Deepali L. Kundnani

I work at the intersection of **biology, statistics,** and **computation** with a strong application focus on the field of genomics and epigenomics. I work with **Dr. Francesca Storici** as a Bioinformatics Ph.D. Graduate Research Assistant in the Storici Lab at Georgia Institute of Technology. My goal is to delineate presence of ribonucleotides(constructs of RNA) in human genomic DNA finding correlations with other DNA metabolic activities in both in cancer and non-cancer cell types.

Through my work in The Storici Lab, I have recently co-authored a **paper** and **received US National Science Foundation Conference Award** for a **poster presentation** in RNA Society 2021

Before coming to Georgia Tech, I have been fortunate to work with amazing doctors and scientists at Hanash Lab in **MD Anderson Cancer Center** and have been a part of incredible effort in diagnostics of **Lung Cancer Risk Assessment Biomarkers.**

Website   **Google Scholar**
LinkedIn   **GitHub**
Email

Education

Ph.D.	**Bioinformatics** – GPA 4.00/4.00 Georgia Institute of Technology Atlanta, GA – USA	Aug 2019 – Present
M.S.	**Molecular Biotechnology** – GPA 3.88/4.00 University of Houston – Clear Lake Houston, TX – USA	Aug 2013 – May 2015
B.E.	**Biotechnology** University of Mumbai Mumbai, India	Aug 2008 – May 2012

Honors and Awards

US National Science Foundation Conference Award   2021
Awarded for Poster presented on "The 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 - RNA 2021.

Jones NAS Biological Sciences Scholarship   2014
Merit based scholarship for students in Biological Sciences department
University of Houston, Clear-Lake, TX, USA

Third Prize in National level Technical Paper Presentation   2012
Prize awarded for presentation on "Genetic Algorithms" by Institute of Electrical and Electronics Engineers (IEEE) committee
University of Mumbai, India

Academic and Industry Research Projects

Studying ribonucleotide incorporation in human non- cancer and cancer cell type   2019-2021
Graduate Research Assistant, Storici Lab, Georgia Institute of Technology, USA
- Studying ribonucleotide composition and sequence context few bases upstream and downstream from site of incorporation.
- Using mathematical models to filter significant highly incorporated locations (hotspots) on the human genome.
- Mapping ribonucleotides on the human genome with different functional regions and annotations to study functional role/association of ribonucleotide incorporation.

Understanding association of RNASEH2A gene in cancer   2020-2021
Graduate Research Assistant, Storici Lab, Georgia Institute of Technology, USA
- Expression correlation of RNASEH2A with cancer proliferation and cell cycle markers in large cancer cell lines and tissue datasets.
- Copy number alteration prevalence of RNASEH2A gene in different cancers from The Cancer Genome Atlas (TCGA)-Pan Cancer Dataset.

Discovery and validation of protein biomarkers (Diagnostic/Therapeutic) in cancer   2015-2019
Research Assistant, Hanash Lab, M.D. Anderson Cancer Research Center, USA
- Utilizing Genomic and expression data to validate proteomic findings in various cancers cell lines.
- Investigating splice variants to find novel antigens in cancer.
- Validation of Protein Biomarker Panel for Early Detection of Lung and Pancreatic Cancer.
- Development of auto-antibody test for Lung and Breast Cancer detection.

2015

Development of Enzyme linked Immuno Assay kits for proteins used in diagnosis of various diseases.
Lab Technician, Ansh Labs, USA
➢ Antibody production for novel diagnostic ELISA kits.
➢ Production of highly sensitive antigens in mammalian cell lines.

Screening human lung cDNA library from Asthma patients for protein interaction with inducible Nitrous Oxide Synthase   2014
Independent student, Bazlur Lab, University of Houston – Clear Lake, USA
➢ Employed a yeast two-hybrid system to detect protein interaction between iNOS (Inducible Nitrous Oxide Synthetase) and human lung cDNA libraries from Asthma patients, followed by sequencing and identification of genes

Creating and testing vectors for high and efficient production of monoclonal Antibodies in the mammalian cells lines   2012-2013
Research Assistant, Usha Biotech, India
➢ Testing of a various proprietary vector (including patented CELL EXPRESS - 100™ system) using eGFP reporter gene on CHO-K1 cell line.

