatics, BMC Bioinformatics, BMC Genomics, Scientific Reports, WIRES RNA, Quantitative Biology, Anals of Applied Statistics, JoVE, Methods (Elsevier), PLoS One.

### **Department and University Services:**

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|--------------|---|
| 2019         | Organizer, Department of Biochemistry and Molecular Biophysics Seminar Series   |
| 2012-present | Member, Center for Motor Neuron Biology and Disease, Columbia University College of Physicians and Surgeons, New York, NY.                                  |
| 2012-present | Member, Cancer Regulatory Networks Group, Herbert Irving Comprehensive Cancer Center, Columbia University College of Physicians and Surgeons, New York, NY. |
| 2016-present | Committee Member, Data Science Institute, Health Analytics.   |
| 2015-present | Scientific and Clinical Steering Committee Member, New York Genome Center.  |
| 2012-present | Faculty Member, Columbia Graduate Program in Cellular, Molecular and Biomedical Studies.  |
| 2015-present | Faculty Member, Columbia Graduate Program in Neurobiology and Behavior.   |
| 2017-present | Department of Systems Biology, Ph.D. Admission Committee.   |
| 2012-present | Interviewer of Ph.D. or M.D./Ph.D. applicants.  |

## Publications:

Google Scholar Citation: 10,637, h-index: 38, i10-index: 44 (as of September 8, 2021).

(\* co-first authors; † co-corresponding authors)

1. Genestine, M., Ambriz, D., Crabtree, G.W., Dummer, P., Molotkova, A., Quintero, M., Mela, A., Biswas, S., Feng, H., Zhang, C., Canoll, P., Hargus, G., Agalliu, D., Gogos, J.A., Au, E. 2020. Vascular-derived SPARC and SerpinE1 regulate interneuron tangential migration and maturation. *eLife*. 10:e56063. DOI: 10.7554/eLife.56063.
2. Alstyne, M.V., Tattoli, I., Delestree, N., Recinos, Y., Workman, E., Shihabuddin, L.S., Zhang, C., Mentis, G.Z., Pellizzoni, L., 2021. Gain of toxic function by long-term AAV9-mediated SMN overexpression in the sensory-motor circuit. *Nat Neurosci*. **24**: 930-940.
3. Feng, H., Moakley, D.F., Chen, S., McKenzie, M.G., Menon, V., Zhang, C. 2021. Complexity and graded regulation of neuronal cell type-specific alternative splicing revealed by single-cell RNA sequencing. *Proc. Nat. Acad. Sci. USA*. **118**: e2013056118.
4. Oku, S., Feng, H., Connor, S.A., Toledo, A., Zhang, P., Zhang, Y., Thoumine, O., Zhang, C., Craig, A.M. 2020. Alternative splicing at neuroligin site A regulates glycan interaction and synaptogenic activity. *eLife*. **9**:e58668.
5. Yu, C., Shen, B., You, K., Huang, Q., Shi, M., Wu, C., Chen, Y., Zhang, C., Li, T. 2020. Proteome-scale analysis of phase-separated proteins in immunofluorescence images. *Brief Bioinform*. DOI: 10.1093/bib/bbaa187.
6. Ustianenko, D., McKenzie, M.G., Zhang, C. 2020. Brain translation – a feather tips the scale. *Mol Cell*. **77**:1155-1156 (preview).
7. Feng, H.\*, Bao, S.\*, Rahman, M., A., Weyn-Vanhentenryck, S.M., Khan, A., Wong, J., Shah, A., Flynn, E.D., Krainer, A.R., Zhang, C., 2019. Modeling RNA-binding protein specificity in vivo by precisely registering protein-RNA crosslink sites. *Mol Cell*. **74**:1189-1204.E6.
8. Wu, D., Schieren, I., Qian, Y., Zhang, C., Jessell, T.M., de Nooij, J.C. 2019. A role for sensory end organ-derived signals in regulating muscle proprioceptor phenotype. *J Neurosci*. **39**:4252-4267.
9. Lee, H. Bao, S., Qian, Y., Geula, S., Leslie, J., Zhang, C., Hanna, J., Ding, L. 2019. Stage-specific requirement for Mettl3-dependent m6A mRNA methylation during haematopoietic stem cell differentiation. *Nat Cell Biol*. **6**:700-709.
10. Bao, S., Moakley, D.F., Zhang, C., 2019. The splicing code goes deep. *Cell*, **176**:414-416 (Leading Edge Preview).
11. Xiao, X.\*†, Zhang, C.\*,† 2018. Special issue on RNA processing and regulation. *Quant Biol*, **6**:193-194 (editorial).

