

Jun Zhang

CURRICULUM VITAE

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Education:

2006-2011 **The University of North Carolina at Chapel Hill**, Chapel Hill, NC, USA
Ph.D. in Biochemistry and Biophysics (May 2011)
Advisor: Dr. [Andrew L. Lee](#)

2003-2006 **Tsinghua University** Beijing, China
M.S. Degree in Biophysics
Advisor: Dr. [Yong-bin Yan](#)

1999-2003 **Nankai University**, Tianjin, China
B.S Degree in Physics
Advisor: Professor Wenxiu Yang

Research and Professional Appointments:

2023-present **University of Alabama at Birmingham**, Department of Chemistry, Birmingham, AL, USA
Associate Professor

2016-2023 **University of Alabama at Birmingham**, Department of Chemistry, Birmingham, AL, USA
Tenure-track Assistant Professor

2011-2016 **National Institute of Environmental Health Sciences, National Institutes of Health**, RTP, NC, USA
Visiting Fellow
Advisor: Dr. [Traci M.T. Hall](#)

2006-2011 **The University of North Carolina at Chapel Hill**, Chapel Hill, NC, USA
Ph.D candidate
Advisor: Dr. Andrew L. Lee

2003-2006 **Tsinghua University**, Beijing, China
Master student
Advisor: Dr. Yong-bin Yan

Fellowships, Honors, and Awards:

UAB Faculty Fellows in Undergraduate Research, 2021-2022
UAB Faculty Development Grant Program, 2017
Paper of the Year, NIEHS, 2016
Paper of the Year, NIEHS, 2014
Visiting Fellow of National Institutes of Health (2011-2016) in the laboratory of Dr. Traci Hall, NIEHS
Student of Comprehensive Excellence, First Place, Tsinghua University, 2005

Professional Societies:

American Chemical Society
RNA Society

Research Interests:

Structure of RNA-binding proteins
Intrinsically disordered proteins
mRNA alternative splicing
Protein dynamics, folding and allostery
Structural Biology approached by NMR, crystallography and SAXS

Funding:

Faculty Development Grant Program, 2017-2018, UAB, PI
National Science Foundation, MCB, “Regulatory Functions of Intrinsically Disordered Electronegative Clusters (ENC) in RNA-Binding Proteins”, 2020-2024, PI
National Institutes of Health, NIGMS, R35, “The Central Roles of SRSF1 in early-stage spliceosome assembly”, 2022-2027, PI

University Committee Responsibilities:

Graduate Student Thesis Committee, Department of Chemistry, UAB
Graduate Student Recruiting Committee, Department of Chemistry, UAB

Ad Hoc Journal Reviewer:

Early Career Reviewer for Journal Biological Chemistry
Nucleic Acids Research
Nature Communications
Biophysical Journal
Biochemistry
Protein & Cell
Protein Science
The Journal of Physical Chemistry
Biochemical and Biophysical Research Communications
PLOS One

Frontiers in Molecular Biosciences
PeerJ
Molecules
Journal of Biomolecular Structure & Dynamics
Journal of Visualized Experiments
Frontiers in Life Science
Biochemistry and Biophysics Reports
BioTechniques

Ad Hoc Grant Reviewer:

The National Science Center in Poland
Breast Cancer Research Foundation of Alabama

Presentations:

1/11/2011, 40th Keystone Symposia, Frontiers of NMR in Biology, Big Sky, Montana, USA.
“Phosphorylation of PDZ3 and its potential function in PSD-95”.

12/18/2013, Center for RNA Biology Meeting. Duke University, Durham, North Carolina, USA.
“How the negatively-charged C-terminal tail of Drosophila stem-loop mRNA binding protein enhances RNA-binding without touching the RNA”

8/28/2014, 26th International Conference on Magnetic Resonance in Biological Systems, Dallas, TX, USA. “Molecular mechanisms for the regulation of histone mRNA stem-loop binding protein by phosphorylation”

3/5/2015, Epigenetics & Stem Cell Biology Laboratory of NIEHS, Research Triangle Park, North Carolina, USA. “Structural study of nop9, an atypical pumilio/FBF protein family essential in ribosomal biogenesis”

1/26/2016, University of Alabama at Birmingham, Birmingham, Alabama. “Structural and Dynamic insights into RNA binding proteins: Stories of Nop9 and histone mRNA stem-loop binding protein”.

3/15/2017, Frontiers of NMR in Life Sciences. Structural analysis reveals the flexible C-terminus of Nop15 undergoes rearrangement to recognize a pre-ribosomal RNA folding intermediate

10/26/2018, “Functions of electronegative clusters in RNA-binding proteins”, Tennessee Technological University, TN, USA.

3/14/2019, UAB-SERCAT Structural Biology Symposium, “Regulation of SRSF1 function via phosphorylation-modulated intramolecular interactions: The tail tells the head what to do”, Birmingham, AL, 35294

4/27/2021, Experimental Biology 2021, ASBMB, “Intrinsically disordered electronegative clusters improve stability and binding specificity of RNA-binding proteins”.