Assessment of Stem Cell Therapy and Analogous Wound Care Techniques for diabetic foot complications in reference to the standard therapy   2011-2012
Trainee, S.L.Raheja Hospital, Mumbai, India (B.E. Thesis)
➢ Track clinical trial from patient inclusion, consent to final day follow up of treatments.
➢ Built statistical analysis to evaluate therapy/drug effectivity.

Publications

Journal Publications

Kundnani D. L., Storici F.2021 . **FeatureCorr: An R package to study feature correlations aided with data transformation for sequencing and microarray data,** *Software Impacts.* (*In Review*)

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. 🔗
📄 **PDF** 📋 **REVIEW**

Ostrin, E. J., Bantis, L. E., Wilson, D. O., Patel, N., Wang, R., Kundnani, D., Adams-Haduch, J., Dennison, J. B., Fahrmann, J. F., Chiu, H. T., Gazdar, A., Feng, Z., Yuan, J. M., & 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., Yu, C.-Y., Cai, Y., Hsiao, F. C., Yang, W.-L., Lu, Z., Celestino, J., Long, J. P., Do, K.-A., Lu, K. H., Ladd, J. J., Urban, N., Bast Jr., R. C., & Hanash, S. M. (2020). **Proteome Profiling Uncovers an Autoimmune Response Signature That Reflects Ovarian Cancer Pathogenesis.** *Cancers*, 12(2), 485. 🔗

📄 **PDF**

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, 1794. 🔗

📄 **PDF** 📊 **IMPACT**

Capello, M., Fahrmann, J. F., Rios Perez, M. V., Vykoukal, J. V., Irajizad, E., Tripathi, S. C., Roife, D., Bantis, L. E., Kang, Y., Kundnani, D. L., Xu, H., Prakash, L. R., Long, J. P., Katayama, H., Fleury, A., Ferri-Borgogno, S., Baluya, D. L., Dennison, J. B., Aguilar-Bonavides, 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. 🔗

📄 **PDF**

Jia, D., George, J. T., Tripathi, S. C., Kundnani, D. L., Lu, M., Hanash, S. M., Onuchic, J. N., Jolly, M. K., & Levine, H. (2019). **Testing the gene expression classification of the EMT spectrum.** *Physical Biology*, 16(2), 025002. 🔗

📄 **PDF** 📊 **IMPACT**

Capello, M., Vykoukal, J. V., Katayama, H., Bantis, L. E., Wang, H., Kundnani, D. L., Aguilar-Bonavides, C., Aguilar, M., Tripathi, S. C., Dhillon, D. S., Momin, A. A., Peters, H., Katz, M. H., Alvarez, H., Bernard, V., Ferri-Borgogno, S., Brand, R., Adler, D. G., Firpo, M. A., … 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. 🔗

📄 **PDF** 📋 **REVIEW**

Fahrmann, J. F., Bantis, L. E., Capello, M., Scelo, G., Dennison, J. B., Patel, N., Murage, E., Vykoukal, J., Kundnani, D. L., Foretova, L., Fabianova, E., Holcatova, I., Janout, V., Feng, Z., Yip-Schneider, M., Zhang, J., Brand, R., Taguchi, A., Maitra, A., … 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** 📰 **NEWS**

Guida, F., Sun, N., Bantis, L. E., Muller, D. C., Li, P., Taguchi, A., Dhillon, D., Kundnani, D. L., Patel, N. J., Yan, Q., Byrnes, G., Moons, K. G. M., Tjønneland, A., Panico, S., Agnoli, C., Vineis, P., Palli, D., Bueno-De-Mesquita, B., Peeters, P. H., … Hanash, S. M. (2018). **Assessment of Lung Cancer Risk on the Basis of a Biomarker Panel of Circulating Proteins**. *JAMA Oncology*, 4(10), 182078. 🔗

📰 **NEWS**

Capello, M., Bantis, L. E., Scelo, G., Zhao, Y., Li, P., Dhillon, D. S., Patel, N. J., Kundnani, D. L., Wang, H., Abbruzzese, J. L., Maitra, A., Tempero, M. A., Brand, R., Brennan, L., Feng, E., Taguchi, I., Janout, V., Firpo, M. A., Mulvihill, S. J., … 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. 🔗

