



# University of Pittsburgh

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September 23, 2012

G. Elisabeta Marai  
Department of Computer Science  
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Dear Liz,

I am writing in support of your tenure dossier at the University of Pittsburgh. As you know, my research focuses on the development of modeling and simulation capabilities for the understanding of complex biological systems. I believe that the rule-based approach that I have developed has the potential to greatly increase the application of computational modeling in molecular biology. By providing an intuitive representation of biological molecules as objects with binding and modification sites acted on by rules that are derived from biochemistry, rule-based modeling provides a powerful alternative to standard approaches to modeling these systems based on differential equations. The advantages of rule-based modeling appear across the spectrum of potential model developers, from computational scientists to bench biologists. However, allowing users to build much more detailed models than was possible before brings new challenges: specifically, the building, debugging, analysis, and management of large-scale models. To realize the full potential of rule-based modeling will require the development of state-of-the-art interfaces that are visually appealing and allow users to perform these tasks in an integrated workflow. Our collaboration has been and continues to be vital to achieving these aims.

For the past four years we have collaborated closely on the development of a visual interface, called RuleBender, for our rule-based modeling tools. Your expertise in visualization research and software development has been critical to the success of this effort. We have jointly managed the project by holding weekly meetings and co-supervising graduate students. Alumni of this project include two Masters' students currently in industry and one PhD student currently still in the program. We have published four papers on RuleBender in the past two years, including two in high-impact journals in the field (*Bioinformatics* and *BMC Bioinformatics*). In addition, our detailed paper on the design and capabilities of RuleBender was awarded Best Paper at the 2011 BioVis Symposium. RuleBender has also become the core component of our training and outreach efforts, which are critical to the future success of the rule-based approach. RuleBender is the preferred interface for nearly all users of our software, and the RuleBender package is the major umbrella for our software distribution efforts. RuleBender is currently used in biology modeling courses by instructors at several major universities, including Pitt, CMU, Yale, and UNAM (Mexico). It is also used in summer schools at [Los Alamos National Laboratory](#) and [Cold Spring Harbor](#). The response to RuleBender is uniformly positive and it has greatly extended the accessibility of both rule-based modeling and computational modeling of biological networks in general. In spite of these successes, much work remains to be done to realize the full potential of visual interfaces for rule-based modeling, and I look forward to our continued collaboration.

Sincerely,

A handwritten signature in blue ink that reads "James R. Faeder".

James R. Faeder, Ph.D.

Associate Professor, Department of Computational and Systems Biology

Co-director, Molecular and Systems Modeling Core, Clinical and Translational Sciences  
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