

Britt H. Park

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Scientific Interests

Amongst other things, I am interested in the use of simulation techniques to design drug candidates, the *ab initio* prediction of protein structure from sequence and the biochemistry and pharmacology of mental illness.

Employment

Principal Engineer **Interwoven, Inc.**
Sunnyvale, California **1997–Present**

Member of the core server group responsible for developing the TeamSite server. TeamSite is a virtual filesystem based web content management system. Instrumental in shipping the first sellable version of TeamSite. Designer and developer of OpenDeploy, a secure content synchronization server. Instrumental in porting TeamSite from Solaris to Microsoft Windows NT. Designer and developer of a sophisticated workflow subsystem for TeamSite. Responsible for initial redesign of TeamSite core server, resulting in a greater than 200% performance increase.

Programmer **Molecular Applications Group**
Palo Alto, California **1996–1997**

Wrote software for protein sequence and structure analysis. Part of the release for MacLook, the company's flagship product, ported to the Macintosh.

Graduate Student **Michael Levitt, Structural Biology,**
Palo Alto, California **Stanford University**
1988–1996

Thesis: *Analysis of Reduced Representation Models of Protein Structure and Empirical Energy Functions Used for The Prediction of Protein Conformations*. Quantified the relationship between protein model complexity and accuracy. Developed a database of decoy misfolded protein conformations, still widely used. Developed empirical energy functions which discriminated between native and non-native protein conformations with high reliability.

Laboratory Technician **Stuart B. Levy, Molecular Biology and**
Boston, Massachusetts **Microbiology, Tufts University Medical**
School
1985–1988

Studied mechanisms of bacterial resistance to tetracyclines. Developed inhibitors of tetracycline efflux proteins. The efflux proteins are proton antiporters encoded by the various tetracycline resistance genes.

Publications

Huang, E. S., Samudrala, R., Park B. H. "Scoring functions for *ab initio* protein structure prediction." *Methods Mol. Biol.* 2000; 143:223-45.

Park, B. H., Huang, E. S., Levitt, M. "Factors affecting the ability of energy functions to discriminate correct from incorrect folds." *J. Mol. Biol.* 1997 Mar 7; 266(4):831-46

Park, B., Levitt, M. "Energy functions that discriminate X-ray and near native folds

from well-constructed decoys." *J. Mol. Biol.* 1996 May 3; 258(2):367-92

Park, B. H., Levitt, M. "The complexity and accuracy of discrete state models of protein structure." *J. Mol. Biol.* 1995 Jun 2; 249(2):493-507

Nelson, M. L., Park, B. H., Levy, S. B. "Molecular requirements for the inhibition of the tetracycline antiport protein and the effect of potent inhibitors on the growth of tetracycline-resistant bacteria." *J. Med. Chem.* 1994 Jan; 70(1):1355-61

Levitt, M., Park, B. H. "Water: now you see it, now you don't." *Structure* 1993 Dec 15; 1(4):223-6

Nelson, M. L., Park, B. H., Andrews, J. S., Georgian, V. A., Thomas, R. C., Levy, S. B. "Inhibition of the tetracycline efflux antiport protein by 13-thio-substituted 5-hydroxy-6-deoxytetracyclines." *J. Med. Chem.* 1993 Feb 5; 36(3):370-7

Park, B. H., Levy, S. B. "The cryptic tetracycline resistance determinant on Tn4400 mediates tetracycline degradation as well as tetracycline efflux." *Antimicrob. Agents Chemother.* 1988 Dec; 32(12):1797-800

Park, B. H., Hendricks, M., Malamy, M. H., Tally, F. P., Levy, S. B. "Cryptic tetracycline resistance determinant (class f) from *Bacteroides fragilis* mediates resistance in *Escherichia coli* by actively reducing tetracycline accumulation." *Antimicrob. Agents Chemother.* 1987 Nov; 31(11):1739-43

McMurry L. M., Park, B. H., Burdett V., Levy, S. B. "Energy-dependent efflux mediated by class L (tetL) tetracycline resistance determinant from streptococci." *Antimicrob. Agents Chemother.* 1987 Oct; 31(10):1648-50

Patents

Method and apparatus for automatically deploying data in a computer network. USPTO 20010044834 patent pending.

Method for enforcing workflow processes for website development and maintenance. USPTO 20010039594 patent pending. Principal inventor.

Method of and apparatus for recovery of in-progress changes made in a software application. USPTO 20010037475 patent pending. Principal inventor.

Method and apparatus for deploying data among data destinations for website development and maintenance. USPTO 20010011265 patent pending. Principal inventor.

System and method for website development. WO 99/40509 patent pending. U. S. patent also pending.

Education

PhD, Structural Biology, Stanford University, 1996.

B. S., Chemistry, *cum laude*, Tufts University, 1985