CONFIDENTIAL

20 October 2005

Yves Brun
Systems Biology/Microbiology Faculty Search
Department of Biology
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Dear Committee Members:

I am writing to recommend **Dr. Yu Xia** for a tenure track position in the Department of Biology at the Indiana University. Dr. Xia is probably the best graduate student I have ever had ("probably" only because I have had so many truly remarkable people in my lab). Xia is definitely in the top 1% of young people I have known at his stage of career. He will be a perfect for your department and has my very strongest recommendation.

I have known Xia since he began his Ph.D. at Stanford in 1995 working in the group of Prof. Harden McConnell. At that time, Prof. Chris Lee who had finished his Ph.D. with me in 1993 was working as a Post Doc in the McConnell lab. Lee alerted me to Xia and about a year latter Xia decided that he wanted to switch to computational biology and transfer to my group. By then, Xia had won a Howard Hughes Pre-doctoral Fellowship in Biological Sciences. In recommending Xia to me, Dr. McConnell used the words "he is one in a billion" and meant it literally. He was certainly right!

After moving to my lab at the beginning of 1997, Yu Xia initially worked on the lattice models pioneered by a previous graduate student, David Hinds. He then went on to collaborate with Ram Samudrala in using these methods rather successfully at CASP3 in 1998. Xia then became more interested in the general properties of proteins. His first work in this area was to generate a very large set of decoys of a 56 residue polypeptide chain folded to a compact shape with secondary structure taken from every 56-residue length in the entire non-redundant scop classification of protein structures.

This work prepared Xia for his most remarkable work with me: the first detailed examination of the sequence and structure space of an artificial 24-mer comprised of two types of amino acids and folding on a two-dimensional square lattice. In spite of it simplicity, this "toy" protein has over 16 million different sequences and over 2 billion different structures. When this model was used to simulate evolution it led to two remarkable findings. (1) When mutation dominates, most sequences in a population will

be far from the most stable sequence and only a few mutations away from being inactive. (2) When recombination dominates, most sequences in a population are much closer to the most stable sequence. These results have far-reaching implications for the role of introns in governing the stability of proteins in higher organisms.

In putting Xia in the "truly outstanding" rank, it is important to know that at Stanford I have been blessed by an incredibly talented group. Of the 14 students and postdocs to leave the group, four are tenured at University of Washington, Yale, UCLA and UCB. Four others currently hold tenure track positions (at Univ. Washington, Texas A & M, Cornell and Ben Gurion University). Xia is truly outstanding even when compared to these other stars.

Yu Xia is a very mature scientist, someone who as a PhD student was consulted by all members of the lab who were generally his senior. He writes remarkably well and I almost never need to edit his texts. He is incredibly intelligent, a very talented programmer and one of the most original thinkers I have ever encountered. He is also a very good group member always helping others, doing more than his share of duties, etc. He is well on his way towards a stellar career as a superstar. I can think of no better candidate for the Department of Biology at the Indiana University.

Yours sincerely,

Michael Levitt
Professor and Associate Chair

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