December 4, 2003

Prof. James A. Glazier
Director, Biocomplexity Institute
Department of Physics
Indiana University, Bloomington
Bloomington, IN 47405-7105

Dear James,

I am writing to recommend Rahul Kulkarni who has applied for a junior faculty position in your department.

I first knew Rahul when he came to NEC about two years ago for an interview for a postdoc position. We were impressed, among other things, by his enthusiasm and energy. We offered him the job, and he joined us in the fall of 2002 working with me and Ned Wingreen. We have been very happy with him. Within a little more than a year, Rahul initiated and accomplished a number of projects. He first started with a bioinformatics study of the co-evolution of the transcription factors (TFs) with their binding sites. I suggested this problem to him in the hope of getting some information about the "transcription code". Rahul quickly became an expert in genome databases and relevant bioinformatics tools, and has invented his own algorithms which allowed him to trace the protein-DNA pairs across different genomes. This comparative genomics study has led to some surprising results, including a new regulatory role of the arginine repressor in some bacteria.

Equipped with his expertise in bioinformatics and his love in biological problems, Rahul initiated (mostly by himself) a couple of projects concerning the regulative roles of small RNAs. The first is an all genome study of sRNAs and their corresponding transcription factors in E. Coli. In this study, Rahul not only identified the TFs for many known sRNAs, thus providing information of the regulative roles of the sRNAs, but can also predict novel sRNAs for further experimental verification. The other project started by Rahul's going to the group meetings of Prof. Bonnie Bassler at Princeton University, and has turned out to be an extremely fruitful collaboration with Bassler's group. Basically, Rahul discovered a number of sRNAs critical to the quorum sensing in the bacterium V. cholerae and related species, which provided new insights into this signaling network. The experimental verifications of Rahul's predictions are underway and have already showed very positive signs.

Rahul has also been working on several other problems, ranging from modeling dynamic localization of proteins, to gene-expression analysis, and to prion diseases. A major difference between Rahul and many others with bioinformatics or other quantitative expertise is that he loves biology. He is always interested in the underlying biological problems. I recommend him highly.

Sincerely yours,

Chao Tang
Senior Research Scientist