# BI ZHAO

Google Scholar Profile ⋄ ResearchGate Profile
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## EDUCATION

**University of South Florida (USF), Tampa, FL, USA** Jan. 2016 - Aug. 2019
*Ph.D. of Science in Cell and Molecular Biology*
**Area of Emphasis:** Bioinformatics, Computational Biology and System Biology
**Dissertation:** Novel Strategies on Characterizing Biologically Specific Protein-protein Interactions

**University of South Florida (USF), Tampa, FL, USA** Aug. 2013 - May. 2015
*Master of Science in Biotechnology*
**Independent Research:** Improve Efficiency of Cancer Vaccines By Comparing Two Types of Immunotherapy Vaccine Modalities

**Henan University, Kaifeng, Henan, China** Sept. 2007 - July 2011
*Bachelor of Bioscience*
**Thesis:** Methylation of H19 gene in ES, IPS, and ntES Cells

## PROFESSIONAL APPOINTMENT

### · RESEARCH APPOINTMENT

**Assistant Professor** Oct. 2022 - present
*University of South Florida, Tampa, Florida, U.S.*

**Applied Research Scientist** June 2022 - Sept. 2022
*Moffitt Cancer Center, Tampa, Florida, U.S.*

**Postdoctoral Fellowship** Sept. 2019 - June 2022
*Virginia Commonwealth University, Richmond, Virginia, U.S.*

**Research/Teaching Assistant** Dec. 2015 - Aug. 2019
*University of South Florida, Tampa, Florida, U.S.*

**Research Assistant** Aug. 2015 - Dec. 2015
*University of South Florida, Tampa, Florida, U.S.*

### · TEACHING APPOINTMENT

**Bio I Cellular Processes Lab** Jan. 2019 - May 2019 & Sept. 2017 - May 2018
*University of South Florida, Tampa, Florida, U.S.*
**Coordinator:** Gemmell, Colbi, Courtesy Faculty.

**Principle of Immunology** Aug. 2018 - Dec. 2018
*University of South Florida, Tampa, Florida, U.S.*
**Supervisor:** Dao, My-Lien, Ph.D.

**The Biology of Humans** May 2018 - July 2018
*University of South Florida, Tampa, Florida, U.S.*
**Supervisor:** Upadhyaya, Ashok, Instructor III.

## PROFESSIONAL SUMMARY

- **RESEARCH INTERESTS**

(1) Developing novel strategies for gene expression analysis (e.g. Zhao, Erwin, & Xue, 2017c);
(2) Characterizing the heterogeneous samples (e.g. Zhao & Xue, 2017d);
(3) Developing structure and function prediction of protein (e.g. Zhao & Xue, 2018; Katuwawala, Zhao, & Kurgan, 2021a);
(4) Predicting binding of small RNA and Protein (e.g. Zhao & Xue, 2017a; Zhao & Xue, 2019);
(5) Establishing structural and functional database (Zhao et al., 2020a);
(6) Establishing protein-protein interaction database;
(7) Discovering and characterizing protein function and mechanism in system (e.g. Zhao et al., 2020b; Zhao et al., 2021b).

## SCHOLARLY WORK

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- **PUBLICATIONS** (**bold font** = representative high impact journal articles; underline = identify corresponding author(s))

**Peng, Z., Li, Z., Meng, Q., Zhao, B., Kurgan, L., (2023). "*CLIP: accurate prediction of disordered linear interacting peptides from protein sequences using co-evolutionary information.*" Briefings in Bioinformatics, bbac502, https://doi.org/10.1093/bib/bbac502.**

**Shaw, T. I., Zhao, B., Li, Y., Wang, H., Wang, L., Manley, B., Stewart, P. A., & Karolak, A. (2022a)."*Multi-omics approach to identifying isoform variants as therapeutic targets in cancer patients.*" Frontiers in oncology, 12, 1051487. https://doi.org/10.3389/fonc.2022.1051487**

**Zhao, B., Kurgan, L., (2022b). "*Compositional Bias of Intrinsically Disordered Proteins and Regions and Their Predictions.*" Biomolecules, 12(7):888. https://doi.org/10.3390/biom12070888.**

**Biro, B., Zhao, B., Kurgan, L., (2022c). "*Complementarity of the Residue-level Protein Function and Structure Predictions in Human Proteins.*" Computational and Structural Biotechnology Journal, 20:2223-2234. PMID: 35615015; PMCID: PMC9118482.**

**Zhao, B., Kurgan, L., (2022d). "*Deep Learning in Prediction of Intrinsic Disorder in Proteins.*" Computational and Structural Biotechnology Journal, https://doi.org/10.1016/j.csbj.2022.03.003. PMID: 35356546; PMCID: PMC8927795.**

**Zhao, B.**, Kurgan, L.. (2021a) "*Surveying over 100 Predictors of Intrinsic Disorder in Proteins.*" Expert Review of Proteomics, doi: 10.1080/14789450.2021.2018304. PMID: 34894985.

