Deepali Lalchand Kundnani

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Ph.D. candidate working at the intersection of biology, computation and statistics at Georgia Institute of Technology. With demonstrated track of excellence in bioinformatics and unbridled passion for solving challenging problems, I am committed to making impactful and meaningful contributions to the field through innovation and interdisciplinary approaches.

EDUCATION

Doctor of Philosophy, Bioinformatics

Georgia Institute of Technology, Atlanta, GA Minor in Machine Learning Thesis - Distribution and features of *ribomes*, genome-wide ribonucleotide embedment in eukaryotic genomes.

Master of Science, Molecular Biotechnology

University of Houston – Clear Lake, Houston, TX

Capstone - Cloning techniques for high yield productivity of monoclonal antibodies in Chinese Hamster Ovarian cells. Independent Research - Screening human lung cDNA library from asthma patients employing a yeast two-hybrid system to detect protein interaction of inducible Nitrous Oxide Synthase.

Bachelor of Engineering, Biotechnology

University of Mumbai, India

Thesis - Assessment of stem cell therapy and analogous wound care techniques for diabetic foot complications in reference to standard therapy.

AWARDS & FUNDS

Student Government Association Conference Award, <i>Georgia Institute of Technology</i> Travel Awards for National / International Conference	2024
Conference Registration Funds, <i>Bio-IT World Conference & Expo</i> <i>Registration funded for aiding as a Consultant for Combinatics Inc.</i>	2023 - 2024
Mark Borodovsky Prize for Excellence in Bioinformatics, <i>Georgia Institute of Technology</i> Award honors top Ph.D. student in the Bioinformatics Interdisciplinary Graduate Program, Georgia Inst	2023 <i>titute of Technology</i>
US National Science Foundation Conference Award, <i>The 26th Annual Meeting of the RNA Society</i> Registration for poster on "The Expression Correlation and Copy Number Alteration (CNA) Pre RNASEH2A in cancer supports a role for RNASEH2A in cancer proliferation."	2021 valence of Human
Performance Excellence Award , <i>University of Texas at MD Anderson Cancer Center</i> Project based performance award recognized internally by the Director/Manager.	2019
Jones NAS Biological Sciences Scholarship, University of Houston – Clear Lake Merit based scholarship for students in Biological Sciences towards academic year.	2014 - 2015
Third Prize, Institute of Electrical and Electronics Engineers (IEEE), India National level technical Paper presentation on "Genetic Algorithms"	2010
Top student honor, <i>National Standard Examination, India</i> Certified in top 10% student against national standard for XI n XII level Chemistry and Biology	2008

EXPERIENCE

Georgia Institute of Technology, Atlanta, GA

Graduate Research and Teaching Assistant, Storici Lab

- Spearheaded first ever investigation on ribonucleotides embedded in human genome as a novel epigenetic layer using ribose-seq data with multi-omics association with expression and methylation.
- Discovered novel features of ribonucleotides in Aicardi-Goutières syndrome (AGS) mutant orthologs in association with replication leading and lagging strand activities.
- Conducted comprehensive analysis of RNASEH2A expression correlations and copy number variations in > 1000 cancer cell lines from Cancer Cell Line Encyclopedia (CCLE) and > 10,000 cancer patient samples from The Cancer Genome Atlas Program (TCGA) in 35+ cancer types to understand its association with cancer proliferation and cell cycle phases.

