# Mansi Srivastava

Doctoral Candidate, Molecular and Cell Biology, Department of Cell Biology and Molecular Genetics, University of Maryland, College Park
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I study how bacteria regulate the expression of long biosynthetic gene clusters. My work focuses on LoaP, a specialized paralog of the transcription factor NusG that promotes RNA-dependent transcriptional antitermination across polyketide synthase operons, combining bacterial genetics in non-model species with reporter assays, transcriptomics and proteomics.

## Research Experience

**Doctoral Candidate, University of Maryland, College Park** **2023–present**

Department of Cell Biology and Molecular Genetics, laboratory of Dr. Wade C. Winkler
Processive antitermination in bacteria: LoaP, a NusG paralog that enhances post-initiation expression of long antibiotic biosynthesis operons. Construction of gene knockouts in diverse bacteria by conjugation-based methods, heterologous reporter assays, RNA-seq and proteomics.

**Graduate Researcher, University of Maryland, College Park** **2021–2023**

Laboratory of Dr. Stephen M. Mount
Computational methods for sequence data: latent Dirichlet allocation for $5'$ splice site prediction and discovery of latent sequence subtypes, and low-rank tensor methods for high-dimensional data.

**Junior Research Fellow, National Centre for Biological Sciences** **2018–2019**

Laboratory of Dr. Shashi Thutupalli
Single-nucleotide polymorphism and copy-number analysis of yeast populations surviving repeated freeze–thaw cycles, identifying genomic regions associated with increased survival and trehalose production.

**Research Intern, Institute of Bioinformatics and Applied Biotechnology** **2018**

Laboratories of Dr. Sanjay Ghosh and Dr. Kshitish Acharya
Cell-based biosensors for heavy metal detection, exploiting native metal-handling pathways. Large-scale expression and purification of ArsM protein in *E. coli*.

## Education

**Ph.D. candidate, Molecular and Cell Biology, University of Maryland, College Park** **in progress**

Department of Cell Biology and Molecular Genetics.

**M.Sc., Bioinformatics and Applied Biotechnology** **2018**

Institute of Bioinformatics and Applied Biotechnology, Bengaluru. CGPA 8.49.

**B.Sc. (Honours), Biomedical Sciences** **2016**

Shaheed Rajguru College of Applied Sciences for Women, University of Delhi. 77.5%.

## Selected Research Contributions

**LoaP-Mediated Antitermination in Non-Model Bacterial Species**

*With Madison D. Jermain, Conor C. Jenkins and Wade C. Winkler*
Tested LoaP homologs from *Bacillus inaquosorum*, *B. cereus*, *B. thuringiensis* ser. *pondicherriensis* and *Paenibacillus polymyxa* in a heterologous *B. subtilis* reporter built from the *B. velezensis dfn* leader fused to *yfp*. Diverse homologs promoted readthrough of the *dfn* terminator in an RNA hairpin-dependent manner, supporting a conserved antitermination mechanism.

**Regulation of the Macrolactin Pathway and Off-Target Effects**

*With Conor C. Jenkins, Madison D. Jermain and Wade C. Winkler*
Deletion of *loaP* in *B. inaquosorum* reduced macrolactin protein levels in stationary phase, while overexpression during exponential growth did not activate the pathway. RNA-seq showed widespread off-target transcriptional changes from LoaP overexpression in *B. subtilis*, enriched in an integrative and conjugative element, whereas NusG overexpression produced minimal changes, indicating that LoaP-mediated regulation is context-dependent.

**Mixtures of Position Weight Matrices for Sequence Subtype Discovery**

*With Shashwat Kumar and Stephen M. Mount*
Used canonical polyadic decomposition to factorize the joint probability distribution over splice site sequences, recovering each subtype's consensus as an interpretable latent factor. A rank-3 decomposition recovered the major (U2) consensus, two subclasses of major sites, and the minor (U12) consensus when minor sites were only 12% of

the data. Mutual information estimated from the fitted distribution identified the most discriminating positions, and classification was comparable to MaxEntScan.

## Conference Presentations

1. *LoaP, a NusG Paralog, Promotes Off-target Effects in Bacillus Species* (poster)
   M. Srivastava, C. C. Jenkins, M. D. Jermain, W. C. Winkler. 22nd Biennial Meeting on Post-Initiation Activities of RNA Polymerases (Mountain Lake Termination Meeting), Mountain Lake Lodge, Virginia, 1–4 October 2026
2. *LoaP Mediated RNA-Based Anti-termination in Non-Model Bacterial Species* (poster, abstract MECH-SAT-460)
   M. Srivastava, M. D. Jermain, W. C. Winkler. ASM Microbe 2026, Washington, DC, June 2026
3. *Investigation of LoaP, a NusG Paralog, Across Non-Model Bacterial Species* (talk)
   Molecular and Cell Biology RIPS seminar, University of Maryland, March 2026
4. *Investigation of LoaP, a NusG Paralog, Across Non-Model Bacterial Species* (talk)
   Molecular and Cell Biology Retreat, University of Maryland, August 2025
5. *LoaP Regulated Operons in Diverse Bacterial Groups* (lightning talk)
   CAFPA–ASM DC, October 2024
6. *Mixture of Position Weight Matrices for Sequence Subtype Discovery* (poster)
   M. Srivastava, S. Kumar, S. M. Mount. NCI RNA Biology Symposium, 27–28 April 2023

## Teaching

- Teaching Assistant, BSCI223: General Microbiology Laboratory, University of Maryland (2023)
- Teaching Assistant, BSCI410: Molecular Genetics, University of Maryland (2022)
- Teaching Assistant, BSCI103: The World of Biology, University of Maryland (2022)
- Teaching Assistant, BSCI161: Principles of Ecology and Evolution Laboratory, University of Maryland (2021)
- Teaching Assistant, BSCI171: Principles of Molecular and Cellular Biology Laboratory, University of Maryland (2021)

## Professional Service

Reviewer for ACM Transactions on Computing for Healthcare (2022–2023).

## Technical Skills

- **Molecular biology:** cloning and primer design, conjugation-based gene knockouts, PCR, RT-PCR and qPCR, restriction digestion, ligation, transformation, cell lysis and nucleic acid isolation
- **Protein biochemistry:** SDS-PAGE and other electrophoresis, size-exclusion, ion-exchange and affinity chromatography, western blotting, protein expression and purification
- **Genomics:** RNA-seq and differential expression analysis, proteomics, ChIP-seq and methylation analysis, metagenomics, genome annotation
- **Computational:** Python, R, Perl, C/C++, Java, shell scripting, Linux; topic models and low-rank methods; homology modelling and docking (Chimera, PyMOL, Maestro)
- **Databases:** NCBI, UCSC, RCSB PDB, UniProt

## Workshops

- Transcriptomics Workshop, University of Maryland, Baltimore County (2025)
- Mathematical and Statistical Explorations in Disease Modelling and Public Health, ICTS Bengaluru (2019)
- Exome Sequencing Workshop, IBAB (2017)
- StartUp Bio, IBAB (2017)
- Spectroscopic and Chromatographic Techniques, SRCASW (2016)