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Education

Ph.D., Biochemistry, University of Wisconsin-Madison, 2002.
M.S., Computer Sciences, University of Wisconsin-Madison, 2001.
M.S., Molecular Biology, Institute of Biophysics, Chinese Academy of Sciences, China, 1997.
B.S., Chemical Physics, University of Science and Technology of China, China, 1994.

Professional Experience

2020–present Professor, Department of Biochemistry, University of California, Riverside.
2017–2020 Associate Professor, Department of Biochemistry, University of California, Riverside.
2012–2017 Assistant Professor, Department of Biochemistry, University of California, Riverside.
2007–2011 Senior Scientist (2010-2011)/Research Associate (2007-2010), Structural Biology Program, Memorial Sloan-Kettering Cancer Center. New York. “Investigation of molecular mechanisms underlying epigenetic regulation”.
2002–2007 Assistant Researcher, NMR Team Leader (2005-2007), Center for Eukaryotic Structural Genomics, University of Wisconsin, Madison.
1997–2002 Research Assistant, Department of Biochemistry, University of Wisconsin, Madison. “Structure-Function Investigation of Proteinases and Proteinase Inhibitors”.
1994–1997 Research Assistant, Biophysics Institute, Chinese Academy of Sciences. Beijing, China. “Study on the folding of N-terminal fragments of *Staphylococcal Nuclease* with various lengths”.

Awards

2013-2015 Basil O'Connor Starter Scholar Research Award, March of Dimes Foundation
2013 Robert T. Poe Faculty Development Grant, Chinese American Faculty Association of Southern California
2013-2014 Regents' Faculty Fellowship, University of California, Riverside
2014-2015 Hellman Fellowship, Hellman Family Foundation
2015-2017 Kimmel Scholar, Sidney Kimmel Foundation for Cancer Research

Scientific Publications

(* These authors have contributed equally to this work; #Corresponding authors)

Institute of Biophysics, Chinese of Academy of Sciences: 1994-1997

1. **Song J**, Dai J, Jing G, Wang J. Study on Folding of N-Terminal Fragments of SnaseR. *Acta Biophysica Sinica* 1997, 13(4):545-550.

University of Wisconsin-Madison: 1997-2007

2. Qasim MA, Lu SM, Ding J, Bateman KS, James MN, Anderson S, **Song J**, Markley JL, Ganz PJ, Saunders CW, Laskowski M Jr. Thermodynamic criterion for the conformation of P1 residues of substrates and of inhibitors in complexes with serine proteinases. *Biochemistry*.1999, 38(22):7142-50.
3. Hemmi H, Studts, JM, Chae YK, **Song J**, Markley JL, Fox BG. Solution structure of the toluene 4-monooxygenase effector protein (T4moD). *Biochemistry*. 2001, 40(12):3512-24.
4. **Song J**, Markley J.L. NMR chemical shift mapping of the binding site of a protein proteinase inhibitor: changes in the (1)H, (13)C and (15)N NMR chemical shifts of turkey ovomucoid third domain upon binding to bovine chymotrypsin A(alpha). *J Mol Recognit*. 2001, 14(3):166-71.
5. **Song J**, Laskowski M Jr, Qasim MA., Markley JL. NMR Determination of pK_a Values for Asp, Glu, His, and Lys Mutants at each Variable Contiguous Enzyme-Inhibitor Contact Position of Turkey Ovomucoid Third Domain. *Biochemistry*. 2003, 42(10):2847-2856.
6. **Song J**, Markley JL. Protein Inhibitors of Serine Proteinases: Role of Backbone Structure and Dynamics in Controlling the Hydrolysis Constant. *Biochemistry*. 2003, 42(18):5186-5194.
7. **Song J**, Qasim MA, Laskowski M Jr., Markley JL. Two Conformational States of Turkey Ovomucoid at Low pH: Three-Dimensional Structures, Internal Dynamics, and Interconversion Kinetics and Thermodynamics. *Biochemistry*. 2003, 42(21):6380-6391.
8. **Song J**, Vinarov, DA, Tyler EM, Shahan MN, Tyler RC, and Markley, JL Hypothetical Protein At2g24940.1 from *Arabidopsis thaliana* Adopts a Cytochrome b5 like Fold. *J Biomol NMR*. 2004, 30(2):215-8.
9. **Song J**, Zhao Q, Thao S, Friederick, RO, and Markley JL. Solution Structure of a Calmodulin-Like Calcium-Binding Domain from *Arabidopsis thaliana*. *J Biomol NMR*. 2004, 30(4):451-6.
10. Tyler RC, Aceti DJ, Bingman CA, Cornilescu CC, Fox BG, Frederick RO, Jeon WB, Lee MS, Newman CS, Peterson FC, Phillips GN Jr, Shahan MN, Singh S, **Song J**, Sreenath HK, Tyler EM, Ulrich EL, Vinarov DA, Vojtik FC, Volkman BF, Wrobel RL, Zhao Q, Markley JL. Comparison of cell-based and cell-free protocols for producing target proteins from the *Arabidopsis thaliana* genome for structural studies. *Proteins*. 2005, 59(3):633-43.
11. Fox BG, Malone TE, Johnson KA, Madson SE, Aceti D, Bingman CA, Blommel PG, Buchan B, Burns B, Cao J, Cornilescu C, Doreleijers J, Ellefson J, Frederick R, Geetha H, Hruby D, Jeon WB, Kimball T, Kunert J, Markley JL, Newman C, Olson A, Peterson FC, Phillips GN Jr, Primm J, Ramirez B, Rosenberg NS, Runnels M, Seder K, Shaw J, Smith DW, Sreenath H, **Song J**, Sussman MR, Thao S, Troestler D, Tyler E, Tyler R, Ulrich E, Vinarov D, Vojtik F, Volkman BF, Wesenberg G, Wrobel RL, Zhang J, Zhao Q, Zolnai Z. X-ray structure of *Arabidopsis* At1g77680, 12-oxophytodienoate reductase isoform 1. *Proteins*. 2005, 61(1):206-8.
12. Zhao Q, **Song J**, Jin Z, Danilova V, Hellekant G, Markley JL. Probing the sweet determinants of brazzein: wild type brazzein and a tasteless variant, brazzein-ins(R18a-I18b),