Aug 2019 – Jul 2025 GPA: 4.00/4.00

Aug 2013 – May 2015

GPA: 3.88/4.00

Aug 2008 – May 2012 First Class

Aug 2020 – present

- Development of R package, FeatureCorr to study feature correlations from sequencing and microarray data, which includes various methods of data normalization of batch effects and allowing multi-omics integration and correlation.
- Conceptualized normalization of ribose-seq data using enrichment factor and ribonucleotide enriched zones (REZ) in human mitochondrial and nuclear genome, now being translated to yeast genome.
- Contributed novel data cleaning solutions for NGS library data from ribose-seq technology, enhancing pattern recognition by 2x and revealed clear sequence preferences around ribonucleotides embedded in yeast and human genome.
- Contributed to securing a \$1 million grant for research by providing hypothesis based on preliminary analysis of riboseseq data.
- Implemented Variational autoencoder (neural networks) integrated with scanpy pipelines on peripheral blood mononuclear cells (PBMCs) single-cell gene expression dataset using Pytorch.
- Led and designed computational pipeline for iGen web application to predict Polygenic Risk Score (PRS) of patients/consumers for 20+ infections using DNA sequencing data from 23andm3 and Ancestry Genomics.
- · Invited and co-hosted well-known cancer researchers to address Georgia Tech community, enhance collaborations and connections.
- Showcased research findings at international conferences, enhancing visibility and impact of research contributions.
- Provided hands on training to 15+ students on linux based cloud computing environment, bioinformatic tool usages, python and R programming.

Georgia Institute of Technology, Atlanta, GA

Graduate Teaching Assistant, rotational PhD student

- Identified differentially methylated regions (DMRs) in smokers vs non-smokers using advanced statistical modeling (Gaussian kernel smoothing) from Yale's Veterans Aging Cohort Study (VACS) having > 900 HIV patient data for survival prediction using machine learning algorithms (k-nearest neighbors, support vector machine).
- Led teams for genome assembly and comparative genomics for successful identification of food borne disease outbreak location and food source on Center for Disease Control's (CDC's) data.
- Lectured, created modules and graded courses with students ranging from 20-250 in complex experimental and computation related undergraduate as well as graduate courses.

University of Texas at MD Anderson Cancer Center, Houston, TX

Research Assistant II, Hanash Lab, Mc Combs Institute for the Early Detection and Treatment of Cancer

- Immune assay optimization and validation of lung and pancreatic cancer biomarkers from more than four universally available human serum/plasma cohorts.
- Patient blood processing in a CLIA certified lab while in a double-blind clinical trial for early diagnosis of lung cancer.
- Large scale production of DNA vaccines for murine studies, in-house antigen and antibody production for immunoassays.
- Batch data normalization and missing data handling for cohorts with large sample size.
- Utilizing existing genomic, transcriptomic data to support novel protein biomarkers and supporting with in house mass spectrometry data in multiple cancers.
- Developing auto-antibody assays for proteins product of alternative splicing in breast and lung cancer.
- Assistance in project related activities of record keeping, compiling research data, placing orders, shipping of crucial time dependent samples, maintaining and stocking inventory, calibration of instruments and other lab duties assigned.

Ansh Labs, Webster, Houston, TX

Intern, Research and Development

- Independently optimized SOP's production of highly sensitive antigens in mammalian cell lines and assisted with FDA audits.
- Screened, scaled up, purified and performed quality control using chromatography and protein assays on monoclonal antibodies from hybridoma clones to be used in commercial ELISA kits for ovarian cancer biomarkers.
- Maintained cell culture labs and calibration of apparatus and equipment.

University of Houston - Clear Lake, Houston, TX

Teaching Assistant, Applied Biotechnology

- Liaison between students and professor for selection of projects and deliverables, while resolving course / exam related queries.
- Trained other teaching assistants for experiment set in basic and advanced molecular biology lab.

Usha Biotech, Hyderabad, India

Research and Teaching Assistant, Cell Culture/Molecular Cloning

Oct 2015 – Jul 2019

Jan 2015 - May 2015

Aug 2014 - Dec 2014

Sep 2012 - Jul 2013

Aug 2019 – Jul 2020

- Assisted in creating and testing proprietary vector (CELL EXPRESS 100[™]) using eGFP reporter gene for stable and efficient expression of monoclonal antibodies in Chinese Hamster Ovarian (CHO-K1) cells.
- Performed molecular cloning to prepare custom plasmid vectors and optimized transfection protocols.
- Selected transfected pools and clones using fluorescence activated cell sorting.
- Trained students in mammalian cell culture handling techniques and maintained lab environment and equipment.