12. Zagore, L.L., Sweet, T.J., Hannigan, M.M., Weyn-Vanhentenryck, S.M., Jobava, R., Hatzoglou, M., Zhang, C., Licatalosi, D.D. 2018. DAZL regulates germ cell survival through a network of polyA-proximal mRNA interactions. *Cell Rep.* **25**: 1225-1240.
13. Yuan, Y., Xie, S., Darnell, J. C., Darnell, A. J., Saito, Y., Phatnani, H., Murphy, E. A., Zhang, C., Maniatis, T. & Darnell, R. B. 2018. Cell type-specific CLIP reveals that NOVA regulates cytoskeleton interactions in motoneurons. *Genome Biol.* **19**:117.
14. Ustianenko, D.\*, Chiu, H.-S.\*, Treiber, T.\*, Weyn-Vanhentenryck, S.M., Treiber, N., Meister, G., Sumazin, P. †, Zhang, C. † 2018. LIN28 selectively modulates a subclass of let-7 microRNAs. *Mol. Cell.* **71**: 271-283.e5.

-cover story, July 19 issue.

15. Weyn-Vanhentenryck, S.M.\*, Feng, H.\*, Ustianenko, D., Duffié, R., Yan, Q., Jacko, M., Martinez, J.C., Goodwin, M., Zhang, X., Hengst, U., Lomvardas, S., Swanson, M.S., Zhang, C. 2018. Precise temporal regulation of alternative splicing during neural development. *Nat Commun.* **9**:2189.
16. Luo, W., Zhang, C., Jiang, Y., Brouwer, C.R. 2018. Systematic reconstruction of autism biology from massive genetic mutation profiles. *Sci Adv.* **4**: e1701799.
17. Bao, X., Guo, X., Yin, M., Tariq, M., Lai, Y., Kanwal, S., Zhou, J., Li, N., Lv, Y., Pulido-Quetglas, C., Wang, X., Ji, L., Khan, M. J., Zhu, X., Luo, Z., Shao, C., Lim, D.-H., Liu, X., Li, N., Wang, W., He, M., Liu, Y.-L., Ward, C., Wang, T., Zhang, G., Wang, D., Yang, J., Chen, Y., Zhang, C., Jauch, R., Yang, Y.-G., Wang, Y., Qin, B., Anko, M.-L., Hutchins, A. P., Sun, H., Wang, H., Fu, X.-D., Zhang, B. & Esteban, M. A. 2018. Capturing the interactome of newly transcribed RNA. *Nat Meth.* **15**:213-220.
18. Jacko, M., Weyn-Vanhentenryck, S.M., Smerdon, J.W., Yan, R., Feng, H., Williams, D.J., Pai, J., Xu, K., Wichterle, H. †, Zhang, C. † 2018. Rbfox splicing factors promote neuronal maturation and axon initial segment assembly. *Neuron*, **97**: 853-868.e6.

-Issue highlight.

-Press release: “Research Unveils a Developmental Splicing Program Controlling Neuronal Maturation and Excitability”. CUMC News Room.

<http://newsroom.cumc.columbia.edu/blog/2018/02/08/new-insights-neurons-become-mature-excitable/>.

19. Ustianenko, D., Weyn-Vanhentenryck, S.M., Zhang, C. 2017. Microexons: discovery, regulation, and function. *WIREs RNA*. e1418. doi: 10.1002/wrna.1418 (review).
  20. Zhang, C.\*, †, Shen, Y.\* † 2017. A cell type-specific expression signature predicts haploinsufficient autism-susceptibility genes. *Hum Mut.* **38**: 204-215.
- News release: “Third-party gene scores added to SFARI Gene”. SFARI.  
<https://www.sfari.org/2017/12/14/third-party-gene-scores-added-to-sfari-gene/>.
21. Shah, A., Qian, Y., Weyn-Vanhentenryck, S.M., Zhang, C. 2017. CLIP Tool Kit (CTK): a flexible and robust pipeline to analyze CLIP sequencing data. *Bioinformatics*, **33**:566-567. DOI: 10.1093/bioinformatics/btw653.

22. 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.* **12**:1159-1168.
23. 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?”, *Nat Meth*, 12:910 (2015).
24. 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.
25. 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.
26. Zhang, Y., Chen, K., Sloan, S., Bennett, M.L., Scholze, A.R., O’Keeffe, S., Phatnani, H.P., Guarnieri, P., Caneda, C., Ruderisch, N., Deng, S., Liddelov, 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.
27. Weyn-Vanhentenryck, 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.
28. 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.
29. 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.
30. 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.
31. 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.
32. 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.