- exhibit different pH-dependent NMR chemical shifts. *Biochem Biophys Res Commun.* 2005, 335(1):256-263.
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 14. **Song J**, Tyler RC, Wrobel RL, Frederick RO, Vojtek FC, Jeon WB, Lee MS, Markley JL. Solution structure of At3g04780.1-des15, an *Arabidopsis thaliana* ortholog of the C-terminal domain of human thioredoxin like protein. *Protein Sci.* 2005, 14(4):1059-63.
 15. **Song J**, Tyler RC, Lee MS, Tyler EM, Markley JL. Solution structure of isoform 1 of Roadblock/LC7, a light chain in the dynein complex. *J Mol Biol.* 2005, 354(5):1043-1051.
 16. Lin I, Chen Y, Fee, JA, **Song J**, Westler WM, Markley JL. Rieske protein from *Thermus thermophilus*: ^{15}N NMR titration study demonstrates the role of ion-ligated histidines in the pH dependence of the reduction potential. *J Am Chem Soc.* 2006, 128(33):10672-10673.
 17. **Song J**, Lee MS, Carlberg I, Vener AV, Markley JL. Micelle-induced folding of spinach thylakoid soluble phosphoprotein of 9 kDa and its functional implications. *Biochemistry.* 2006, 45 (51): 15633-15643.
 18. **Song J**, Markley JL. Three-dimensional structure determined for a subunit of human tRNA splicing endonuclease (Sen15) reveals a novel dimeric fold. *J Mol Biol.* 2007, 366(1):155-164.
 19. Frederick RO, Bergeman L, Blommel PG, Bailey LJ, McCoy JG, **Song J**, Meske L, Bingman CA, Ritters M, Dillon NA, Kunert J, Yoon JW, Lim A, Cassidy M, Bunge J, Aceti DJ, Primm JG, Markley JL, Phillips GN Jr, Fox BG. Small-scale, semi-automated purification of eukaryotic proteins for structure determination. *J Struct Funct Genomics.* 2007, 8(4):153-66.
 20. **Song J**, Markley JL. Cautionary Tail: the presence of an N-terminal tag on dynein light-chain roadblock/LC7 affects its interaction with a functional partner. *Protein Pept Lett.* 2007, 14(3):265-268.
 21. **Song J**, Zhao Q, Vinarov DA, Loushin Newman C, Markley JL. Solution structure of human sorting nexin 22. *Protein Sci.* 2007, 16(5):807-14.
 22. Phillips GN Jr., Fox BG, Markley JL, Volkman BF, Bae E, Bitto E, Bingman CA, Frederick RO, Lytle BL, McCoy JG, Pierce BS, **Song J**, Twigger SN. Structures of Proteins of Biomedical Interest from the Center for Eukaryotic Structural Genomics. *J Struct Funct Genomics.* 2007, 8(2-3):73-84.
 23. **Song J***, Guo LW*, Muradov H, Artemyev NO, Ruoho AE, Markley JL. Intrinsically disordered γ subunit of cGMP phosphodiesterase encodes functional relevant transient secondary and tertiary structures. *Proc. Natl. Acad. Sci.* 2008, 105(5):1505-10.
 24. **Song J**, Bettendorff L., Tonelli, M., Markley JL. Structural Basis for the Catalytic Mechanism of Mammalian 25 kDa Thiamine Triphosphatase. *J Biol Chem.* 2008, 283(16):10939-48.
 25. **Song J***, McGivern JV*, Nichols KW, Markley JL, Sheets MD. Structural basis for RNA recognition by a type II poly(A)-binding protein. *Proc. Nat. Acad. Sci.* 2008, 105(40):15317-22.
 26. Lytle BL, **Song J**, de la Cruz NB, Peterson FC, Johnson KA, Bingman CA, Phillips GN Jr, Volkman BF. Structures of Two Arabidopsis Thaliana Major Latex Proteins Represent Novel Helix-grip Folds. *Proteins.* 2009, 76(1):237-43.
 27. Chu UB, **Song J**, Mavlyutov TA, Guo LW. In Vitro Interaction of tubulin with the photoreceptor cGMP phosphodiesterase γ -subunit. *Neurosci Lett.* 2010, 482(3):225-229.