S L Raheja Hospital, Mumbai, India

May 2011 - Apr 2012

Trainee assistant for Senior Research Coordinator

- Conducted literature survey, monitored stem cell therapy clinical study reports for diabetic foot complications, toxicology reports and clinical study results.
- Conducted patient selection using inclusion and exclusion criteria and assisted in performing relevant biochemical tests.
- Formulated a statistical standard for evaluating the effectiveness of stem cell therapy using would closure measurements

PUBLICATIONS

- Kundnani, D. L., Yang. T., Channagiri, T., Xu, P., Lee, Y., ... Jonoska, N. & Storici, F. (2025). Human nuclear ribomes reveal DNA-embedded ribonucleotides as a novel epigenetic layer. *in preparation*.
- Moalic, Y., Reveil, M., Kundnani, D. L., Balachander, S., Yang, T., ..., Storici, F., & Henneke, G. (2025). Genomewide ribonucleotide detection in Archaea. *BioRxiv*, 2025.03.17.643674. Henneke, G. (2025).
- Bazzani, V, Kundnani, D. L., Redin, M. E., Agostini, F., Corso, A., ... Storici, F. & Vascotto, C. (2025). Characterization of a new mutation of mitochondrial ND6 gene in hepatocellular carcinoma and its effects on Complex I. *Sci Reports.* & BPDF
- Kundnani, D. L., Yang, T., Gombolay, A., Mukherjee, K., Newnam, G., Meers, C., ... & Storici, F. (2023). Distinct features of ribonucleotides within genomic DNA in Aicardi-Goutières syndrome ortholog mutants of Saccharomyces cerevisiae. *IScience*, 27 (6), 110012. EPF CODE
- Xu, P., Yang, T., Kundnani, D. L., Sun, M., Marsili, S., Gombolay, A. L., ... Storici, F. (2023). Light-strand bias and enriched zones of embedded ribonucleotides are associated with DNA replication and transcription in the human-mitochondrial genome. *Nucleic Acids Research*, 52 (3) 1207–1225. DEF CODE
- Yang J., Sun M., Ran Z., Yang T., Kundnani D. L., Storici F. & Xu P. (2024). rNMPID: a database for riboNucleoside MonoPhosphates in DNA. *Bioinformatics Advances*, 4 (1). *P* → PDF → WEBSITE
- Kundnani, D., & Storici, F. (2021). FeatureCorr: An R package to study feature correlations aided with data transformation for sequencing and microarray data. *Software Impacts*, 10, 100144. DEF DEF CODE
- Marsili, S., Tichon, A., **Kundnani, D.**, & Storici, F. (2021). Gene co-expression analysis of human rnaseh2a reveals functional networks associated with dna replication, dna damage response, and cell cycle regulation. *Biology*, 10(3), 221. *I* → DF **E** REVIEW
- Ostrin, E. J., Bantis, L. E., Wilson, D. O., Patel, N., Wang, R., Kundnani, D., ... & Hanash, S. M. (2021). Contribution of a Blood-Based Protein Biomarker Panel to the Classification of Indeterminate Pulmonary Nodules. *Journal of Thoracic Oncology*, 16(2), 228–236. & IMPACT
- Kobayashi, M., Katayama, H., Irajizad, E., Vykoukal, J. V., Fahrmann, J. F., Kundnani, D. L., ... & Hanash, S. M. (2020). Proteome Profiling Uncovers an Autoimmune Response Signature That Reflects Ovarian Cancer Pathogenesis. *Cancers*, 12(2), 485. & EPDF
- Subbalakshmi, A. R., Kundnani, D., Biswas, K., Ghosh, A., Hanash, S. M., Tripathi, S. C., & Jolly, M. K. (2020). NFATc Acts as a Non-Canonical Phenotypic Stability Factor for a Hybrid Epithelial/Mesenchymal Phenotype. *Frontiers in Oncology*, 10, 553342. *Implies PDF* → IMPACT
- Capello, M., Fahrmann, J. F., Rios Perez, M. V., Vykoukal, J. V., Irajizad, E., Tripathi, S. C., ... & Hanash, S. M. (2020). CES2 Expression in Pancreatic Adenocarcinoma Is Predictive of Response to Irinotecan and Is Associated with Type 2 Diabetes. *JCO Precision Oncology*, 4, 426–436. *Contemposition* (2007)
- Jia, D., George, J. T., Tripathi, S. C., Kundnani, D. L., Lu, M., Hanash, S. M., ... & Levine, H. (2019). Testing the gene expression classification of the EMT spectrum. *Physical Biology*, 16(2), 025002. *Constant Physical Biology*, 16(2), 025002.
- Capello, M., Vykoukal, J. V., Katayama, H., Bantis, L. E., Wang, H., Kundnani, D. L., ... & Hanash, S. M. (2019). Exosomes harbor B cell targets in pancreatic adenocarcinoma and exert decoy function against complement-mediated cytotoxicity. *Nature Communications*, 10(1), 1–13. *P* ² □ PDF ² REVIEW
- Fahrmann, J. F., Bantis, L. E., Capello, M., Scelo, G., Dennison, J. B., Patel, N., ... & Hanash, S. (2019). A Plasma-Derived Protein-Metabolite Multiplexed Panel for Early-Stage Pancreatic Cancer. *JNCI: Journal of the National Cancer Institute*, 111(4), 372–379. & PDF III NEWS

