

Amika Sood, PhD

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EXPERIENCE

Senior Research Associate

Complex Carbohydrate Research Center, University of Georgia | 2022 - 2024

- Developed a novel representation and scoring function to assess structural similarities, predict pharmacophores from known binders, and conduct substructure searches among monosaccharides.
- Showcased enhanced capabilities in sugar analysis by outperforming RDKit in comparative evaluations.
- Utilized Molecular Modeling to reveal insights into Brucella antigen-antibody interactions and TREM2-Heparan Sulfate binding, advancing collaborative research.

Post-Doctoral Research Associate

Department of Biostatistics and Bioinformatics, Duke University | 2019 - 2022

- Developed a program to estimate admixture and co-ancestry from kinship matrices.
- Performed GWAS to identify variants associated with steroid response in pediatric nephrotic syndrome.

Post-Doctoral Research Associate

Institute of Bioinformatics, University of Georgia | 2017 - 2019

- Improved the scoring function of AutoDock Vina-Carb by 25% for Glycosaminoglycans (GAGs).
- Modified Vina-Carb code to implement the scoring function, leading to more accurate docking simulations.
- Compared the performance of docking software (AutoDock 4.2.6 and Vina) for Protein-GAG blind docking.

Graduate Research Assistant

Institute of Bioinformatics, University of Georgia | 2010 - 2016

- 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 MMGBSA 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.

Assistant System Engineer

Tata Consultancy Services, Bangalore, India | 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..

EDUCATION

PhD in Bioinformatics, University of Georgia | 2016

Dissertation Title: "Development of Computational methods to characterize Carbohydrate-Protein interactions"

Relevant Graduate level courses: 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

B.Tech in Biotechnology (Biochemical Engineering), Vellore Institute of Technology | 2008

Thesis Title: "Role of Ispa protein in the pathogenesis of Mycobacterium Tuberculosis"

CERTIFICATIONS

- Python for Data Science, AI & Development, IBM, 2024.
- Machine Learning with Python, IBM, 2024.

PUBLICATIONS

1. Carpenter EJ, Peng C, Twells N, Woudstra L, **Sood A**, et. al. Atom-level machine learning of protein-glycan interactions and cross-chiral recognition in glycobiology. **Science Advances** (under review)
2. Tu T, Ochoa A, **Sood A**, et. al. Polygenic Risk Scores and HLA Class II Variants are Biomarkers of Corticosteroid Response in Childhood Nephrotic Syndrome. (Submitted: *Kidney International*)
3. **Sood A**, Bundle DR, Woods RJ. Towards understanding the basis of specificity between Brucella Antigen-Antibody Interactions. **Molecules** 2025; 30(14):2906
4. McMillan IO, Liang L, Su G, Song X, Drago K, Yang H, Alvarez C, **Sood A**, et. al. TREM2 on microglia cell surface binds to and forms functional binary complexes with heparan sulfate modified with 6-O-sulfation and iduronic acid. **JBC** 2024; 300(9):107691
5. Lane BM, Chryst-Stangl M, Wu G, Shalaby M, El Desoky S, Middleton CC, Huggins K, **Sood A** et. al. Steroid-sensitive nephrotic syndrome candidate gene CLVS1 regulates podocyte oxidative stress and endocytosis. **JCI Insight**. 2022;7(2):e152102.
6. Olson LJ, Misra SK, Ishihara M, Battaile KP, Grant OC, **Sood A**, et. al. Allosteric regulation of lysosomal enzyme recognition by the cation-independent mannose 6-phosphate receptor. **Commun. Biol.** 2020;3(1):1-15.
7. Kim SY, Jin W, **Sood A**, et. al. Characterization of heparin and severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) spike glycoprotein binding interactions. **Antivir. Res.** 2020;181:104873.
8. **Sood A**, et. al. Defining the Specificity of Carbohydrate-Protein Interactions by Quantifying Functional Group Contributions. **J. Chem. Inf. Model.** 2018;58(9):1889-1901.
9. Xie B, **Sood A (first co-author)**, et. al. Quantitative Protein Topography Measurements by High Resolution Hydroxyl Radical Protein Footprinting Enable Accurate Molecular Model Selection. **Sci Rep.** 2017;7(1):4552.
10. Misra SK, **Sood A**, et. al. Mapping of the Fondaparinux Binding Site of JR-FL gp120 by High Resolution Hydroxyl Radical Protein Footprinting and Computational Docking. **BioRxiv**. 2017.
11. Ng S, Lin E, Kitov PI, Tjhung KF, Gerlits OO, Deng L, Kasper B, **Sood A**, et. al. Genetically encoded fragment-based discovery of glycopeptide ligands for carbohydrate-binding proteins. **J Am Chem Soc.** 2015;137:5248–525.
12. Poor TA, Jones LM, **Sood A**, et. al. 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:

1. **Sood A**, Woods RJ. Optimizing AutoDock Vina-Carb: A Novel Scoring Function for Improved Docking of Glycosaminoglycans. (Target Journal: *Nature Methods*)
2. **Sood A**, Foley BL and Woods RJ. A Novel Representation and Scoring Function for Enhanced Structural Similarity Assessment and Pharmacophore Prediction in Monosaccharides. (Target Journal: *Glycobiology*)
3. **Sood A** and Ochoa AJ. Estimating ancestry from a population kinship matrix under arbitrary ancestral subpopulation structure. (Target Journal: *Oxford Bioinformatics*)