

BIOGRAPHICAL SKETCH

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NAME: Zheng Zuo

eRA COMMONS USER NAME (credential, e.g., agency login): ZHENGZUO1

POSITION TITLE: Postdoctoral Researcher

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Peking University, Beijing, China	B.S.	05/2008	Physics
Washington University in St. Louis, MO, U.S.	PhD	01/2015	Biomedical Engineering
Washington University in St. Louis, MO, U.S.	Postdoc	01/2018	Genetics
Stanford University, CA, U.S.	Postdoc		Genetics

A. Personal Statement

My past research work in Washington University in St. Louis is focused on transcriptional gene regulation, or more specifically, using high-throughput sequencing combined with other biophysical techniques to characterize protein-DNA interactions, and deciphering their molecular mechanism of various genetic diseases. Currently I'm combining sequencing, microfluidics and chemical biology approaches to study post-translational modifications (PTMs) on protein-DNA and protein-protein interactions.

B. Positions and Honors

Cold Spring Harbor Asia Fellowship Award
Suzhou, Oct 2014

11th International Conference on Bioinformatics and Biomedical Engineering (iCBBE 2017),
Invited speaker and technical session chair, Hangzhou, May 2017

C. Contributions to Science

Development of Spec-seq method to quantitatively characterize protein-DNA interactions specificity;
Development of Methyl-Spec-seq to characterize methylation sensitivity of protein-DNA interactions;
Development of Two-Color fluorescence anisotropy to characterize protein-ligands interactions in general;
Discovery of non-independent recognition of tandem zinc finger proteins;

D. Additional Information: Research Support and/or Scholastic Performance

Zuo Z, Billings T, Walker M, Petkov P, Fordyce P, Stormo GD (2019). Why do long zinc finger proteins have short motifs? A case study of ZFY and CTCF reveals non-independent recognition of tandem zinc fingers. BioRxiv. Under review by Genome Research.

Chang, Y. K., Zuo, Z., & Stormo, G. D. (2018). Quantitative profiling of BATF family proteins/JUNB/IRF heterotrimers using Spec-seq. BMC molecular biology, 19(1), 5.

Zuo Z, Roy B, YK Chang, Granas DG, Stormo GD. Measuring quantitative effects of methylation on transcription factor-DNA binding affinity. Science Advances. (co-corresponding author) 2017 Nov 17

Roy B, Zuo Z, Stormo GD. Quantitative specificity of STAT1 and several variants. Nucleic acids research. 2017 May 16.

Chang YK, Srivastava Y, Hu C, Joyce A, Yang X, Zuo Z, Havranek JJ, Stormo GD, Jauch R. Quantitative profiling of selective Sox/POU pairing on hundreds of sequences in parallel by Coop-seq. Nucleic Acids Research. 2016 Dec 2:gkw1198.

Sasse SK, Zuo Z, Kadiyala V, Zhang L, Pufall MA, Jain MK, Phang TL, Stormo GD, Gerber AN. Response element composition governs correlations between binding site affinity and transcription in glucocorticoid receptor feed-forward loops. Journal of Biological Chemistry. 2015 Aug 7;290(32):19756-69.

Zuo Z, Chang Y, Stormo GD. A quantitative understanding of lac repressor's binding specificity and flexibility. Quantitative biology (Beijing, China). 2015 Jun 1;3(2):69. (Illustrated in Journal Cover and highlighted in Cold Spring Harbor 2017 System biology conference manual cover)

Stormo GD, Zuo Z, Chang YK. Spec-seq: determining protein-DNA-binding specificity by sequencing. Briefings in functional genomics. 2015 Jan 1;14(1):30-8.

Zuo Z, Stormo GD. High-resolution specificity from DNA sequencing highlights alternative modes of Lac repressor binding. Genetics. 2014 Nov 1;198(3):1329-43.

A modified bacterial one-hybrid system yields improved quantitative models of transcription factor specificity. Christensen RG, Gupta A, Zuo Z, Schriefer LA, Wolfe SA, Stormo GD. Nucleic Acids Res. 2011 Jul;39(12)

Hemme CL, Fields MW, He Q, Deng Y, Lin L, Tu Q, Mouttaki H, Zhou A, Feng X, Zuo Z, Ramsay BD. Correlation of genomic and physiological traits of Thermoanaerobacter species with biofuel yields. Applied and environmental microbiology. 2011 Nov 15;77(22):7998-8008.