• Capello, M., Bantis, L. E., Scelo, G., Zhao, Y., Li, P., Dhillon, D. S., ... & Hanash, S. M. (2017). Sequential Validation of Blood-Based Protein Biomarker Candidates for Early-Stage Pancreatic Cancer. *Journal of the National Cancer Institute*, 109(4), djw266. C DF INTERS

CONFERENCE PRESENTATIONS, PAPERS AND POSTERS

- Presentation Kundnani, D. L., Yang T., Gombolay L. A., Sun, M., Randhawa S., Mukherjee K., Meers C, Mehta Z., Mouawad C., Balachander S., Verma I., Chhatlani K., Storici, F. Aicardi–Goutières syndrome (AGS) orthologous mutation in RNase H2C subunit mimics embedded ribonucleotides patterns of mutation in RNase H2B PIP-box. Georgia Tech School of biological Sciences (SOBS) retreat, Georgia, USA 2024. Z Received full funding to attend the conference.
- Presentation Kundnani, D. L., Yang T., Gombolay L. A., Sun, M., Randhawa S., Mukherjee K., Meers C, Mehta Z., Mouawad C., Balachander S., Verma I., Chhatlani K., Storici, F. Aicardi–Goutières syndrome (AGS) orthologous mutation in RNase H2C subunit mimics embedded ribonucleotides patterns of mutation in RNase H2B PIP-box. Federation of American Societies for Experimental Biology (FASEB) Conference, Florida, USA 2024 Received travel funding to attend the conference.
- Poster Kundnani, D. L., Yang T., Gombolay L. A., Sun, M., Randhawa S., Mukherjee K., Meers C, Mehta Z., Mouawad C., Balachander S., Verma I., Chhatlani K., Storici, F. Aicardi–Goutières syndrome (AGS) orthologous mutation in RNase H2C subunit mimics embedded ribonucleotides patterns of mutation in RNase H2B PIP-box. Bio-IT World Conference & Expo, Boston USA, 2024 **7** Received partial funding from Combinatics Inc.
- Expo Consultant CellKb, Cell type makers for annotation and discovery in scRNA-seq datasets, Combinatics Inc. Bio-IT World Conference & Expo, Boston USA, 2024 Z Received partial funding from Combinatics Inc.
- Presentation & Poster Kundnani, D. L., Yang T., Gombolay L. A., Sun, M., Randhawa S., Mukherjee K., Meers C, Mehta Z., Mouawad C., Balachander S., Verma I., Chhatlani K., Storici, F. Aicardi–Goutières syndrome (AGS) orthologous mutation in RNase H2C subunit mimics embedded ribonucleotides patterns of mutation in RNase H2B PIP-box. Midsouth computational biology and bioinformatics society (MCBIOS) Conference, Georgia, USA 2024 Received full funding to attend the conference.
- Expo Consultant CellKb, Cell type makers for annotation and discovery in scRNA-seq datasets, Combinatics Inc. Bio-IT World Conference & Expo, Boston USA, 2023 Z Received partial funding from Combinatics Inc.
