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Biocomplexity Faculty Search c/o C. Howard
Department of Physics, Indiana University
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November 30, 2004

Dear Dr. Howard:

I am writing in my strongest support of Dr. Yang Zhang for his application of a faculty position at your department.

After finishing a postdoctoral fellow position at Harvard University, I accepted in 2000 a tenure-track position at the newly establishing Howard Hughes Medical Institute Center for Single Molecule Biophysics at Department of Physiology and Biophysics of State University of New York at Buffalo. Yang was one of many people who applied a postdoctoral position in my then yet-to-be-established lab. However, his resume was so outstanding. I immediately accepted him. I also had an intensive communication with him in order to convince him to join my lab. He finally decided to join Professor Jeffrey Skolnick's lab at St. Louis instead. I understood his decision although it was a great loss to me.

That was mostly email communication. I personally met Yang two years later when he accepted a research assistant professor position at the Center of Excellence in Bioinformatics in our university. This gave me a chance to know him more scientifically as well as personally. He joined my group meetings several times and he also came to the parties at my house many times. I have enjoyed and been benefited from many scientific discussion with him because one of my major research interests is also in the field of protein-structure prediction using theoretical and bioinformatic approaches. These contacts re-enforce my early impression about him. That is, he is one of the brightest persons I ever met.

That Yang is highly creative and productive is demonstrated by 15 high-quality peer-reviewed publications in a little over three years (since 2001) and without prior experience in bioinformatics. For example, one of the most difficult problems in structure prediction of proteins is how to refine the initial structures generated from structural templates obtained from protein data bank. More often than not, refinement leads to reduction of prediction accuracy. Yang creatively developed a novel algorithm, called *TASSER*, which assembles the protein models from the fragments of the templates. The algorithm is the first algorithm showing that it is possible to improve over initial structures. This original algorithm will likely make a great impact to the bioinformatic field by setting a new level of accuracy for structure prediction. The paper was published in *Proc. Natl. Acad. Sci.* (2004).

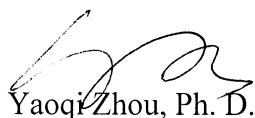
Perhaps, more importantly, Yang initiates his work and completes them mostly independently. This is based on my frequent discussion with him and with his advisor. This is also reflected from his successful transition from high-energy physics (Ph.D), to folding mechanism of macromolecules such as DNA/RNA and proteins, and to protein structure prediction. In each field, he has left a successful tracking record through his extensive publications and is becoming the known expert in the field of biophysics and bioinformatics.

Yang is a cooperative and easy-going person. He got along with his colleagues in Jeff's lab very well. He has no problem in explaining his ideas and work to other people in the seminars and in discussion. Thus, I am sure that he will be a fine teacher.

I strongly believe that Yang will be a valuable asset to your department if accepted. Based on his academic record and experience, he has my strongest support for his application of the faculty position at your university. If you have any further questions, please feel free to contact me at (716) 829-2985.

Thank you very much for your consideration.

Sincerely yours,



Yaoqi Zhou, Ph. D.
Associate Professor