9/10/2021, University of North Dakota, Department of Chemistry, “Intrinsically disordered electronegative clusters improve stability and binding specificity of RNA-binding proteins”.

10/8/2021, University of South Florida, Department of Molecular Medicine, “Intrinsically disordered electronegative clusters improve stability and binding specificity of RNA-binding proteins”.

11/10/2021, Southeastern Regional Meeting of ACS (SERMACS), Session Chair of General Biochemistry.

2/10/2022, Middle Tennessee State University, Department of Chemistry, Regulatory Roles of Unstructured Regions in RNA-binding proteins.

2/18/2022, Mississippi State University, Department of Chemistry, Regulatory Roles of Unstructured Regions in RNA-binding proteins.

4/28/2022, University of Alabama, Department of Chemistry & Biochemistry, The central role of Arg-Ser repeats in early-stage spliceosome assembly.

10/13/2022, 2022 RNA Society of North Carolina Symposium, RTP, NC, USA. The central role of SRSF1 in spliceosome assembly.

8/24/2023, University of Alabama at Birmingham, Department of Microbiology, Birmingham, AL, USA. The central role of Arg-Ser repeats in early-stage spliceosome assembly.

9/1/2023, University of Missouri, Department of Biochemistry, Columbia, MO, USA. The central role of Arg-Ser repeats in early-stage spliceosome assembly.

Teaching Responsibilities:

Fundamental Biochemistry, CH460/CH760

Advanced Biochemistry, CH461/CH761

Fundamentals, CH700

Special Topics in Biochemistry, CH669/769

Publications:

1. Zaharias, S., Fargason, T., Greer, R., Song, Y. and Zhang, J. (2023) Electronegative clusters modulate folding status and RNA binding of unstructured RNA-binding proteins. *Protein Sci*, **32**, e4643.
2. Fargason, T., De Silva, N.I.U., King, E., Zhang, Z., Paul, T., Shariq, J., Zaharias, S. and Zhang, J. (2023) Peptides that Mimic RS repeats modulate phase separation of SRSF1, revealing a reliance on combined stacking and electrostatic interactions. *Elife*, **12**.
3. Brettrager, E.J., Cuya, S.M., Tibbs, Z.E., Zhang, J., Falany, C.N., Aller, S.G. and van Waardenburg, R. (2023) N-terminal domain of tyrosyl-DNA phosphodiesterase I regulates topoisomerase I-induced toxicity in cells. *Sci Rep*, **13**, 1377.

4. Yang, Y., Kozlovskaya, V., Zhang, Z., Xing, C., Zaharias, S., Dolmat, M., Qian, S., Zhang, J., Warram, J.M., Yang, E.S. *et al.* (2022) Poly(N-vinylpyrrolidone)-block-Poly(dimethylsiloxane)-block-Poly(N-vinylpyrrolidone) Triblock Copolymer Polymersomes for Delivery of PARP1 siRNA to Breast Cancers. *ACS Appl Bio Mater*, **5**, 1670-1682.
5. De Silva, N.I.U., Fargason, T., Zhang, Z., Wang, T. and Zhang, J. (2022) Inter-domain Flexibility of Human Ser/Arg-Rich Splicing Factor 1 Allows Variable Spacer Length in Cognate RNA's Bipartite Motifs. *Biochemistry*, **61**, 2922-2932.
6. Zaharias, S., Zhang, Z., Davis, K., Fargason, T., Cashman, D., Yu, T. and Zhang, J. (2021) Intrinsically disordered electronegative clusters improve stability and binding specificity of RNA-binding proteins. *J Biol Chem*, **297**, 100945.
7. Zhang, J., Teramoto, T., Qiu, C., Wine, R.N., Gonzalez, L.E., Baserga, S.J. and Tanaka Hall, T.M. (2020) Nop9 recognizes structured and single-stranded RNA elements of preribosomal RNA. *RNA*, **26**, 1049-1059.
8. Fargason, T., Wang, T., De Silva, N.I.U., Zhang, Z., McKelvey, H., Knapp, T., Zaharias, S. and Zhang, J. (2020) Amide additives improve RDC measurements in polyacrylamide. *J Biomol NMR*, **74**, 119-124.
9. Davis, K.B., Zhang, Z., Karpova, E.A. and Zhang, J. (2018) Application of tyrosine-tryptophan fluorescence resonance energy transfer in monitoring protein size changes. *Anal Biochem*, **557**, 142-150.
10. Zhang, J., Gonzalez, L.E. and Hall, T.M.T. (2017) Structural analysis reveals the flexible C-terminus of Nop15 undergoes rearrangement to recognize a pre-ribosomal RNA folding intermediate. *Nucleic Acids Res*, **45**, 2829-2837.
11. Skrajna, A., Yang, X.C., Bucholc, K., Zhang, J., Hall, T.M.T., Dadlez, M., Marzluff, W.F. and Dominski, Z. (2017) U7 snRNP is recruited to histone pre-mRNA in a FLASH-dependent manner by two separate regions of the stem-loop binding protein. *RNA*, **23**, 938-951.
12. Law, A.B., Sapienza, P.J., Zhang, J., Zuo, X. and Petit, C.M. (2017) Native State Volume Fluctuations in Proteins as a Mechanism for Dynamic Allostery. *J Am Chem Soc*, **139**, 3599-3602.
13. Zhou, X., Liu, Z., Zhang, J., Adelsberger, J.W., Yang, J. and Burton, G.F. (2016) Alpha-1-antitrypsin interacts with gp41 to block HIV-1 entry into CD4+ T lymphocytes. *BMC Microbiol*, **16**, 172.
14. Zhang, J., McCann, K.L., Qiu, C., Gonzalez, L.E., Baserga, S.J. and Hall, T.M. (2016) Nop9 is a PUF-like protein that prevents premature cleavage to correctly process pre-18S rRNA. *Nat Commun*, **7**, 13085.
15. McCann, K.L., Teramoto, T., Zhang, J., Tanaka Hall, T.M. and Baserga, S.J. (2016) The molecular basis for ANE syndrome revealed by the large ribosomal subunit processome interactome. *Elife*, **5**.
16. Zhang, J., Tan, D., DeRose, E.F., Perera, L., Dominski, Z., Marzluff, W.F., Tong, L. and Hall, T.M. (2014) Molecular mechanisms for the regulation of histone mRNA stem-loop-binding protein by phosphorylation. *Proc Natl Acad Sci U S A*, **111**, E2937-2946.
17. Zhang, J., Lewis, S.M., Kuhlman, B. and Lee, A.L. (2013) Supertertiary structure of the MAGUK core from PSD-95. *Structure*, **21**, 402-413.
18. Zhang, J., Petit, C.M., King, D.S. and Lee, A.L. (2011) Phosphorylation of a PDZ domain extension modulates binding affinity and interdomain interactions in postsynaptic density-