- Poster Kundnani, D. L., Yang T., Gombolay L. A., Mukherjee K., Meers C, Mehta Z., Mouawad C., Storici, F. Ribonucleotide incorporation in Aicardi–Goutières syndrome (AGS) orthologous mutants of yeast RNase H2 subunits. Bio-IT World Conference & Expo, Boston USA, 2023 Z Received partial funding from Combinatics Inc.
- Presentation Kundnani, D. L., Yang T., Gombolay L. A., Mukherjee K., Meers C, Mehta Z., Mouawad C., Storici, F Effect of AGS-orthologous mutations on ribonucleotide incorporation rates and patterns in Saccharomyces cerevisiae. RNASEH Conference, Maryland, USA 2022
- Presentation Kundnani, D. L., Marsili, S., Tichon, A., & Storici, F. Expression correlation of RNASEH2A in cancer datasets confirms its association with cancer proliferation and specific cell cycle markers, Global Virtual Congress on Cancer research & Drug Development Cancer Research, Online 2022
- Poster Kundnani, D. L., Marsili, S., Tichon, A., & Storici, F. Expression Correlation and Copy Number Alteration (CNA) Prevalence of Human RNASEH2A in cancer supports a role for RNASEH2A in cancer proliferation. The 26th Annual Meeting of the RNA Society, Online, 2021. Z Received NSF Conference Award
- Paper Kobayashi, M., Katayama, H., Irajizad, E., Vykoukal, J. V., Fahrmann, J. F., Kundnani, D. L., … Bast Jr., R. C., & Hanash, S. M. (2020). Proteome Profiling Uncovers an Autoimmune Response Signature That Reflects Ovarian Cancer Pathogenesis. *Cancers*, 12(2), 485. *Image PDF*
- Presentation Kundnani D. L., Railkar S., Genetic Algorithms, National Technical Paper Presentation, Institute of Electronical and Electronics Engineers Engineering in Medicine & Biology Society (IEEE-EMBS), Mumbai India, 2011 Von Third Prize
- Presentation Kundnani D. L., Water Purification Systems, BIOZEAL, Mumbai India, 2009

INVITED TALKS AND LECTURES

- Importance of Bioinformatics, Ribose-map and using Pace Cloud Computational server, Research Project Laboratory Lecture (BIOL-4590), Georgia Institute of Technology, 2025
- Distribution of ribonucleotides embedded in the nuclear genome of multiple human cell types. MBM Seminar Series, Georgia Institute of Technology, USA 2024
- Distinct features of ribonucleotides in genomic DNA of Aicardi-Goutières syndrome (AGS)-ortholog mutants in yeast. MBM Seminar Series, Georgia Institute of Technology, USA 2024
- Role of RNA in DNA repair and modification, RNA Biology and Biotechnology (BIOL-8560/4560), Georgia Institute of Technology, 2023

