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- An experienced hybrid biomedical scientist with a demonstrated history of working in a professional and academic setting for over 8 years.
 - Currently, working on autoimmune disease associated non-coding variants for their possible target genes and underlying disease mechanism.
 - Prioritized regulatory variants by combining GWAS hits and epigenomic features such as enhancer marks, ATAC-Seq peaks.
 - Identified possible target genes/genomic regions for 5600 autoimmune disease related enhancer variants using capture Hi-C in Th1, Th2 and Th17 cells.
 - Allelic activity for regulatory variants in disease relevant primary cell types such as Th1, Th2 and Th17 using allelic MPRA
 - Validated MPRA hits and Capture Hi-C regulatory variant-target gene pairs using arrayed and pooled genome editing approaches in primary T cells and Jurkat T cells.
 - Previously successfully completed projects in the areas ranging from protein engineering, Structure-functional studies, biophysics of small molecule-DNA interactions, protein purification and activity optimization for novel high fidelity CAS9 enzymes for genome editing, optimizing RNP approaches for genome editing, Off target CRISPR integration and on target analysis for Adenovirus mediated CRISPR edits.
 - **Key Skills:**
Benchwork: Functional genomics using ChIP seq, RNA-Seq, Sc RNA-Seq (droplet and combinatorial indexing based approach), Hi-C, Capture HiC, MPRA, STARR-Seq, CRISPR screens , On target off target library preparation, library sequencing using illumina platform (Next-seq 550)
 - **Computational work:**
NGS data analysis for RNA-Seq, Sc RNA-Seq, HI-C, Capture Hi-C, CRISPR off target on target analysis, and data visualization using Shell scripting, R and Python packages, version control with GIT, (<https://github.com/bioarpit1>)
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Professional Experience (Recent)

University of Washington Seattle

Senior Fellow, 2017 to Present

- Delineating target genes for autoimmune disease-associated regulatory variants using 3D genomics, MPRA and genome editing Optimization and implementation of CRISPR-CAS9-mediated gene editing in primary T helper cells.
- Generated NGS libraries for different omics assays such as ChIP-Seq, RNA-Seq, ScRNA-Seq (Split-pool), Hi-C, capture Hi-C, MPRA libraries, CRISPR off target NGS libraries.
- Library QC using bioanalyzer and NGS run using Next-Seq 550 platform.
- Demultiplexing data and NGS data analysis using appropriate pipeline such as HiCUP, Chicago (Hi-C, capture Hi-C), DE-Seq 2 (RNA-Seq), MACS and Deeptools (ChIP-Seq), Scanpy, ScPrep, Seurat and monocle3 (ScRNA-Seq), MPRAalyze (MPRA, STARR-seq), CRISPRESSO2 (CRISPR NGS libraries).

Institute of Genomics & Integrative biology

Postdoctoral Associate, 2015-2017

Continued...

Genome editing:

- Heterologous Purification and characterization of naturally occurring high fidelity CAS9 from *Francisella novicida* (FnCAS9)
- Optimized in vitro cleavage assay (IVC) for comparing SpCAS9 and FnCAS9
- Comparison of enzyme kinetics for cleavage using IVC and bio-physical methods.
- In vivo genome editing optimization for FnCAS9 in mouse embryonic stem cells.
- Off target comparison between FnCAS9 and Sp CAS9 using ChIP-seq.
- supplied FPLC Purified and activity tested SpCAS9 and FnCAS9 to many labs across the institute.

Synthetic biology:

- investigated the effects of various ionic liquids on DNA-small molecule interaction using bio physical method such as CD spectroscopy, UV melting and isothermal titration calorimetry (ITC)

Educational Background

PhD in Bio-Technology Institute of Genomics and integrative biology , New Delhi and Savitribai Phule Pune University, Pune India

Masters (MSc) in Microbiology – The Maharaja Sayajirao University of Baroda, Vadodara, India

Bachelors (BSc) in Zoology – The Maharaja Sayajirao University of Baroda, Vadodara, India

