#### BIOGRAPHICAL SKETCH

Provide the following information for the key personnel and other significant contributors. Follow this format for each person. **DO NOT EXCEED FOUR PAGES.** 

NAME		POSITION TITLE			
Abhijeet Kapoor	Postdoctora	Postdoctoral Research Associate			
eRA COMMONS USER NAME (credential, e.g., agency login) NA					
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)					
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY		
Jaypee University of Information Technology, India	B.Tech.	2004-2008	Bioinformatics		
Iowa State University, USA	Ph.D.	2009-2014	Bioinformatics and Computational Biology		
Icahn School of Medicine at Mount Sinai, USA	Post-Doc	2015-	Computational Structural Biology		

#### A. Personal Statement

My PhD studies focused on using computational techniques such as coarse-grained and all-atom simulations to understand functional motions in Ras proteins, an oncology target of exceptional importance. The primary focus of the work was to develop a generic coarse-grained model of proteins, use it to study conformational transitions in Ras proteins with the goal to identify specific structural features controlling the intrinsic conformational transitions, and complement the results using all-atom simulations. First, I developed the coarse-grained model that successfully folded nineteen proteins to their native state starting from completely random conformations. Next, using the coarse-grained simulations in combination with all-atom simulations, I identified the structural features that regulate the intrinsic nucleotide (GDP) exchange reaction based on which a model for regulatory protein assisted exchange process was presented. Finally, I provided a comprehensive comparison of the dynamics of all the three Ras isoforms using extensive all-atom molecular dynamics simulations. Such an understanding is critical for the design of inhibitors that can selectively target a particular malfunctioning isoform.

I joined the Filizola lab to conduct simulation studies of important protein targets, such as G protein coupled receptors and integrins, with the aim of using the mechanistic insights obtained from simulations for drug designing.

#### B. Positions and Honors.

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2008-2009	Research Assistant, Department of Biochemistry, University of Delhi South Campus, New
	Delhi, India
2009-2014	Research Assistant / Ph.D., Bioinformatics and Computational Biology, Iowa State
	University, USA
2014	Teaching Assistant / Ph.D., Bioinformatics and Computational Biology, Iowa State
	University, USA
2015-	Postdoctoral Research Associate, Department of Chemical and Structural Biology, Icahn
2010	School of Medicine at Mount Sinai, USA
	School of Medicine at Mount Sinal, OSA

## Other Experience, Professional Memberships, and Awards

2012-2014	Member, Biophysical Society
2012	Bioinformatics and Computational Biology Travel Fellowship Award, Iowa State University
2012	Best Oral Presentation Award at International Interdisciplinary Science Conference on
	Protein Folding and Diseases, Jamia Millia Islamia, New Delhi, India
2014	James Cornette Research Fellowship in Bioinformatics and Computational Biology, Iowa
	State University

# C. Selected Peer-Reviewed Publications (in chronological order)

- 1. Kapoor A, Shandilya M, Kundu S. Structural insight of dopamine β-hydroxylase, a drug target for complex traits, and functional significance of exonic single nucleotide polymorphisms. PLoS One. 2011;6(10):e26509.
- 2. Kapoor A, Travesset A. Folding and stability of helical bundle proteins from coarse-grained models. Proteins. 2013 Jul;81(7):1200-11.
- 3. Kapoor A, Travesset A. Folding 19 proteins to their native state and stability of large proteins from a coarse-grained model. Proteins. 2014 Mar;82(3):505-16.
- 4. Kapoor A, Travesset A. Mechanism of the exchange reaction in HRAS from multiscale modeling. PLoS One 2014;9(10):e108846.

## D. Research Support

None