- Importance of Bioinformatics and Introduction on Ribose-Map Tool kit, Research Project Laboratory Lecture (BIOL-4590), Georgia Institute of Technology, 2023
- Data Preprocessing and Dimensionality reduction in Biomedical and Clinical settings, Biostatistics Lecture (APPH-6225), Georgia Institute of Technology, 2020
- DNA sequencing and Phylogenetic Analysis, Genetics Lab (BIOL-2345), Georgia Institute of Technology, 2019
- Time Management, Management Course, University of Mumbai India, 2010

ARTICLES REVIEWED

- Haiqiang Wang, Xiyan Lu & Jiakuan Chen., Construction and experimental validation of an acetylation-related gene signature to evaluate the recurrence and immunotherapeutic response in early-stage lung adenocarcinoma, *BMC Med Genomics* 15, 254 *P*
- Reijns MAM, Parry DA, Williams TC, et al. Signatures of TOP1 transcription-associated mutagenesis in cancer and germline [published correction appears in Nature. 2022 May;605(7910): E7]. Nature. 2022; 602(7898):623-631.
- Penghao Xu, Francesca Storici, Frequency and patterns of ribonucleotide incorporation around autonomously replicating sequences in yeast reveal the division of labor of replicative DNA polymerases, Nucleic Acids Research, Volume 49, Issue 18, 11 October 2021, Pages 10542–10557.
- Gombolay, A.L., Storici, F. Mapping ribonucleotides embedded in genomic DNA to single-nucleotide resolution using Ribose-Map. Nat Protoc (2021).
- El-Sayed, W. M. M., Gombolay, A. L., Xu, P., Yang, T., Jeon, Y., Balachander, S., Newnam, G., Tao, S., Bowen, N. E., Brůna, T., Borodovsky, M., Schinazi, R. F., Kim, B., Chen, Y., & Storici, F. (2021). Disproportionate presence of adenosine in mitochondrial and chloroplast DNA of Chlamydomonas reinhardtii. IScience, 24(1), 102005.

MENTORING EXPERIENCE

Research mentor for 5 B.S. / M.S. Bioinformatics Students	2021-2024
Georgia Institute of Technology	
 Prerna Kokil, BS/MS, Medical Student (<u>F'23 [▼] Sp'24 [▼]</u>) 	2022-2024
• Ishika Verma, MS, Intern at Moderna, Ph. D student at Penn State University (<u>S'23 ₹ Sp'24</u> ₹)	2022-2024
Yashas Appaji, BS Biology student	2022-2023
 Kirti Chhatlani, MS, Clinical bioinformatician at Mayo Clinic (<u>S'22 Z Spr'23 Z</u>) 	2021-2023
 Ashlesha Gogate, Computational Biologist at UT Southwestern Medical Center (<u>S'22</u>) 	2021-2022
Computational Biology Faculty Research Awards	
Trainer for cell culture techniques	2018
University of Texas at MD Anderson Cancer Center	
Hansini Krishna, Research Intern	2018

TEACHING POSITIONS

Course	Position/Title	<u>Institute</u>	Semester
RNA Biology & Biotech (BIOL 4560/8560)	Teaching Assistant	Georgia Institute of Technology, USA	Fall 2023
Research Project Lab (BIOL-4590)	Teaching Assistant	Georgia Institute of Technology, USA	Spring 2023
Biostatistics (APPH-6225)	Teaching Assistant	Georgia Institute of Technology, USA	Summer 2020
Scientific Foundations of Health (APPH 1040)	Teaching Assistant	Georgia Institute of Technology, USA	Spring 2020
Genetics Lab (BIOL-2345)	Teaching Assistant	Georgia Institute of Technology, USA	Fall 2019
Applied Biotechnology (BIOT 5031)	Teaching Assistant	University of Houston – CL, USA	Fall 2014
Mammalian Cell Culture Techniques	Teaching Assistant	Usha Biotech, India	Spring 2013

COURSEWORK

Graduate

Applied Genomics, Human computational Genomics, Machine Learning in Biosciences and Computational biology, Biostatistics, Probability and Statistics, Advanced molecular biotechnology Labs, Applied Biotechnology, Bioinformatics, Bacterial taxonomy, Marine biology, Plant genomics, Bioethics.

