

Department of Biochemistry
and Molecular Biophysics

(314) 362-4195

December 19, 2003

Biocomplexity Faculty Search Committee
c/o Prof. Rob de Ruyter van Steveninck
Biocomplexity Institute
Indiana University
Swain Hall West 117
Bloomington IN, 47405-7105

Dear Search Committee:

This letter is written in strong support of the application of Dr. Yong (Mike) Kong for a tenure-track faculty position in the area of computational biology in the Biocomplexity Institute at Indiana University. Dr. Kong is presently on the research staff at 454 Corporation, a wholly-owned subsidiary of CuraGen, in New Haven, Connecticut. He is currently looking to move back into an academic research environment.

Mike Kong did his Ph.D. thesis in my lab as a student in the Molecular Biophysics program at the Washington University School of Medicine. He completed our Ph.D. program, from course work to thesis research to defense, in somewhat under 4 years – which I believe to be the shortest time of any Ph.D. student at the Medical School during the last decade. Mike was a stellar student in all respects. The faculty, myself included, just pointed him in the right direction, got out of the way, and watched him go.

Dr. Kong's work in my lab focused on using multipole electrostatics to extend and improve the accuracy of empirical force fields for protein structural modeling. These force fields, such as the well-known AMBER and CHARMM, are central to structural biology and molecular modelling. He used atomic multipole expansions to model direct electrostatic interactions within proteins, and a general Cartesian polytensor formalism to organize the computation. Parameters derived from Stone's distributed multipole analysis decomposition of high-level quantum calculations were determined for the natural amino acids with classical induced dipole terms to treat polarizability. In addition, Mike developed a novel linear CPU time extension of classical reaction field techniques, and used this in simulations with his new multipole-based water model and as a solvation model for peptide/protein simulation. He incorporated all of the above into the TINKER molecular modeling package available from <http://dasher.wustl.edu/tinker/>. His initial work on water simulation formed the basis of the AMOEBA polarizable force field, nearing completion our ongoing research.

In addition to his work with me, Mike did some very interesting theoretical research on 2-D and 3-D Ising lattice models for macromolecular binding. Prof. Enrico DiCera piqued Mike's interest in this area, but their published results were entirely a result of Mike's independent progress in his "spare time". Mike also has previous training in electrical engineering (while in China) and in experimental molecular biology (at the University of Illinois). He surprised me on several occasions with his detailed knowledge of scientific areas far removed from his graduate research.

Compared to the approximately 25 people that have been through my lab during 13 years in Saint Louis, I would consider Dr. Kong to be my finest graduate student and in the top 3-5 coworkers overall. Of the two postdocs I would rank as equivalent to Mike, one is now a senior group leader at the Pfizer Discovery Technology Center in Cambridge and an Adjunct Assistant Professor of Bioinformatics at Boston University. The second has just returned to take up a tenure-track position in Biomedical Engineering at Washington University after considering offers from three schools of similar caliber.

Mike Kong's strongest point is that he is just plain brilliant. In addition to his deep understanding of biophysics and bioinformatics, he is as fine an applied mathematician as I have ever known. For example, Mike would routinely submit answers to the monthly problems in the bulletin of the Mathematical Association of America. These problems are intended to challenge an audience of professional mathematicians. As I recall, he won at least one prize from the MAA for his solutions while a graduate student. Mike has an easy going, understated personality. He was always willing to help in tutoring other students in our program. His spoken English was serviceable during his time in St. Louis, and has obviously improved in the years since he left my lab. His written English was and is excellent due to voracious reading of the research literature across much of biomedical and computational science. I have no doubt that he will be able to write strong grant proposals in search of funding for his research.

Finally, I should say that Dr. Kong is someone who really deserves the chance to develop an academic research program. When he left my lab, I tried hard to push him down the usual path to postdoctoral research followed by a faculty position. Shortly before leaving St. Louis, Mike married a fellow student and his father passed away back in China. His new wife had lined up an excellent postdoc at Yale, and Mike was attracted to the CuraGen offer not only for the science, but as a chance to make some money and apply for US citizenship. Now, some years later, he has contributed directly to the development of numerous bioinformatics tools at Curagen. The group at Curagen has been extensively dismantled for business reasons; for example, Mike's co-worker and immediate boss, Joel Bader, has just taken a faculty position at Johns Hopkins. I know from discussions with Dr. Bader that he thinks highly of Mike Kong's work in bioinformatics, and I suspect you will hear from him separately. Indeed, Dr. Kong is well-positioned to continue with his own independent ideas in bioinformatics, modeling or more likely a combination of the two.

If you are looking to fill a faculty position in computational biology, but would like someone who can interface with mathematicians and biophysicists as well as experimental biomedical scientists, Dr. Kong would be an excellent choice. Please contact me by phone (314-362-4195) or email (ponder@dasher.wustl.edu) if I can be of further assistance.

Sincerely,



Jay W. Ponder
Associate Professor
Biochemistry & Molecular Biophysics