Research Publications

- ND Jayavelu, A Jajodia, **A Mishra**, RD Hawkins - Nature communications, 2020, Candidate silencer elements for the human and mouse genomes
- Acharya S, **Mishra A**, Paul D, Ansari AH, Azhar M, Kumar M, Rauthan R, Sharma N, Aich M, Sinha D, Sharma S, Jain S, Ray A, Jain S, Ramalingam S, Maiti S, Chakraborty D. *Francisella novicida* Cas9 interrogates genomic DNA with very high specificity and can be used for mammalian genome editing. Proc Natl Acad Sci U S A. 2019 Oct 15;116(42):20959-20968. doi: 10.1073/pnas.1818461116. Epub 2019 Sep 30. PubMed PMID: 31570623; PubMed Central PMCID: PMC6800334. **(co-first author)**
- Li C, **Mishra AS**, Gil S, Wang M, Georgakopoulou A, Papayannopoulou T, Hawkins RD, Lieber A. Targeted Integration and High-Level Transgene Expression in AAVS1 Transgenic Mice after In Vivo HSC Transduction with HDAd5/35++ Vectors. Mol Ther. 2019 Dec 4;27(12):2195-2212. doi: 10.1016/j.ymthe.2019.08.006. Epub 2019 Aug 19. PubMed PMID: 31494053; PubMed Central PMCID: PMC6904827.
- **Mishra A**, Hawkins RD. Three-dimensional genome architecture and emerging technologies: looping in disease. Genome Med. 2017 Sep 30;9(1):87. doi:10.1186/s13073-017-0477-2. Review. PubMed PMID: 28964259; PubMed Central PMCID: PMC5623062.
- **Mishra A**, Ekka MK, Maiti S. Influence of Ionic Liquids on Thermodynamics of Small Molecule-DNA Interaction: The Binding of Ethidium Bromide to Calf Thymus DNA. J Phys Chem B. 2016 Mar 17;120(10):2691-700. doi: 10.1021/acs.jpcc.5b11823. Epub 2016 Mar 4. PubMed PMID: 26907668.
- Kumar A, Kumar S, Kumar D, **Mishra A**, Dewangan RP, Shrivastava P, Ramachandran S, Taneja B. The structure of Rv3717 reveals a novel amidase from Mycobacterium tuberculosis. Acta Crystallogr D Biol Crystallogr. 2013 Dec;69(Pt 12):2543-54. doi: 10.1107/S0907444913026371. Epub 2013 Nov 19. PubMed PMID: 24311595; PubMed Central PMCID: PMC3852659.
- **Mishra A**, Vij M, Kumar D, Taneja V, Mondal AK, Bothra A, Rao V, Ganguli M, Taneja B. Integration host factor of Mycobacterium tuberculosis, mIHF, compacts DNA by a bending mechanism. PLoS One. 2013 Jul 26;8(7):e69985.

Awards & Fellowships

- Senior Research Fellowship Council for Scientific and Industrial Research, India
- Junior Research Fellowship Council for Scientific and Industrial Research, India
- Best poster/oral presentation at the EMBO global exchange lecture course on “structural and bio-physical methods for biological macromolecules in solution”held at CSIR-CCMB,hydrabad india 2012
- Selected in prestigious STEP(science teaching experience for post-doctoral).
- Designed and taught senior year 2 credit course on genome editing in disease treatment as a STEP fellow.

Technical Proficiencies

Molecular Biology Tools & Techniques	PCR Primer/probe design quantitative real time PCR (qRT-PCR) CRISPR-Cas9 Gene editing analysis DNA, RNA and protein isolation, plasmid library preparation Gibson assembly of highthroughput MPRA and CROP-Seq libraries In vitro transcription Gene cloning Site-directed mutagenesis vector design using Benchling tool ChIP-Seq libraries Hi-C and Capture Hi-C libraries ATAC-Seq libraries RNA-Seq libraries Single cell RNA-Seq libraries (combinatorial indexing based) lentiviral packaging
Protein Analysis	Recombinant protein expression and purification in <i>E. coli</i> , animal cells western blots Immunoprecipitation EMSA FPLC CD spectroscopy ITC titrations
Bioinformatics and NGS analysis	ChIP-Seq ATAC-Seq RNA-Seq Sc RNA-Seq Hi-C, Capture Hi-C MPRA data analysis using R and Python packages from Bioconductor and Bioconda repositories Input data preparation for variety of R/Python packages using Awk Pandas and Numpy reproductive pipeline environment stored using Jupyter notebooks and pushed them to git repository
Mammalian Cell Culture Assays	Mammalian cell culture (representing adherent cell lines such as HEK 293-T, mESCs, Hela, and suspension cell lines such as K562, Jurkat, primary T cell culture) PBMC to CD4 isolation T cell activation/proliferation Genome-editing in naïve CD4 T Cells electroporation using NEON system transduction using lentiviral and adenoviral particles Stable cell line generation using lentivirus Flow cytometry Cryopreservation