
Zheng Wang - Publications

1. Liu, T. and Wang, Z. (2018) [SOV refine: A further refined definition of segment overlap score and its significance for protein structure similarity](https://doi.org/10.1186/s13029-018-0068-7). **Source Code for Biology and Medicine**, 13:1, <https://doi.org/10.1186/s13029-018-0068-7>.
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3. Liu, T. and Wang, Z. (2017) [scHiCNorm: A software package to eliminate systematic biases in single-cell Hi-C data](https://doi.org/10.1093/bioinformatics/btx104). **Bioinformatics**, 34:6, 1046-1047.
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5. Liu, H., Li, J., Koirala, P., Ding, X., Chen, B., Wang, Y., Wang, Z., Wang, C., Zhang, X., and Mo, Y. (2016) [Long non-coding RNAs as prognostic markers in human breast cancer](#). *Oncotarget*, DOI: 10.18632/oncotarget.7828.
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8. Eickholt, J., Wang, Z. (2014) [PCP-ML: Protein characterization package for machine learning](#). *BMC Research Notes*, 7:810.
9. Cao, R., Wang, Z. (co-first author), Wang, Y., and Cheng, J. (2014) [SMOQ: a tool for predicting the absolute residue-specific quality of a single protein model with support vector machines](#). *BMC Bioinformatics*, 15:120.
10. Cao, R., Wang, Z., and Cheng, J. (2014) [Designing and evaluating the MULTICOM protein local and global model quality prediction methods in the CASP10 experiment](#). *BMC Structural Biology*, 14:13.
11. Taylor, K., Briley, A., Wang, Z., Cheng, J., Shi, H., and Caldwell, C (2013) [Aberrant epigenetic gene regulation in lymphoid malignancies](#). *Seminars in Hematology*, 50(1), 38-47.
12. Wang, Z., Cao, R., Taylor K., Briley A., Caldwell C., and Cheng, J. (2013) [The properties of genome conformation and spatial gene interaction and regulation networks of normal and malignant human cell types](#). *PLoS ONE*, 8(3): e58793. doi:10.1371/journal.pone.0058793.
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21. Joshi, T., Patil, K., Fitzpatrick, M.R., Franklin, L.D., Yao, Q., Wang, Z., Libault, M., Brechenmacher, L., Valiyodan, B., Wu, X., Cheng, J., Stacey, G., Nguyen, H., and Xu, D. (2011) [Soybean knowledge base \(SoyKB\): A web resource for soybean translational genomics](#). *BMC Genomics*, 13(Suppl 1):S15, doi:10.1186/1471-2164-13-S1-S15.
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26. Wang, Z., Tegge, A.N., and Cheng, J. (2009) [Evaluating the absolute quality of a single protein model using structural features and support vector machines](#). **Proteins**, 75, 638-647.
27. Tegge, A.N., Wang, Z. (co-first author), Eickholt, J., and Cheng, J. (2009) [NNcon: Improved protein contact map prediction using 2D-recursive neural networks](#). **Nucleic Acids Research**, 37(Web Server issue), W515-8.
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Conference proceedings

1. Joshi, T., Patil, K., Fitzpatrick, M.R., Franklin, L.D., Yao, Q., Wang, Z., Libault, M., Brechenmacher, L., Valiyodan, B., Wu, X., Cheng, J., Stacey, G., Nguyen, H., and Xu, D. (2011) [Soybean knowledge base \(SoyKB\): A web resource for soybean translational genomics](#). *The Tenth Asia Pacific Bioinformatics Conference*, Melbourne, Australia.
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Book chapters

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2. Tegge, A.N., Wang, Z., and Cheng, J. (2009) [Integrative protein fold recognition by alignments and machine learning](#). *Protein Structure Prediction: Method and Algorithms*, Rangwala, H., and Karypis, G., Wiley.

Ph.D. dissertations

1. [Wang, Z. \(2012\) Revealing the conformation and properties of human genome, protein molecules and protein domain co-occurrence network](#), Ph.D. in Computer Science dissertation, University of Missouri-Columbia.

Master's theses

1. Wang, Y., (2016) [Predicting DNA methylation state of CpG dinucleotide using genome topological features and deep networks](#), M.S. in Computer Science thesis, University of Southern Mississippi, 2016
2. [Wang, Z. \(2007\) Consensus prediction of protein secondary structures](#), Master in Computer Science thesis, University of New Brunswick, Canada.