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29. Wang GG, **Song J**, Wang Z, Dormann HL, Casadio F, Li H, Luo JL, Patel DJ, Allis CD. Haematopoietic Malignancies Caused by Dysregulation of a Chromatin-binding PHD Finger. **Nature**. 2009, 459(7248): 847-51.
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31. Teplova M, **Song J**, Gaw HY, Teplov A, Patel DJ. Structural insights into RNA recognition by the Alternate-splicing Regulator CUG Binding Protein 1. **Structure**. 2010, 18(10):1364-77.
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35. Kuo AJ*, **Song J***, Cheung P*, Ishibe-Murakami S, Yamazoe S, Chen JK, Patel DJ, Gozani, O. ORC1 BAH domain links dimethylation of H4K20 to DNA replication licensing and Meier-Gorlin syndrome. **Nature**. 2012, 484:115-110.

University of California, Riverside: 2012-

36. Cai L, Rothbart SB, Lu R, Xu B, Chen WY, Tripathy A, Rockowitz S, Zheng D, Patel DJ, Allis CD, Strahl BD, **Song J[#]**, **Wang GG[#]**. An H3K36 methylation-engaging Tudor motif of polycomb-like proteins mediates PRC2 complex targeting. *Mol. cell*. 2013; 49(3):571-82.
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39. Ji D, Lin K, **Song J**, Wang Y. Effects of Tet-induced oxidation products of 5-methylcytosine on Dnmt1- and DNMT3a-mediated cytosine methylation. *Mol. Biosyst*. 2014; 10(7):1749-52.
40. Zhang W, Sankaran S, Gozani O, **Song J[#]**. A Meier-Gorlin syndrome mutation impairs the ORC1-nucleosome association. *ACS chemical biology*. 2015; 10(5):1176-80.
41. Zhang ZM, Liu S, Lin K, Luo Y, Perry JJ, Wang Y, **Song J[#]**. Crystal Structure of Human DNA Methyltransferase 1. *J. Mol Biol*. 2015; 427(15):2520-31.
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46. Harter MR, Liu CD, Shen CL, Gonzalez-Hurtado E, Zhang ZM, Xu M, Martinez E, Peng CW[#], **Song J[#]**. BS69/ZMYND11 C-Terminal Domains Bind and Inhibit EBNA2. *PLoS pathogens.* 2016; 12(2):e1005414.
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48. Wang B, Tan XF, Thurmond S, Zhang ZM, Lin A, Hai R[#], **Song J[#]**. The structure of Zika virus NS5 reveals a conserved domain conformation. *Nature Commun.* 2017; 8:14763.
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51. Zhang ZM, Lu R, Wang P, Yu Y, Chen D, Gao L, Liu S, Ji D, Rothbart SB, Wang Y, Wang GG[#], **Song J[#]**. Structural basis for DNMT3A-mediated de novo DNA methylation. *Nature.* 2018; 554: 387-391.
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55. Wang B, **Song J[#]**. Structural basis for the ORC1-Cyclin A association. *Protein Sci.* 2019; 28(9):1727-1733.
56. Structure and regulation of ZCCHC4 in m⁶A-methylation of 28S rRNA. Ren W, Lu J, Huang M, Gao L, Li D, Wang GG, **Song J[#]**. *Nat. Commun.* 2019; (10): 5042.
57. A DNA Aptamer for Binding and Inhibition of DNA methyltransferase 1. Wang L, Lee J, Gao L, Yin J, Duan Y, Jimenez LA, Adkins GB, Ren W, Li L, Fang J, Wang Y, **Song J[#]** and Zhong W[#]. *Nucleic Acids Res.* 2019; 47(22):11527-11537.
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59. Dong X, Gao L, Song J, Wang Y. Chemical Proteomic Profiling of Lysophosphatidic Acid-Binding Proteins. *Anal. Chem.* 2019; 91 (24): 15365-15369.
60. Anteneh H, Fang J, **Song J[#]**. Structural basis for impairment of DNA methylation by the DNMT3A R882H mutation. *Nat. Commun.* 2020; 11: 2294.

