# AMIKA SOOD

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## EDUCATION

**The University of Georgia (UGA), Athens, GA** 2016
Doctor of Philosophy in Bioinformatics

- Dissertation Title: "Development of Computational methods to characterize Carbohydrate-Protein interactions"
- Advisor: Robert J. Woods, Ph.D.
- *Relevant Graduate level courses*: Bioinformatics II, Statistical Methods in Bioinformatics I and II, Computational Genome Organization, Algorithms for Computational Biology, Computational Methods in Bioinformatics, Mathematical Biology, Computer Simulation Methods in Physics, Computer Simulations of Materials

**Vellore Institute of Technology, Vellore, India** 2008

- Bachelor of Technology in Biotechnology (Biochemical Engineering)
- Thesis Title: "Role of lspa protein in the pathogenesis of Mycobacterium Tuberculosis"

## SKILLS

*Software & Languages:* FORTRAN, C, C++, JAVA, JSP, Servlets, JavaBeans, JDBC, XML/HTML, Bash, Linux, Molecular Visualization Software, Eclipse, AMBER MD package, AutoDock, SMMP Monte Carlo package, Gaussian, GaussView.

Molecular Modeling, Molecular Dynamics, Monte Carlo simulation, Protein-Carbohydrate docking, Force field development, Pharmacophore design, Homology modeling, Programming; Scientific writing.

## EXPERIENCE

**Complex Carbohydrate Research Center (CCRC), UGA**
***Post-Doctoral Research Associate*** 2017 -

- Designing a scoring function for prediction of Glyosaminoglycan (GAG) binding to proteins using AutoDock Vina.
- Modified the AutoDock Vina code to add the new scoring function.
- Compared the performance of docking software (AutoDock 4.2.6 and Vina) for Protein-GAG blind docking.

***Graduate Research Assistant*** 2010 – 2016

- Created a scoring function for quantification of similarities in monosaccharides to explain cross-reactivity observed in several glycan binding proteins (GBP) and prediction of binders.
- Derived glycan pharmacophores for GBPs with broad specificity using known binders.
- Developed a scoring function based on per-residue Solvent Accessibility Surface Area (SASA) and footprinting for assessment of the quality of theoretical protein models.
- Generated parameters for non-standard molecule compatible with AMBER/GLYCAM force field for MD and MM-GBSA analysis.
- Developed a new term for all-atom AMBER force field based on the backbone dipoles for improved secondary structure sampling. Modified the AMBER code to calculate the new term.
- Trained 3 graduate and 2 undergraduate students and handled communications with collaborators.

**Tata Consultancy Services, Bangalore, India**
***Assistant System Engineer*** 2008 – 2009

- Trained in JavaScript, JSP, Servlets, JavaBeans, JDBC and Struts II Framework.
- Involved in software development for a multinational retail client for their order consolidation.
- Contributed to the development of a website using Scheme Programming Language.

**B. R. Ambedkar Centre for Biomedical Research, University of Delhi, India**
***Undergraduate Researcher*** Jan – June 2008

- Cloned lspA enzyme (Lipoprotein Signal Peptidase) of Mycobacterium tuberculosis in pET29 plasmid.
- Purified recombinant lspA using affinity and ion exchange chromatography.
- Performed protein characterization using SDS-PAGE and biochemical assays.

## PROFESSIONAL ACTIVITIES & AWARDS

- Reviewer for PLOS Computational Biology, 2018 onwards.
- UGA Graduate School Travel Award, 2013.
- Sun Certification of Java Programmers 1.5, 2009.

## POSTERS AND PRESENTATIONS

Sood A. Performance of MM-PB/GBSA calculations using six different carbohydrate ligands interacting with ECL. AMBER Developers meeting. Oral presentation. Tampa, FL. Feb 2018.

Sood A, Wang X, Sharp J, and Woods RJ. Integrating MS footprinting data in protein structure modeling. GRC: Biological Molecules in the Gas Phase & in Solution. Poster presentation. Holderness, NH. July 2013.

Sood A, Wang X, Sharp J, and Woods RJ. Integrating MS footprinting data in protein structure modeling. Research Resource Advisory Committee meeting. Poster presentation. Athens, GA. Oct 2012.

Sood A. Solvent Excluded Surface Area Restraints. AMBER Developers meeting. Oral presentation. Athens, GA. Feb 2011.

## PUBLICATIONS

**Sood A**, Gerlits OO, Ji Y, Bovin NV, Coates L and Woods RJ. Defining the Specificity of Carbohydrate–Protein Interactions by Quantifying Functional Group Contributions. J. Chem. Inf. Model. 2018;58(9):1889-1901.

Xie B, **Sood A (first co-author)**, Woods RJ and Sharp JS. Quantitative Protein Topography Measurements by High Resolution Hydroxyl Radical Protein Footprinting Enable Accurate Molecular Model Selection. Sci Rep. 2017;7(1):4552.

Ng S, Lin E, Kitov PI, Tjhung KF, Gerlits OO, Deng L, Kasper B, **Sood A**, Paschal BM, Zhang P, Ling CC, Klassen JS, Noren CJ, Mahal LK, Woods RJ, Coates L and Derda R. Genetically encoded fragment-based discovery of glycopeptide ligands for carbohydrate-binding proteins. J Am Chem Soc. 2015;137:5248–525.

Poor TA, Jones LM, **Sood A**, Leser GP, Plasencia MD, Rempel DL, Jardetzky TS, Woods RJ, Gross ML and Lamb RA. Probing the paramyxovirus fusion (F) protein-refolding event from pre- to postfusion by oxidative footprinting. Proc. Natl. Acad. Sci. U.S.A. 2014;111:E2596–E2605.

***Articles in Preparation (Manuscripts available if required):***

Viola JA, **Sood A (first co-author)**, Lee JK, McBride R, Smith DF, Cummings RD, Paulson JC, Moremen K, Woods RJ and Pierce M. Comparative microbial glycan binding specificities of three intelectins: hIntL-1, hIntL-2, and XCG-1. (in preparation).

**Sood A**, Foley BL and Woods RJ. Monosaccharide similarity analysis to understand protein-carbohydrate specificity. (in preparation).

Misra SK, **Sood A**, Soares PA, Pomin VH, Woods RJ and Sharp JS. Mapping of the Fondaparinux Binding Site of JR-FL gp120 by High Resolution Hydroxyl Radical Protein Footprinting and Computational Docking. (in preparation). Preprint: https://doi.org/10.1101/207910