PROMOTION RECOMMENDATION
UNIVERSITY OF MICHIGAN
MEDICAL SCHOOL
DEPARTMENT OF COMPUTATIONAL MEDICINE AND BIOINFORMATICS
DEPARTMENT OF BIOLOGICAL CHEMISTRY

Yang Zhang, Ph.D., associate professor of computational medicine and bioinformatics, with tenure, Department of Computational Medicine and Bioinformatics, and associate professor of biological chemistry, without tenure, Department of Biological Chemistry, Medical School, is recommended for promotion to professor of computational medicine and bioinformatics, with tenure, Department of Computational Medicine and Bioinformatics, and professor of biological chemistry, without tenure, Department of Biological Chemistry, Medical School.

Academic Degrees:

Ph.D.	1996	Central China Normal University, Wuhan, China

Professional Record:

2011-present	Associate Professor of Biological Chemistry, University of Michigan
2009-present	Associate Professor of Computational Medicine and Bioinformatics, University of Michigan
2009-present	Adjunct Associate Professor, Center for Bioinformatics, University of Kansas
2008-2009	Associate Professor, Center for Bioinformatics, Department of Molecular Biosciences, University of Kansas
2005-2008	Assistant Professor, Center for Bioinformatics, Department of Molecular Biosciences, University of Kansas

Summary of Evaluation:

Teaching: Dr. Zhang has been rated by his students and by faculty colleagues in the Department of Computational Medicine and Bioinformatics (DCMB) as a fine teacher, receiving very favorable to outstanding reviews for his advanced bioinformatics methods course, BIOINF 528, Advanced Applications of Bioinformatics. Dr. Zhang is the course director and only lecturer of this course. This course has received 'outstanding' reviews from nearly half of the students who have taken it. Dr. Zhang also participates in BIOINF 527, Introduction to Bioinformatics and Computational Biology. Dr. Zhang is one of 13 faculty members who give lectures to the class. Dr. Zhang also contributes substantively to the teaching mission of the Department of Biological Chemistry; making substantive contributions to three courses: BioChem 711 a graduate seminar, BioChem 552, Macromolecular Structure and Function, and Chemical Biology 501. Dr. Zhang is a well-recognized mentor of students and post-doctoral fellows. His lab has kept a size of ~20 members which include post-doctoral fellows (five-eight), Ph.D. students (six-eight), and masters students and undergraduate students (four-six). He conducts a three-four hour lab meeting every Tuesday to discuss research results and trace the difficulty and progress of each

lab member. The presentations at each lab meeting include two reports of research progress and one report on journal articles. On every Thursday, Dr. Zhang conducts three-four hours of open meetings with students who have general questions and issues in their research. Dr. Zhang has served as chair of the Bioinformatics Graduate Program, he regularly attends and engages students in the weekly seminar series which involve ~20-40 graduate students within the bioinformatics Ph.D. program. He has served as a thesis committee member for students from the DCM&B, the Department of Chemistry, the Department of Biological Chemistry, and the Department of Mechanical Engineering.

Research: Dr. Zhang's major research activity and accomplishments since his arrival at Michigan are in the following six areas: Protein structure prediction, protein function annotation, protein-protein interactions, protein design, genome-wide protein structure and function predictions, bioinformatics tools and public services. This work has resulted in 66 scientific articles published or accepted for publication in peer-reviewed journals since he came to Michigan in the fall of 2009. Many of these articles have generated a wide impact within the fields of molecular biology and computational biology. Of note, the two articles describing the I-TASSER server (BMC Bioinf 2008, Nat Prot 2010) have been cited 750 and 853 times, respectively. Dr. Zhang's lab is well funded with two R01's. He also has an NSF Career Award, a Sloan Award, funding from the UM-SJTU Foundation and a UM M-Cubed grant. In addition, he has submitted another R01 for funding on "New methods for template-based protein quaternary structure." Dr. Zhang's remarkable success in the application and continued improvement of his iterative threading assembly refinement (I---TASSER) server, and his historic three successive wins of the biennial international competition entitled the Critical Assessment of protein Structure Prediction (CASP) is unparalleled in the field of computational structural biology. This competition recognizes the fastest/most accurate computational protein folding results, going from the primary sequence of amino acids to a hidden (unknown to the contestants) 3D structure, whose structure is known by x-ray crystallography to the judges. The best laboratories in the world work continuously to improve their methods in the duration between competitions, and the stakes are very high. He has led the world in this since 2006, while publishing his methods and results widely in the best peer-reviewed journals (including 27 publications this year alone). His advice and collaboration with colleagues in Biological Chemistry have been highly valued advantages of his secondary appointment.

Recent and Significant Publications:

Mitra P, Shultis D, Brender JR, Czajka J, Marsh D, Gray F, Cierpicki T, Zhang Z: An evolution-based approach to de novo protein design and case study on Mycobacterium Tuberculosis. *PLoS Computational Biology*, in press, 2013.

Xu D, Zhang Y: Ab Initio protein structure assembly using continuous structure fragments and optimized knowledge-based force field. *Proteins: Structure, Function, and Bioinformatics* 80: 1715-1735, 2012.

Roy A, Zhang Y: Recognizing protein-ligand binding sites by global structural alignment and local geometry refinement. *Structure* 20:987-997, 2012.

