

Lincong Wang

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Research Interests

Elucidate the biochemical function of proteins through structure determination and the characterization of dynamics using both computational methods and experimental techniques, especially solution nuclear magnetic resonance spectroscopy (NMR).

Education

Postdoctoral

1998–2000 Biophysics Research Division, the University of Michigan, Ann Arbor, MI.
Supervisor: Prof. Erik R. P. Zuiderweg.

Graduate

1992–1998 Ph.D. in Biochemistry, Michigan State University, East Lansing, MI.
Supervisor: Prof. Honggao Yan.

1998–2000 Computer Science, Eastern Michigan University, Ypsilanti, MI.

2000–2001 Computer Science, University of Maryland, College Park, MD.

Undergraduate

1986–1990 B. Sc. in Biology, Zhejiang University, P. R. China.

Research Experience

Research Associate

2001–now Development of algorithms for high throughput structural determination using very sparse restraints and for automatic NMR resonance assignment.

Senior Scientist

2000–2001 Development of software for the Protein Data Bank (PDB), National Institute of Standard and Technology.

Research Fellow

1998–2000 Development of NMR techniques and computational methods for studying

protein dynamics, structure and function.

Research Assistant

1992–1998 Biochemical and NMR studies of human cellular retinoic acid binding proteins (CRABPs).

Teaching Experience

Committee Members

2001–now Serving as a committee member for a Ph.D. and a Master student and supervising the research of a undergraduate in computer science at Dartmouth College.

Teaching Assistant

1993–1994 Biochemistry, Michigan State University.

Awards

Best Poster Award at the Computational Systems Bioinformatics Conference (CSB 2003) sponsored by the IEEE Computer Society in cooperation with the ACM.

Publications

Wang, L., Li, Y., and Yan, H. (1997) Human Cellular Retinoic Acid Binding Proteins: Quantitative Analysis of the Ligand Binding Properties of the Wild-Type and Site-Directed Mutants. *J. Biol. Chem.* 272, 1541-1547.

Yan, H., Wang, L., and Li, Y. (1997) A Novel Method for Measuring the Binding Properties of the Site-Directed Mutants of The Proteins that Binding Hydrophobic Ligands: Application to Cellular Retinoic Acid Binding Proteins. In *Techniques in Protein Chemistry VIII* (Marshak, D. R., Ed.), 449-456. Academic Press, San Diego.

Wang, L., Li, Y., Abildgaard, F., Markley, J. L., and Yan, H. (1998) NMR Solution Structure of Type II Human Cellular Retinoic Acid Binding Protein: Implications for Ligand Binding. *Biochemistry* 37, 12727-36.

Wang, L., and Yan, H. (1998) NMR Study Suggests a Major Role for Arg111 in Maintaining the Structure and Dynamical Properties of Type II Cellular Retinoic Acid Binding protein. *Biochemistry* 37. 13021-32.

Chen, X., Tordova, M., Gilliland, G. L., Wang, L., Li, Y., Yan, H., and Ji, X. (1998) Crystal Structure of Cellular Retinoic Acid Binding Protein Type II: Suggestions a Mechanism of Ligand Entry. *J. Mol. Biol.* 278, 641-653.

Wang, L., and Yan, H. (1999) NMR Studies of Type II Human Cellular Retinoic Acid Binding Protein. *Biochimica et Biophysica Acta* 1433, 240-252.

Pang, Y., **Wang, L.**, Pellecchia, M., Kurochkin, A. V., and Zuiderweg, E. R. P. (1999) Evidence for Extensive Anisotropic Local Motions in a Small Enzyme Using a New Method to Determine NMR Cross-Correlated Relaxation Rates in the Absence of Resolved Scalar Coupling. *J. Biomol. NMR* 14(4), 297-306.

Pellecchia, M., Pang, Y., **Wang, L.**, Kurochkin, A. V. Kumar A., and Zuiderweg, E. R. P. (1999) Quantitative Measurement of Cross-Correlations Between ^{15}N and ^{13}CO Chemical Shift Anisotropy Relaxation Mechanisms by Multiple Quantum NMR. *J. Am. Chem. Soc.* 121, 9165-9170.

Wang, L., Kurochkin, A. V., and Zuiderweg, E. R. P. (2000) An Iterative Fitting Procedure for the Determination of Longitudinal NMR Cross-Correlation Rates. *J. Magn. Reson.* 144,175-185.

Wang, L., Pang, Y., Holder, T., Brender, J. R., Kurochkin, A. V., and Zuiderweg E. R. P. (2001) Functional Dynamics in the Active Site of the Ribonuclease Binase. *Proceedings of the National Academy of Sciences, USA*, 98, 7684–7689.

Langmead, C., Yan, A., Lilien, R., **Wang, L.**, and Donald B. (2003). A Polynomial-Time Nuclear Vector Replacement Algorithm for Automated NMR Resonance Assignments. *Proceedings of the Seventh Annual International Conference on Research in Computational Molecular Biology (RECOMB2003)*, 176-187. Berlin, Germany, April 10-13.

Wang, L., Mettu, R., Lilien, R. and Donald B. (2003). An Exact Algorithm for Determining Protein Backbone Structure from NH Residual Dipolar Couplings. IEEE Computer Society Bioinformatics Conference (CSB2003), 611-612. Stanford University, CA, August 11-14. (*Winner of Best Poster Award*).

Wang, L., and Donald B. (2003). An Exact Algorithm for Determining Protein Backbone Structure from a Minimum Number of Residual Dipolar Couplings. *Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB2004)*, San Diego, CA, March 27-31, 2004 (in review).

Wang, L., and Donald B. (2003). Exact Solutions for Internuclear Vectors and Backbone Dihedral Angles from NH Residual Dipolar Couplings in *Two Media*, and Their Application in a Systematic Search Algorithm for Determining Protein Backbone Structure. *J. Biomol. NMR* (in review).

Wang, L., and Donald B. Exact Solutions for Internuclear Vectors and Backbone Dihedral Angles from NH and CH Residual Dipolar Couplings in *a Single Medium*, and Their Application in a Systematic Search Algorithm for Determining Protein Backbone Structure. (prepared)

References

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