BI ZHAO

[Google Scholar Profile](#) ⋄ [ResearchGate Profile](#)

Genomics Program, Department of Global, Environment, & Genomic Health Science, College of Public Health

University of South Florida ⋄ 3720 Spectrum Blvd., Suit 304, Tampa, FL 33612 ⋄ Ph.813-396-2812 ⋄ bizhao@usf.edu

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**

AI in Public Health Research   Jan. 2026
University of South Florida, Tampa, Florida, U.S.
Instructor: Zhao, Bi, Ph.D.
Fundamental Genomics   Aug. 2023 - Present
University of South Florida, Tampa, Florida, U.S.
Instructor: Zhao, Bi, Ph.D.
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 analyzing omics data (e.g. 2022a);
(2) Establising protein residue-level putative structural and function annotations (e.g. 2024 & 2020a) ;
(3) Developing structure and function prediction of protein (e.g. 2021a & 2018);
(4) Discovering and characterizing protein function and mechanism in system (e.g. 2020b & 2021b).

SCHOLARLY WORK

· **PUBLICATIONS** (**bold font** = representative high impact journal articles; <u>underline</u> = identify corresponding author(s); * = the co-first author(s))
Yu, J.*, <u>Zhao, B.*</u>, <u>Kurgan, L.</u> (2025). Comprehensive assessment of AlphaFold's predictions of secondary structure and solvent accessibility at the amino acid-level in eukaryotic, bacterial and archaeal proteins. Computational and Structural Biotechnology Journal. Basu, S.*, Zhao, B.*, Biró, B., Faraggi, E., Gsponer, J., Hu, G., Kloczkowski, A., Malhis, N., Mirdita, M., Söding, J., Steinegger, M., Wang, D., Wang, K., Xu, D., Zhang, J., <u>Kurgan, L.</u>, (2024). *"DescribePROT in 2023: more, higher-quality and experimental annotations and improved data download options."* **Nucleic Acids Research, 52(D1), D426-D433.**

Zhao, B., Ghadermarzi, S., <u>Kurgan, L.</u> (2023a). *"Comparative evaluation of AlphaFold2 and disorder predictors for prediction of intrinsic disorder, disorder content and fully disordered proteins."* **Computational and Structural Biotechnology Journal, 21, 3248-3258.**

<u>Kurgan, L.</u>, Hu, G., Wang, K., Ghadermarzi, S., Zhao, B., Malhis, N., Erdős, G, Gsponer, J, Uversky, V., Dosztányi, Z. (2023b). *"Tutorial: a guide for the selection of fast and accurate computational tools for the prediction of intrinsic disorder in proteins."* **Nature Protocols, 18(11), 3157-3172. Peng, Z., Li, Z., Meng, Q., Zhao, B., <u>Kurgan, L.</u>, (2023c).** *"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.**

<u>Shaw, T. I.</u>, **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., <u>Kurgan, L.</u>, (2022b). *"Compositional Bias of Intrinsically Disordered Proteins and Regions and Their Predictions."* **Biomolecules, 12(7):888. https://doi.org/10.3390/biom 12070888.**

Biro, B.*, <u>Zhao, B.*</u>, <u>Kurgan, L.</u>, (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., <u>Kurgan, L.</u>, (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., <u>Kurgan, L.</u>. (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.**, & <u>Kurgan, L.</u>. (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., <u>Kurgan, L.</u>. (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. (2025). " *Prediction of Intrinsically Disordered Lipid Binding Residues with DisoLipPred*". In Protein Function Prediction: Methods and Protocols (pp. 301-312). New York, NY:

Springer US.

Zhao, B., Basu, S., & Kurgan, L. (2024). "*DescribePROT Database of Residue-Level Protein Structure and Function Annotations*". In Prediction of Protein Secondary Structure (pp. 169-184). New York, NY: Springer US.

Zhao, B. & Kurgan, L.(2023). "*Machine Learning for Intrinsic Disorder Prediction*", in Machine Learning in Bioinformatics of Protein Sequences. p. 205-236.

Zhao, B. & Kurgan, L. (2023). "*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. (2022). "*Computational Strategies for Biological and Biomedical Research.*" Department of Biomolecular Science, University of South Florida.

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

Zhao, B., (2019). "*Novel Strategies on Characterizing Biologically Specific Protein-protein Interaction Networks*" 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.

PROFESSIONAL SERVICES

Early Career Editorial Board Member, Biomolecules	2025 - present
Invited Reviewer, Briefings in bioinformatics	2024 - present
Invited Reviewer, Nature Communications	2022 - present
Invited Reviewer, MDPI	2022 - present
Program Committee, BIBM	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

USF new research grant ($20,000), USF, Tampa, Florida, U.S.	2023
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

CERTIFICATIONS

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