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62. Ren W, Fan H, Grimm SA, Guo Y, Kim, JJ, Li L, Petell CJ, Tan XF, Zhang ZM, Coan JP, Yin J, Gao L, Cai L, Detrick B, Çetin B, Wang Y, Cui Q, Strahl BD, Gozani O, Miller KM, O’Leary SE, Wade PA, Patel DJ[#], Wang GG[#], Song J[#]. Direct readout of heterochromatic H3K9me3 regulates DNMT1-mediated maintenance DNA methylation. *Proc Nat Acad Sci USA.* 2020; 117(31):18439-18447.
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64. Sarkar P, Li Z, Ren W, Wang S, Shao S, Sun J, Ren X, Perkins, N, Guo Z, Chang CE, Song J, Xue M. Inhibiting Matrix Metalloproteinase-2 Activation by Perturbing Protein–Protein Interactions Using a Cyclic Peptide. *J Med Chem.* 2020; 63, 13, 6979–6990.
65. Fan H, Lu J, Guo Y, Li D, Zhang ZM, Tsai YH, Pi WC, A JH, Gong W, Xiang Y, Allison DF, Geng H, He S, Diao Y, Chen WY, Strahl BD, Cai L, **Song J[#]**, Wang GG[#]. BAHCC1 binds H3K27me3 via a conserved BAH module to mediate gene silencing and oncogenesis. *Nat Genet.* 2020; 52(12):1384-1396.
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69. Fang J, Leichter SM, Jiang J, Biswal M, Lu J, Zhang ZM, Ren W, Zhai J, Cui Q, Zhong X[#], **Song J[#]**. Substrate deformation regulates DRM2-mediated DNA methylation in plants. *Sci Adv.* 2021; 7:eabd9224.
70. Biswal M, Diggs S, Xu D, Khudaverdyan N, Lu J, Fang J, Blaha G, Hai R[#], **Song J[#]**. Two conserved oligomer interfaces of NSP7 and NSP8 underpin the dynamic assembly of SARS-CoV-2 RdRP. *Nucleic Acids Res.* 2021; 48:5956-5966.

Review Article

1. **Song J[#]**, Pfeifer GP[#]. Are there specific readers of oxidized 5-methylcytosine bases? *BioEssays.* 2016; 38(10):1038-1047.
2. Wang B, Thurmond S, Hai R[#], **Song J[#]**. Structure and function of Zika virus NS5 protein: perspectives for drug design. *Cell Mol Life Sci.* 2018; 75: 1723-1736.
3. Ren W, Gao L, **Song J[#]**. Structural Basis of DNMT1- and DNMT3A-Mediated DNA Methylation. *Genes.* 2018; 9(12), 620.
4. Thurmond S, Wang B, **Song J[#]**, Hai R[#]. Suppression of Type I Interferon Signaling by Flavivirus NS5. *Viruses.* 2018; 10(12):712.

5. Pfeifer GP, Szabó PE and **Song J**. Protein interactions at oxidized 5-methylcytosine bases. *J. Mol. Biol.* 2020; 432(6):1718-1730.

Book Chapter

1. Wrobel RL, Bingman CA, Jeon WB, **Song J**, Vinarov DA, Frederick RO, Aceti DJ, Sreenath HK, Zolnai Z, Vojtik FC, Fox BG, Phillips GN Jr., and Markley JL. (2006) Structural Proteomics. *Plant Proteomics*, 99-128. Blackwell Publishing, Oxford.