

Postdoc Position –RNA, Neuronal Cell Biology & Evolution- Columbia University

Keywords: RNA, alternative splicing, neuron, evo-devo, cilia & ciliopathies



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 as funded by NIH and other funding sources. **This posting is to search for candidates to work on a project the role of lineage alternative exons in the context neurodevelopment, including cilia function & ciliopathies.**

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>.

The candidates will lead an exciting project that aims to understand the function of lineage-specific alternative exons, especially in a group of cilia genes, in neurodevelopment and genetic diseases. The candidates will use an array of molecular and cell biology approaches, such as cloning, transient/stable expression, RT-PCR/qPCR, westernblots, IP/co-IP, RNASeq, flow cytometry, CRISPR/gene editing, stem cell differentiation, molecular biology, and other cutting-edge methods. Studies will be performed in both cell (including ESC/iPSC) and mouse models. The candidates will work in a dynamic and interdisciplinary environment at Columbia University Medical Center. 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.](#), [Kraimer, 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-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.

Required/desired qualifications:

A Ph.D. or equivalent degree in a Molecular Biology, Cell Biology, Neurobiology, or related fields

This position requires independence, effective communication, critical thinking, creativity, multi-tasking, organization, and the ability to work in a collaborative research environment.

The ideal candidate will have previous experience with cilia biology in cell culture and animal models, strong background in molecular & cell biology, and familiarity with neurobiology.

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

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