Katuwawala, AI., **Zhao, B.**, & Kurgan, L.. (2021b). "*DisoLipPred: Accurate prediction of disordered lipid binding residues in protein sequences with deep recurrent networks and transfer learning.*" Bioinformatics. doi:10.1093/bioinformatics/btab640. PMID: 34487138.

Zhang, F., **Zhao, B.**, Shi, W., Li, M., Kurgan, L.. (2021c). "*DeepDISOBind: Accurate Prediction of RNA-, DNA- and Protein-binding Intrinsically Disordered Residues with Deep Multi-task Learning.*" Briefings in Bioinformatics, doi: 10.1093/bib/bbab521. PMID: 34905768.

**Zhao, B., Katuwawala, AI., Oldfield CJ., Hu, G., Wu, Z., Uversky VN., & Kurgan, L. (2021d). "*Intrinsic Disorder in Human RNA-binding Proteins.*" J Mol Biol, 433(21), 167229. doi:10.1016/j.jmb.2021.167229. PMID:34487791.**

**Zhao, B., Katuwalala, AI., Oldfield, CJ., Dunker, AK., Faraggi, E., Gsponer, J., Kloczkowski, AI., Malhis, N., Mirdita, M., Obradovic, Z., Söding, J., Steinegger, M., Zhou, Y., & Kurgan, L., (2020a). "*DescribePROT: Database of Amino Acid-level Protein Structure and Function Predictions.*" Nucleic Acids Research, 49(D1), D298–D308. https://doi.org/10.1093/nar/gkaa931. PMID: 33119734; PMCID: PMC7778963.**

**Zhao, B., Katuwawala, A., Uversky, VN., & Kurgan, L., (2020b). "*IDPology of the Living Cell: Intrinsic Disorder in the Subcellular Compartments of the Human Cell.*" Cellular and Molecular Life Sciences, CMLS, 78(5), 2371–2385. https://doi.org/10.1007/s00018-020-03654-0. PMID: 32997198.**

Sun, X., Malhis, N., **Zhao, B.**, Xue, B., Gsponer, J. & Rikkerink, H., (2020c). "*Computational Disorder Analysis in Ethylene Response Factors Uncovers Binding Motifs Critical to Their Diverse Functions.*" International Journal of Molecular Sciences, 21(1), 74. https://doi.org/10.3390/ijms21010074. PMID: 31861935; PMCID: PMC6981732.

Palumbo, E., **Zhao, B.**, Xue, B., Uversky, VN., & Dave, V., (2019). "*Analyzing aggregation propensities of clinically relevant PTEN mutants: a new culprit in pathogenesis of cancer and other PTENopathies.*" Journal of Biomolecular Structure and Dynamics, 38(8), 2253–2266. https://doi.org/10.1080/07391102.2019.1630005. PMID: 31232187.

**Zhao, B.** & Xue, B. (2019). "*Significant improvement of miRNA target prediction accuracy in large datasets using meta-strategy based on comprehensive voting and artificial neural networks.*" BMC genomics, 20(1), 158. doi:10.1186/s12864-019-5528-1. PMID: 30813885; PMCID: PMC6391818.

**Zhao, B. & Xue, B. (2018). "*Decision-Tree Based Meta-Strategy Improved Accuracy of Disorder Prediction and Identified Novel Disordered Residues Inside Binding Motifs.*" International journal of molecular sciences, 19(10), 3052. https://doi.org/10.3390/ijms19103052. PMID: 30301243; PMCID: PMC6213717.**

**Zhao, B. & Xue, B. (2017a). "*Improving prediction accuracy using decision-tree-based meta-strategy and multi-threshold sequential-voting exemplified by miRNA target prediction.*" Genomics, 109(3-4), 227-232. doi:10.1016/j.ygeno.2017.04.003. PMID: 28435088.**

**Zhao, B.** & Xue, B. (2017b). "*Consensus datasets of mouse miRNA-mRNA interactions from multiple online resources.*" Data Brief, 14, 143-147. doi:10.1016/j.dib.2017.07.035. PMID: 28795090; PMCID: PMC5537373.

**Zhao, B., Erwin, A., & Xue, B. (2017c)."*How many differentially expressed genes: A perspective from the comparison of genotypic and phenotypic distances.*" Genomics, 110(1), 67–73. https://doi.org/10.1016/j.ygeno.2017.08.007. PMID: 28843784.**

**Zhao, B.** & Xue, B. (2017d). "*Measuring the inter-sample heterogeneity by dynamic PCA-biplot.*" 2017 Ieee International Conference on Bioinformatics and Biomedicine (BIBM), 2017: p. 2333-2335.

