Postdoc Positions – Computational or Experimental RNA Biology - Columbia University

Keywords: Bioinformatics, AI/ML, RNA, splicing, new technology development, Precision Medicine, CLIP, Protein-RNA interactions, neuron, cilia, deno-evo, health, disease

Chaolin Zhang lab – networking in the RNA world

The Laboratory of **Dr. Chaolin Zhang** in Department of Systems Biology, Columbia University Irving Medical Center (CUIMC) has multiple postdoctoral openings to conduct research on mammalian RNA regulatory networks and RNA-based precision medicine.

Taking a multidisciplinary approach that tightly integrates biochemistry, molecular biology, genome engineering and high-throughput data analysis and integrative modeling, the Zhang Laboratory studies how RNA and proteins interact to form regulatory networks in the nervous system at the mechanistic and systems levels, how these networks contribute to intrinsic neuronal functional properties, and how such properties are implicated in health and disease. We are working to translate fundamental discoveries to RNA-based precision medicine for devastating disorders with unmet medical needs. The Zhang lab consists of a group of inspired and creative scientists from diverse background. Recent lab members have successfully transitioned into prominent

academic and pharmaceutical industry positions. More information about the Zhang laboratory can be found at http://zhanglab.c2b2.columbia.edu.

Experimental RNA biology, especially those interested in high-throughput genomics technology development.
The candidates will lead exciting projects that aim to understand fundamental mechanisms of RNA-protein interactions and alternative RNA splicing regulation in normal and disease contexts, as well as evolutionary changes of RNA regulation with functional implications. The candidates will develop new technologies to probe protein-RNA interactions that push the boundaries of the current state of the art, with powerful applications in human genetic studies and precision medicine. The candidates will also have opportunities to use CRISPR genome editing to engineer pluripotent stem cell (ESC/iPSC) lines, differentiate these cells to neurons, and apply various cutting-edge technologies to characterize protein-RNA interactions, alternative splicing regulation, and function on a genome-wide scale. The candidates will work in a dynamic environment and also work closely with computational biologists. Strong mentorship will be provided to help them achieve their career goals.

AI/ML, bioinformatics, computational genomics interested in RNA biology.
The candidates will participate in and lead exciting projects that aim to understand fundamental mechanisms of RNA-protein interactions and alternative RNA splicing regulation in normal and disease contexts. Innovative computational and machine learning-based approaches will be used to develop predictive models for analysis of high-throughput genomic data, including large scale bulk/scRNA-seq and CLIP-seq in various cellular contexts, as well as other genomic and genetic variant datasets. The candidates will work in a dynamic environment and also work closely with experimental biologists. Strong mentorship will be provided to help them achieve their career goals.

Selected recent publications:

1. 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.

2. 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.

3. Bao, S., Moakley, D.,F., Zhang, C., 2019. The splicing code goes deep. Cell, 176:414-416 (Leading Edge Preview).

4. 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).

5. 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.

6. 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).

7. Ustianenko, D., Weyn-Vanhentenryck, S.M., Zhang, C. 2017. Microexons: discovery, regulation, and function. WIREs RNA. e1418. doi: 10.1002/wrna.1418 (review).

8. 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.

9. 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 (highlighted by Nat Meth, 12:910).

10. Yan, Q.* , Weyn-Vanhentenrycka, 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.

Required/desired qualifications:

Wet lab:
1. A Ph.D. or equivalent degree in a Molecular Biology/Biochemistry/Molecular Neuroscience, or related fields

2. Strong background in experimental RNA biology. Experience of performing high-throughput genomic assays such as CLIP is a plus.

3. Extensive experience in mammalian cell culture. Experience working with stem cells and neuronal differentiation and characterization is a plus.

4. Experience in genomic technology development is a plus.

5. Basic bioinformatics, programming and quantitative analysis skills is not required but a plus.

6. Highly motivated and ability to work independently as well as to collaborate in a group setting.

7. Excellent written and verbal communication skills

8. A minimal of one first-author paper published in related peer-reviewed journals

Dry lab:
1. A Ph.D. degree in Computational or Systems Biology, Bioinformatics, Computer Sciences, or related fields

2. A genuine interest in solving complex biological problems using quantitative approaches

3. Strong background in statistical modeling and machine learning; experience in genomic analysis using deep neural networks is a plus.

4. Solid programing skills (eg., C/C++ and/or python/perl)

5. Extensive experience in handling large-scale genomic data. Experience in deep sequencing data analysis is a plus.

6. Highly motivated and ability to work independently as well as to collaborate in a team setting

7. Excellent written and verbal communication skills

8. A minimal of one first-author paper published in related peer-reviewed journals

Compensation:

Salary range: $60,000 - $70,000
The salary of the finalist selected for this role will be set based on a variety of factors, including but not limited to departmental budgets, qualifications, experience, education, licenses, specialty, and training. The above hiring

range represents the University's good faith and reasonable estimate of the range of possible compensation at the time of posting.

Applicants should send a curriculum vitae and names and contacts of three references to:

Dr. Chaolin Zhang
630 W 168th Street
P&S Building, Room 4-448
New York NY 10032
(212)305-9354
cz2294@columbia.edu
zhanglab.c2b2.columbia.edu