Roy A, Kucukural A, Zhang Y: I-TASSER: a unified platform for automated protein structure and function prediction. *Nature Protocols* 5:725-738. 2010.

Zhang Y: Template-based modeling and free modeling by I-TASSER in CASP7. *Proteins: Structure, Function, and Bioinformatics*, 69 (Suppl 8):108-117, 2007.

Service: Dr. Zhang is currently the associate editor of *BMC Research Notes, Frontiers in Bioinformatics and Computational Biology, PLoS One* and *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. In addition, he sits on the editorial boards of Computational Biology and Chemistry: Advances and Applications, Open Access Bioinformatics, and the *Journal of Health & Medical Informatics*. Since 2002, he has been a reviewer for *Science, Cell, Nature, Nature Biotechnology, Nature Protocols, PLoS Biology, PNAS*, and 38 other journals. Dr. Zhang is a member of NIH Special Study Sections (ZGM1 CBB-3, MABS, ZRG1 BCMB-P, ZRG1 CB-L and others), a review panelist for NSF (CDI, MCB, PGRP, Office of Cyberinfrastructure, and others), and has been on the Program Committee for ISMB. Since 2009, he has served as international reviewer for the Israel Science Foundation and as a reviewer for the Luxembourg National Science Foundation, in 2010 was appointed to the Recruitment Commission in Structural Biology for ISAAC PERAL Program Spain and in 2011 appointed to the Scientific Committee of CIBB International meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics. He has also been a reviewer for The Danish Council for Independent Research and Natural Sciences, The Swiss National Science Foundation (SNSF), the UK Biotechnology and Biological Sciences Research Council (BBSRC) and the French National Research Agency. He is a member of the American Chemical Society and the Biophysical Society and has given keynotes, seminars, workshops all over the world. Most recently, he was the keynote speaker at the Twenty-Seventh AAAI Conference, and the section chair at the 3rd Annual World Congress of Molecular & Cell Biology in Suzhou, China. Other keynotes in 2012 alone include: the 8th Symposium Soft Matter and Life Science in Guiyang, China, the IEEE 6th International Conference on System Biology, in Xian, China, the Chinese Academy of Science, in Beijing, China, and the 22nd Brazilian Synchrotron (LNLS) annual user' meeting, in Sao Paulo, Brazil. In 2011, he was a keynote speaker at the US HUPO Annual Conference and at the Leeds Annual Statistical Research Workshops at the University of Leeds, U.K. Within the University of Michigan, Dr. Zhang has served on the Bioinformatics Graduation Affairs Committee, the Graduation Admissions Committee, and the Curriculum Committee. He currently chairs the department's Seminar Program, serves on its Executive Committee and represents the Department as the associate chair for research.

External Reviewers:

Reviewer A: "Dr. Zhang is one of the top three investigators worldwide in modeling protein structures. The other two who I consider equal...are considerably more senior that Dr. Zhang and have been endowed professors for a long time. This placement is highly significant since the field is very competitive and includes at least 100 active groups that regularly participate in CASP. As such, Dr. Zhang's publications and software are of very high impact."

Reviewer B: "...it is clear that Yang is a superb researcher and his work is very creative and provides new avenues for protein structure prediction, as well as protein-protein interactions. His prolific scientific research record places him at the top group of researchers in the protein structure prediction area..."

Reviewer C: "Dr. Zhang participates widely in peer organizational service, which includes his work on Editorial Boards of several journals, frequent participation in review of NIH proposals and proposals from other organizations, including international, and other peer reviews. He is an invited and keynote speaker at many meetings and conferences."
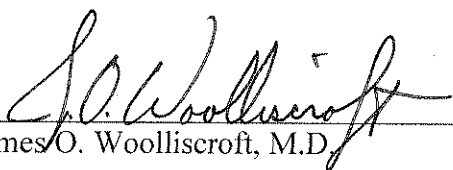
Reviewer D: "He is clearly performing better than any of his peers at CASP. He is absolutely the foremost protein structure predictor in the world. It is interesting to see that he is looking ahead and his recent papers indicate some significant and important efforts to diversify his research, readying him for new grant submissions as a re-invented scientist - something everyone must do. This ensures that he will maintain his scientific leadership."

Reviewer E: "Dr. Zhang has had a major impact on the field of protein modelling achieving number one position in the CASP trials held every two years since 2006....I consider that having Dr. Zhang as a faculty member markedly enhances the international reputation of computational biology at that university."

Reviewer F: "He is innovative in developing bioinformatics methods and software tools. Some of his tools are very popular. For example, his tools TM-align and TM-score are two of the most popular software tools for protein structure comparison and protein structure model assessment....His publication record is outstanding. He has published a number of landmark papers in protein structure modeling with high impact and citations."

Summary of Recommendation:

Dr. Zhang has made superior research contributions in the field of protein structure. He is a solid leader with an international reputation. I am pleased, therefore, to recommend Yang Zhang, Ph.D. for promotion to professor of computational medicine and bioinformatics, with tenure, Department of Computational Medicine and Bioinformatics, and professor of biological chemistry, without tenure, Department of Biological Chemistry, Medical School.

James O. Woolliscroft, M.D.
Dean
Lyle C. Roll Professor of Medicine

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