**Zhao, B.** & Xue, B. (2016). "*Self-regulation of functional pathways by motifs inside the disordered tails of beta-catenin.*" 17 Suppl 5(Suppl 5), 484. https://doi.org/10.1186/s12864-016-2825-9. PMID: 27585692; PMCID: PMC5009561.

**Zhao, B.**, & Xue, B. (2015). "*Systematic Analyses Reveal Regulatory Mechanisms of the Flexible Tails on Beta-catenin.*" In Bioinformatics Research and Applications: 11th International Symposium, ISBRA 2015 Norfolk, USA, June 7-10, 2015 Proceedings (Vol. 9096, p. 440). Springer.

## · BOOK CHAPTERS

**Zhao, B.**& Kurgan, L., "*Machine Learning for Intrinsic Disorder Prediction*", in Machine Learning in Bioinformatics of Protein Sequences. p. 205-236.

**Zhao, B.**& Kurgan, L., "*Databases of Protein Structure and Function Predictions at the Amino Acid Level*", in Machine Learning in Bioinformatics of Protein Sequences. p. 329-353.

## · PRESENTATIONS

Zhao, B. (2020). "*Intrinsic Disorder in the Human Cell.*" Department Seminar, Department of Computer Science, Virginia Commonwealth University.

Zhao, B., (2019). "*Novel Strategies on Characterizing Biologically Specific Protein-protein Interaction Networks*" Department Seminar, Department of Cellular, Microbiology, and Molecular Biology, University of South Florida.

Zhao, B. (2015). "*Systematic Analyses Reveal Regulatory Mechanisms of the Flexible Tails on Beta-catenin.*" *11nd* International Symposium on Bioinformatics Research and Applications (ISBRA).

## · POSTERS

**Zhao, B.** & Xue, B. (2019). "*Dual-threshold Decision-tree Based Meta-strategy Improving Predictive Performance of Protein Binding Region in Disorder Proteins.*" 2019 Biophysical Society Annual Meeting.

**Zhao, B.** & Xue, B. (2016). "*Regulation of Neuropeptides by Their Mutual Interactions.*" *24th* conference on intelligent systems for molecular biology (ISMB).

**Zhao, B.** & Xue, B. (2015). "*Flexible Tails Regulate the Functions of Beta-Catenin.*" 2015 Biomedical Engineering Society (BMES).

**Zhao, B.** & Xue, B. (2014). "*Structural Flexibility Characterizes the Function of Natriuretic Peptides.*" *6th* USF Graduate Student and Post-Doctorate Research Symposium.

**Zhao, B.** & Xue, B. (2014). "*Structure Flexibility Characterizes Essential Role in Neuropeptides*" *8th* USF CAS Annual Oktoberfest, 2014, Tampa, Florida.

## SKILLS

**Technical** Deep Learning, Meta-analysis, Machine Learning, Data Mining, Algorithm, Polymerase chain reaction, Western blot, Enzyme-linked immunosorbent assay

**Computing** Python, Matlab, C, C++, Linux, SAS, R, SQL

## CERTIFICATIONS

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|---|---|
| **Machine Learning Foundations**, License 8Z9E7T9XQGYV, Coursera. | Apr. 2017 - Present |
| **Programming for Everybody (Python)**, License Z5EU5BHCHH, Coursera. | Aug. 2015 - Present |
| **SAS base certification**, License SAS1120694, Pearson Professional Program. | Mar. 2015 - Present |
| **Bioinformatics Certification**, Univ. of South Florida (USF) | Mar. 2015 - Present |

## PROFESSIONAL SERVICES

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| **Invited Reviewer**, Nature Communications, 2022 | 2022 - present |
| **Invited Reviewer**, MDPI, 2022 | 2022 - present |
| **Program Committee**, BIBM 2021-2022. | 2021 - present |
| **Reviewer Board Member**, Frontiers in Bioscience-Elite | 2021 - present |
| **Member**, Sigma Xi. USF, Tampa, Florida, U.S. | 2018 - present |
| **Associate Faculty Member**, F1000 Research. | 2014 - 2018 |

## AWARDS AND HONORS

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| **Chih Foundation and Publication Award ($1,250)**, USF, Tampa, Florida, U.S. | 2018 |
| **Summer Fellowship from CMMB ($2,900)**, USF, Tampa, Florida, U.S. | 2018 |
| **CMMB Outstanding Graduate Student Research Award**, USF, Tampa, Florida, U.S. | 2017 |
| **Travel Fellowship from CMMB ($200)**, USF, Tampa, Florida, U.S. | 2016 |
| **Summer Fellowship from CMMB ($2,150)**, USF, Tampa, Florida, U.S. | 2016 |
| **Travel Fellowship from ISBRA conference ($600)**, Norfolk, Virginia, U.S. | 2015 |