Undergraduate

Coursework: Immunology, Genetic Engineering and Technology, Protein & Enzyme Engineering, Analytical Techniques in Biotechnology, Biochemistry, Bioinformatics, Molecular Genetics, Plant Cell and Tissue Culture, Bioprocess and Downstream Technology, Biomaterials and Components, Transport Phenomena in Biotechnology, Mass and Heat Transfer Operations, Thermodynamics and Biochemical Engineering, Process Calculations, Information Technology, Statistics and Database Management.

Introduction to Gen AI - Art of the Possible, Amazon Web Services	2025
Pivot Tables in Depth, LinkedIn	2018
Clinical Laboratory Improvement Amendments (CLIA) Certification, UT MD Anderson Cancer Center	2018
R programming, Coursera	2017
Data Scientist Toolbox, Coursera	2016
ISO 9001:2008 Rules and Regulations, Ansh Labs, Houston, TX	2015
Mammalian Cell Culture and Molecular Cloning Techniques, India	2012
Applications of Immunology in Health and Medicine, Haffkine Institute, India	2011
Workings of Clinical Research, Institute of Clinical Research, India	2010
PROFESSIONAL SERVICE & AFFILIATIONS	
Founding Student Committee Member, Molecular BioMedical (MBM) Cancer Talk Series	2022-2024
Member, American Association for the Advancement of Science (AAAS)	2020-2022

Member, American Association for the Advancement of Science (AAAS)	2020-2022
Member, Georgia Tech Bioinformatic PhD Orientation Panel	2021
Member, Georgia Tech Bioinformatics T-shirt committee	2021
Assisted in Storici Lab's Grant Writing (received \$1M from W.M. Keck Foundation)	2021
Member of Association for Women in Science – Gulf Coast Houston (AWIS-GCH)	2014 - 2019

COMMUNITY SERVICE

CERTIFICATIONS

SKY at Georgia Tech, Advisor

Training new executives in running the registered student organization SKY at GeorgiaTech, gain funding to make comprehensive well-being and resilience programs available for Georgia Tech students

Emerging Leaders Advisory Board (ELAB), member

Nominated and selected to advise Vice President of Student Engagement in Georgia Tech to improve mental health and well-being on campus.

SKY at Georgia Tech, President

Raised >\$20,000 for making comprehensive well-being and resilience programs available to >1000 university students in two years. Led organization of group meditation with GeorgiaTech leadership and 700+ students and staff as a part of #techmeditates initiative.

Asha for Education (AfE-Atlanta), Secretary	2020-2022
Trained for half marathon while raising funds for under-privileged children in India	
Efforts of Hurricane Harvey Relief	2018

Volunteered to clean homes and provide accommodation during

National Service Scheme (India) - Blood Donation Camps, Volunteer

Check hemoglobin levels and provide refreshments to blood donors while making sure they are okay to leave donation camps.

REFERENCES

Francesca Storici, Professor, Biological Sciences, Georgia Institute of Technology, francesca.storici@biology.gatech.edu Greg Gibson, Regents Professor, Biological Sciences, Georgia Institute of Technology, greg.gibson@biology.gatech.edu Matthew Torres, Associate Professor, Biological Sciences, Georgia Institute of Technology, mtorres35@gatech.edu Johannes Fahrmann, Associate Professor, Clinical Cancer Prevention, UT MD Anderson, jffahrmann@mdanderson.org Amin Momin, Principal Bioinformatics Scientist, Biomea Fusion, momin.amin@gmail.com

2024-2025

F'2023

2022-2024

2009-2011