- 95 (PSD-95) protein, a membrane-associated guanylate kinase (MAGUK). *J Biol Chem*, **286**, 41776-41785.
19. Zhang, J., Sapienza, P.J., Ke, H., Chang, A., Hengel, S.R., Wang, H., Phillips, G.N. and Lee, A.L. (2010) Crystallographic and nuclear magnetic resonance evaluation of the impact of peptide binding to the second PDZ domain of protein tyrosine phosphatase 1E. *Biochemistry*, **49**, 9280-9291.
 20. Petit, C.M., Zhang, J., Sapienza, P.J., Fuentes, E.J. and Lee, A.L. (2009) Hidden dynamic allostery in a PDZ domain. *Proc Natl Acad Sci U S A*, **106**, 18249-18254.
 21. Zhang, J. and Yan, Y.B. (2008) Oligomerization and aggregation of bovine pancreatic ribonuclease A: backbone hydration probed by infrared band-shift. *Protein Pept Lett*, **15**, 650-657.
 22. Whitley, M.J., Zhang, J. and Lee, A.L. (2008) Hydrophobic core mutations in CI2 globally perturb fast side-chain dynamics similarly without regard to position. *Biochemistry*, **47**, 8566-8576.
 23. Jiang, Y., Su, J.T., Zhang, J., Wei, X., Yan, Y.B. and Zhou, H.M. (2008) Reshaping the folding energy landscape of human carbonic anhydrase II by a single point genetic mutation Pro237His. *Int J Biochem Cell Biol*, **40**, 776-788.
 24. Zhang, J., He, H.W., Wang, Q. and Yan, Y.B. (2006) Sequential events in ribonuclease A thermal unfolding characterized by two-dimensional infrared correlation spectroscopy. *Protein Pept Lett*, **13**, 33-40.
 25. Yan, Y.B., Zhang, J., He, H.W. and Zhou, H.M. (2006) Oligomerization and aggregation of bovine pancreatic ribonuclease A: characteristic events observed by FTIR spectroscopy. *Biophys J*, **90**, 2525-2533.
 26. Kim, S.H., Zhang, J., Jiang, Y., Zhou, H.M. and Yan, Y.B. (2006) Assisting the reactivation of guanidine hydrochloride-denatured aminoacylase by hydroxypropyl cyclodextrins. *Biophys J*, **91**, 686-693.
 27. Zhang, J. and Yan, Y.B. (2005) Probing conformational changes of proteins by quantitative second-derivative infrared spectroscopy. *Anal Biochem*, **340**, 89-98.
 28. He, H.W., Zhang, J., Zhou, H.M. and Yan, Y.B. (2005) Conformational change in the C-terminal domain is responsible for the initiation of creatine kinase thermal aggregation. *Biophys J*, **89**, 2650-2658.