33. 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.
34. 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.
35. 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.
36. 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.
37. 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.
38. 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.
39. 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.
40. **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.
41. **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.
42. 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.

43. 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.
44. **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.
45. **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.
46. **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.
47. **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.
48. **Zhang, C.**, Zhang, X., Zhang, M.Q., Li, Y. 2007. Neighbor number, valley seeking and clustering. *Pattern Recogn. Lett.* **28**:173-180.
49. 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.
50. **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.
51. **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)
52. **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

53. **Weyn-Vanhentenryck, S.M.**, **Zhang, C.** 2016. mCards: genome-wide prediction of clustered sequence motifs as binding sites for RNA-binding proteins. *Methods Mol Biol.* 1421:215-226.
54. **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.
55. **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.
56. **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 Lectures:**

- 11/2021. 2021 Precision Medicine Scholars' Day (zoom; invited talk).
- 11/2021. Deciphering the role of RNA-binding proteins in neurodevelopment and disease. Webinar organized by Science Magazine (zoom; invited talk).
- 10/2021. Biogen (zoom; invited talk)
- 07/2021. Human Genetics in NYC (zoom; invited talk)
- 05/2021. Genetics, Genomics, and Systems Biology (GGSB) Seminar Series. University of Chicago (zoom; invited talk)
- 04/2020. Center for RNA Science and Therapeutics. Case Western Reserve University (invited talk, to be rescheduled)
- 10/2019. Francis Crick Institute (invited talk)
- 10/2019. Wellcome Trust Workshop on Neuronal Maturation. London, UK (invited talk).
- 09/2019. EMBO Workshop on RNP Network Dynamics in Development and Disease. Ljubljana, Slovenia (invited talk).
- 05/2019. Biomedical Informatics Seminar Series, Ohio State University. Columbus, OH (canceled).
- 03/2019. Department of Pharmacology, Northwestern University, Chicago, IL.
- 03/2019. UCLA Bioinformatics Seminar Series. UCLA, Los Angeles, CA.
- 01/2019. Department of Microbiology, Biochemistry and Molecular Genetics and Public Health Research Institute Joint Seminar Series, Rutgers New Jersey Medical School, Newark, NJ.
- 11/2018. Institute for Basic Science (IBS) Conference on RNA Biology, Seoul, Korea (canceled).
- 10/2018. Cold Spring Harbor Asia Conference on RNA Biology. Suzhou, China (canceled).
- 10/2018. Institute for Computational Biomedicine, Weill Cornell Medicine, New York, NY.
- 09/2018. Emory Graduate Program in Genetics and Molecular Biology (GMB) & Department of Pharmacology Joint Seminar, Emory University, Atlanta, GA.
- 07/2018. ISMB RNA-SIG Meeting. Chicago, IL.
- 04/2018. New York Genome Center Five Points Seminar Series. New York, NY.
- 03/2018. American Society for Neurochemistry Symposium. Irvine, CA.
- 08/2017. Otto Warburg Summer School Symposium. Shanghai, China.
- 07/2017. Tsinghua University Biology (THUBio) Reunion, New York, NY.

07/2016. Bioinformatics Division, TNLIST, Tsinghua University, Beijing, China.

04/2016. Department of Biological Sciences Seminar Series, St John's University. Queens, NY.

02/2016. Penn State University Neuroscience Seminar. University Park, PA.

02/2016. Amgen Inc. Boston, MA.

01/2016. Robert H Lurie Comprehensive Cancer Center, Northwestern University. Chicago, IL.

09/2015. Center for RNA Biology, Ohio State University. Columbus, OH.

06/2014. International Congress of Endocrinology & the Endocrine Society (ICE/Endo) Annual Meeting. Chicago, IL.

10/2012. Bioinformatics Division, TNLIST, Tsinghua University, Beijing, China.

10/2012. Tsinghua Symposium on Genomics and Epigenomics. Beijing. China.

10/2012. CSHA meeting on RNA Biology. Suzhou. China.

09/2012. CAS-MPG Partner Institute for Computational Biology. Shanghai, China.

11/2011. ASN Annual meeting Advances in Research Conference: MicroRNA. Philadelphia. PA.

10/2011. Rockefeller Bioinformatics/Biostatistics Collaborative Group meeting. Rockefeller University, New York NY.

07/2010. FASEB Posttranscriptional Control of Gene Expression: Mechanisms of mRNA Decay. Carefree, AZ.

11/2009. New York Illumina Genome Analyzer User Group Meeting. New York, NY.

## **Teaching Experience and Responsibilities:**

### Course Teaching

2015-present      Co-Instructor, Graduate Course "Deep Sequencing" (G4017).

