



University at Buffalo
The State University of New York

Buffalo Center of Excellence in Bioinformatics

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Biocomplexity Faculty Search
c/o C. Howard
Department of Physics
Indiana University
Swain West 117
727 East 3rd Street
Bloomington, IN 47405-7105

To Whom It May Concern:

This letter is on behalf of **Dr. Yang Zhang** who has applied for a faculty position at Indiana University. In 2001, Yang started out as a very promising postdoctoral fellow in my research group. Based on his superb performance, he was subsequently promoted to a research assistant professor here in the Center of Excellence in Bioinformatics. As such, I am extremely well acquainted with his abilities and promise. At this point in time, we both agree that it is time for him to seek an independent faculty position and to strike out on his own. I have every expectation that he will be extraordinarily successful.

Yang is a highly creative, hard working and talented scientist. Not only is he very smart and a very quick study, but he is exceptionally productive. It was Yang who gave life to the very promising *TASSER* method of protein structure prediction that he developed in collaboration with me. In the field of protein structure prediction, there are two issues that must be solved: the formulation of an efficient conformational search scheme and the development of an energy function whose global minimum is the native state of the protein. In this regard, he developed the parallel hyperbolic conformational sampling method and conformational search scheme and came up with the idea of a combined continuous space/lattice model. He then succeeded in optimizing the force field to give the best to date correlation of energy and structure quality. Furthermore, the resulting *TASSER* approach is the first general method that systematically improves the quality of the predicted structure relative to that of the template. It also does well in modeling the loop regions. Based on recent CASP6 results, it appears that *TASSER* is among the best, if not the best, of the approaches to protein structure prediction.

Yang's group seminars are always well prepared and insightful, and I have every expectation that he will be a good teacher as well as an excellent scientist. His English is excellent and he is very effective at communicating his ideas.

On a personal level, he is very thoughtful and honest and is a very effective collaborator. He is extremely well organized, and he has played a significant mentoring role with other postdoctoral fellows in our group.

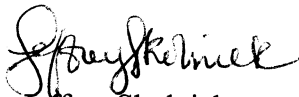
I would rank him as the very best of my postdoctoral fellows and close collaborators. He is superior in every respect to my long time collaborator, Andrzej

Kolinski and is a much deeper thinker than Adam Godzik. Indeed, I am hard pressed to think of someone more talented in the field of protein structure prediction. There is no doubt in my mind that he will have a very successful and productive scientific career.

I strongly urge you to consider him for a faculty position in your department. In Yang, you have a clear winner.

Please feel free to contact me if I can provide any additional information.

Sincerely,



Jeffrey Skolnick

Director, Center of Excellence in Bioinformatics

UB Distinguished Professor