📄 **PDF** 📰 **NEWS**

Conference Papers

Makoto Kobayashi, Katayama, H., Xu, H., Vykoukal, J. V, Fahrmann, J. F., Kundnani, D. L., Wang, H., Celestino, J., Liu, J., Lu, K. H., & Hanash, S. M. (2019). **In-depth proteomics profiling of ovarian cancer ascites-derived tumor cells for therapeutic target discovery.** , JPrOS JES 2019. 🔗

📄 **PDF**

Web Posts

Kundnani, D., Thomas, S., Ulukaya, G. B., Kesar, D., Feldman, J., & Duan, J. (Nicole). (2019). **Differential gene expression in lung cancer cell lines between wildtype and mutant/variant p53**. *Biology Computes | Genomics and Bioinformatics at Georgia Tech.* Ⓦ

Kesar, D., Kundnani, D., Feldman, J., Thomas, S. T., Ulukaya, G. B., & Duan, J. (Nicole). (2019). **Exome Analysis of Utah Resident with Northern and Western European Ancestry.** *Biology Computes | Genomics and Bioinformatics at Georgia Tech.* Ⓦ

Presentations and Lectures

Oral Presentations
Kundnani, D. L., Marsili, S., Tichon, A., & Storici, F. (2022) **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 2022 (*Abstract accepted*)

Poster Presentation

Kundnani, D. L., Marsili, S., Tichon, A., & Storici, F. (2021). 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 - RNA 2021. 🔗 📄 **PDF** 🏆 **Received Conference AWARD**

Lectures

Data Preprocessing and Dimensionality reduction in Biomedical and Clinical settings, Biostatistics, Georgia Institute of Technology, 2020

DNA sequencing and Phylogenetic Analysis, Genetics Lab, Georgia Institute of Technology, 2019

Time Management, Thadomal Shahani Engineering College, 2010

Technical Paper Presentation

Genetic Algorithms, National Technical Paper Presentation, Mumbai, 2011 🏆 **Won Third Prize**

Workshops

Water Purification Systems, BIOZEAL, 2009.

Teaching Experience

Course	Position/Title	Institute	Semester
Biostatistics (APPH-6225)	Teaching Assistant	Georgia Institute of Technology	Summer 2020
Scientific Foundations of Health (APPH 1040)	Teaching Assistant	Georgia Institute of Technology	Spring 2020
Genetics Lab (BIOL-2345)	Teaching Assistant	Georgia Institute of Technology	Fall 2019
Applied Biotechnology (BIOT 5031)	Teaching Assistant	University of Houston – Clear Lake	Fall 2014

Professional Training

ISO 9001:2008 Rules and Regulations   2015
Ansh Labs, USA

Mammalian Cell Culture and Molecular Cloning Techniques   2012
Usha Biotech, India

Applications of Immunology in Health and Medicine   2011

Haffkine Institute, India

Workings of Clinical Research, 2010
Institute of Clinical Research, India

Professional Affiliations

RNA Society, member 2021-Present

American Association for the Advancement of Science (AAAS), member 2020-Present

International Society for Computational Biology (ISMB) , member 2019-Present

Association for Women in Science, Gulf Coast Houston (AWIS-GCH), member 2014-2019

Institute of Electrical and Electronics Engineers – Engineering in 2009-2010
Medicine & Biology Society(IEEE-EMBS), member

Professional Service

Member of Georgia Tech **Bioinformatic PhD Orientation Panel** 2021

Member of Georgia Tech **Bioinformatics T-shirt committee** 2021

Assisted in Storici Lab's **Grant Writing** 2021

Reviewed articles: 2019 - Present
➢ 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. 🔗

Community Service

ASHA for Education, Fundraising 2020-Present
10K and half marathon Runner, Atlanta, USA

National Service Scheme, Blood Donation Camps 2009-2011

Volunteer, Mumbai, India

Skills

Programming: R Bioconductor, Python, Bash, MATLAB, MySQL, C++,HTML, Markdown

Applications: SPSS, GraphPad prism, Excel, Tableau, Mendeley, AutoCAD, Adobe Illustrator

Platforms and Environments: Linux, Windows OS, Visual Studio Code, Sublime, Jupyter and Google Colab

Spoken Languages: English, Hindi, Sanskrit

Other

Citizenship: Indian