2016-present      Lecturer, Graduate Course "Biochemistry, Cell and Molecular Biology I" (G6300).

2019                CUMC Integrated Program Orientation on Experimental Design.

2018                Lecturer, MD Course "Molecular Mechanisms and Disease".

### Other Teaching Activities

2018                Invited Speaker, Current Topics in Molecular Genetics (IBS 515), Graduate Program in Genetics and Molecular Biology (GMB) at Emory University

2017	Invited Speaker, Otto Warburg Summer School on RNA Biology: Diverse Functions Revealed by Global Analysis. Shanghai, China.
2017	Speaker, Department of Systems Biology Faculty, Ph.D. Student Recruit.
2016	Speaker, Columbia University Graduate Program in Neurobiology and Behavior Bootcamp.
2016-present	Speaker, Department of Systems Biology Faculty Research Seminar Series.
2013, 2014, 2016	Speaker, Department of Systems Biology Retreat.
2013	Speaker, Department of Biochemistry and Molecular Biophysics Retreat.
2013	Invited Speaker, RNA-seq in Biomedical Research Workshop, Columbia University Genome Center.
2007	Invited Speaker, New York Illumina Genome Analyzer User Group Meeting.

### **Advising and Mentorship:**

#### Post Doctoral Research Scientists

2021-present	Brian Joseph, PhD, Memorial Sloan Kettering Cancer Center.
2021-present	Georgia Dermentzaki, PhD, University of Athens.
2019-present	Melissa McKenzie, MD/PhD, New York University.
2016-present	Huijuan Feng, Ph.D., Tsinghua University, Beijing.
2017-2021	Suying Bao, Ph.D., University of Hong Kong. - Columbia Precision Medicine Research Fellowship (2018-2020)
2015-2021	Dmytro Ustianenko, Ph.D., Masaryk University, Brno, Czech Republic.
2018-2019	Brittany L Phillips, Ph.D., Emory University. - Currently Medical Writer 2 at Chrysalis Medical Communications
2013-2015	Qinghong Yan, Ph.D., Stony Brook University. - Currently Senior Scientist at Amgen.
2013-2014	Yong Zhang, Ph.D., The Chinese Academy of Science.

#### Graduate Students

2018-present	Daniel Moakley, Integrated Program in CMBS.
2018-present	Yocelyn Recinos, Integrated Program in CMBS. - NSF Graduate Research Fellowship.
2013-2017	Sebastien Weyn, Integrated Program in CMBS, Columbia University.

- Recipient of the 2018 Titus M Coan Prize for Excellence in Research
  - Currently Bioinformatics Scientist at Stoke Therapeutics.
- 2013-2017      Martin Jacko, Pathobiology & Molecular Medicine (joint with Hynek Wichterle).
- Currently Postdoc at Stanford University.
- 2015              Huijuan Feng, Visiting Ph.D. student from Tsinghua University, Beijing.
- Winner of Outstanding Thesis Award at Tsinghua University and National Scholarship based on work in the lab.
  - Currently Postdoctoral Research Scientist in the lab.
- 2012-2013      Jie Wu, Visiting Ph.D. student from CSHL.
- Joined MIT as a Bioinformatics Scientist upon graduation.
  - Currently Senior Research Scientist at Philips.

### Undergraduate and Master Students

- 2017-present      Lekha Yesantharao, Columbia College, Undergraduate Research Student.
- 2017-present      Justin Wong, Columbia College, Undergraduate Research Student.
- Simons scholarship for undergraduate summer research (2017).
- 2017              Helene Lovett, Harvard University, Summer Undergraduate Research Student. Amgen Scholarship (2017).
- 2015-2017      Ankeeta Shah, Barnard College, Undergraduate Research Student.
- Amgen Scholarship (2016).
  - Goldwater Scholarship (2016).
  - Currently Graduate Student, University of Chicago.
- 2015-2016      Kevin Huynh, M.S. Technician.
- Currently MD Program, UCSF.
- 2016              Jiaye Li, Master Student, Biotechnology Program, Columbia University. Master thesis research.
- 2016              Jingxian You, Fudan University (Shanghai, China), Summer Undergraduate Research Student.
- Currently Master Student, Imperial College London.
- 2015-2017      Jonah Lee, Columbia College, Undergraduate Research Student.
- 2013-2016      Joy Pai, Columbia College, Undergraduate Research Student.
- Amgen Scholarship.
  - Currently Bioinformatician, Rockefeller University.
  - Will join Stanford University for graduate study.
- 2015              Kernyu Park, Columbia College, Undergraduate Research Student.
- Currently Master student, Biomedical Informatics Program, Columbia University.