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TO WHOM IT MAY CONCERN

December 9, 2005

Dear Chairperson of the Faculty Search Committee:

I am writing this letter to express my strongest support for the application of **Dr. Jiajian Liu** for a faculty position at your Institute.

I am an Assistant Professor in the Department of Computational Biology, School of Medicine, University of Pittsburgh with joint appointments at the Department of Human Genetics, Graduate School of Public Health and the University of Pittsburgh Cancer Institute (UPCI), School of Medicine. My background is on Mathematics (undergraduate) and molecular biology (graduate) and I have worked on the development of Bioinformatics tools for more than eight years. Currently, in my laboratory, we develop computational algorithms and biochemical techniques to study the DNA identification and binding of transcription factors to their target DNA sequences.

I came to know Dr. Liu when he joined the laboratory of Prof. Stormo in Washington University in St. Louis, where I was working as post-doctoral Research Associate. My main project was consisted of the modeling of the protein-DNA interactions for the Cys₂His₂ zinc finger protein family. By studying published base and amino acid selection data of the wild type protein and mutants we found that the *additivity hypothesis* (i.e. individual base-amino acid contacts contribute independently to the total binding affinity) is a very good approximation for the Cys₂His₂ zinc finger family of transcription factors. Dr. Liu continued this study by collecting additional data and refining the computational model. His work showed that certain "key" amino acid residues determine the overall affinity of the protein to the DNA. Once the overall affinity has been determined the interactions are additive at the DNA level. This is a very important finding that Dr. Liu used it to further improve the computational predictions of the DNA binding for this model family of transcription factors. Note that traditional DNA target prediction methods usually model the binding preferences of a single member of a family at a time. Thus, achieving an accurate model for a transcription factor **family** is of great importance.

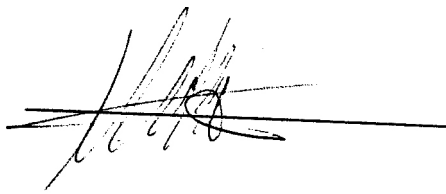
Although Dr. Liu's background is in Biology, his recent work shows that he has excelled in computational biology and bioinformatics. This is not surprising given his strong interest on the computational modeling of properties of biomolecules and his quick learning capabilities. Shortly after he joined the laboratory of Prof. Stormo, Dr. Liu became familiar with all the projects and he was able to make useful suggestions to many of us. Dr. Liu is very

methodical and careful with his work and he has very strong work ethic. He is also self-motivated and academically oriented.

In conclusion, I believe that Dr. Liu's qualities and his interdisciplinary background and training will make him an excellent candidate in your Institute and I strongly support his candidacy.

If you think that I can be of any further help, please do not hesitate to contact me.

Sincerely yours,

A handwritten signature in black ink, appearing to be 'Panagiotis Benos', written over a horizontal line.

Panagiotis (Takis) Benos, Ph.D.
University of Pittsburgh