Nafiul Huda, Ph.D. (Expected 2026)

Molecular Biologist • Next-Generation Sequencing • Clinical & Functional Genomics

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Authorized to work in the U.S.

PROFESSIONAL SUMMARY

PhD-trained molecular biologist with 9+ years of bench-to-bioinformatics experience spanning clinical human genetics and large-scale functional genomics. Hands-on expert in bulk and single-cell RNA-seq library preparation (Illumina), nucleic acid extraction from blood and tissue samples, sample QC (Agilent 2100 TapeStation, Qubit), PCR, and recombinant DNA. Power user of Benchling for SOP authoring, ELN management, sample tracking, and protocol versioning across multi-year studies. Designed and delivered multifactor RNA-seq experiments of 320+ samples end-to-end — from sample collection through differential expression, splicing analysis, and biological interpretation. Strong record of building reproducible computational pipelines, troubleshooting novel assays, and training junior scientists in collaborative research environments.

EDUCATION

Expected 2026 **Ph.D., Biological Sciences** — Auburn University, Auburn, AL
Dissertation: Sex Differences in the Regulatory Architecture of Insulin Signaling in *Drosophila melanogaster* • Advisor: Dr. Rita M. Graze

2017 **M.Sc., Biochemistry and Molecular Biology** — University of Dhaka, Bangladesh

2015 **B.Sc., Biochemistry and Molecular Biology** — University of Dhaka, Bangladesh

TECHNICAL EXPERTISE

Next-Generation Sequencing: Bulk and single-cell RNA-seq library preparation (Illumina kits); ATAC-seq processing; library QC; high-throughput transcript analysis; end-to-end NGS workflows on 320+ sample studies.

Nucleic Acid Extraction & QC: RNA and DNA extraction from whole blood, fresh/frozen tissue, and cultured cells (Zymo, QIAGEN, RCC-5); nucleic acid integrity and purity assessment with Agilent 2100 TapeStation and Qubit.

Molecular Biology: Conventional PCR, ARMS-PCR, qPCR, colony PCR; RFLP and SNP genotyping; gel electrophoresis; SDS-PAGE; Western blotting; bacterial transformation; plasmid isolation; restriction digestion; molecular cloning; site-directed mutagenesis; recombinant protein expression and purification.

Cell Culture & Lab Operations: Animal cell culture; BSL-2 lab practices and biosafety; slide preparation for microscopy; lab equipment operation, maintenance, and troubleshooting; reagent and supply management; *Drosophila* husbandry.

Lab Informatics & LIMS: Power user of Benchling for SOP authoring, electronic lab notebook (ELN) management, sample inventory and tracking, plasmid and sequence management, and experimental protocol versioning; reproducible workflow documentation and lab data integration.

Experimental Design: Multifactor design of experiments (sex × genotype × treatment × environment); power analysis and sample-size estimation; biological and technical controls; case-control cohort design with patient-derived samples.

Bioinformatics & Data Analysis: RNA-seq alignment, QC, and quantification; differential expression (DESeq2, edgeR); alternative splicing (rMATS turbo); WGCNA co-expression networks; isoform-level analysis; functional enrichment; SNP association testing; NCBI, UniProt, KEGG.

Programming & Visualization: R, Python, Bash, C; Linux command line and HPC environments; Git/GitHub; reproducible pipeline development; ggplot2, matplotlib, seaborn; Adobe Photoshop and Illustrator for figure preparation.

RESEARCH EXPERIENCE

May 2026–Present **Graduate Research Assistant (NGS Focus)**
Stevison Lab, Department of Biological Sciences, Auburn University • PI: Dr. Laurie Stevison

- Perform single-cell RNA-seq library preparation (Illumina kits) for a multi-lab thermal-stress study across two *Drosophila* species; contributing to a first-author publication in preparation (Hatch-seed and NIH MIRA support).
- Analyze integrated RNA-seq and ATAC-seq datasets to characterize transcriptomic and chromatin-accessibility responses to thermal stress during oogenesis (NIH R35-funded program).

Aug 2017–May 2026 **Graduate Researcher (Molecular Biology & NGS)**

Graze Lab, Department of Biological Sciences, Auburn University • Advisor: Dr. Rita M. Graze

- Executed end-to-end NGS workflows on 320+ *Drosophila* samples: RNA extraction, library QC (TapeStation, Qubit), Illumina bulk and single-cell RNA-seq library preparation, sequencing submission, and downstream analysis.
- Managed sample inventory, protocol versioning, and SOP documentation in Benchling across a multi-year, 320-sample study; authored ELN entries and maintained reproducible records shared across collaborators.
- Designed and ran a four-factor RNA-seq study (genotype × sex × treatment × environment) across multiple genetic backgrounds, including power analysis, biological controls, and randomization to support rigorous statistical inference.
- Built and documented a reproducible RNA-seq analysis pipeline (DESeq2 differential expression, dose-response clustering, rMATS-turbo alternative splicing, WGCNA co-expression networks, functional enrichment) used across multiple lab projects.

Fall 2022 & 2025 **Graduate Assistant — Recombinant DNA Technology (BIOL 5521)**

Auburn University • with Dr. Rita M. Graze

- Led hands-on, SOP-driven training for ∼40 upper-division students per term across two parallel sections through an end-to-end recombinant protein workflow: bacterial transformation, plasmid isolation, restriction digestion, mutagenic PCR, site-directed mutagenesis, and SDS-PAGE validation.
- Supported real-time experimental troubleshooting, protocol adherence, and manuscript-quality data write-up.

Jul 2015–Jun 2017 **Graduate Researcher (Clinical Molecular Genetics)**

Population Genetics Lab, University of Dhaka, Bangladesh • Advisor: Dr. A. H. M. Nurun Nabi

- Performed DNA extraction from whole-blood patient samples and downstream genotyping by ARMS-PCR, RFLP, and qPCR across multiple case-control cohorts investigating type 2 diabetes and cancer biology (hTERT/telomere length).
- Quantified leukocyte telomere length and analyzed hTERT promoter and VNTR polymorphisms in clinical samples; results published in five peer-reviewed journal articles.

TEACHING & TRAINING

2018–2026 **Graduate Teaching Assistant** — Auburn University

- **BIOL 1031/1037 Honors: Organismal Biology Laboratory** (8 years). Independently led 2 sections per semester (∼64 students/term); instruction spanned microbiology and microscopy, botany, animal diversity, and vertebrate dissection.
- **BIOL 1021: Principles of Biology Laboratory** (2018–2019). Instructed sections on scientific method, evolutionary biology, and quantitative data analysis; developed an active-learning lab exercise for core evolutionary concepts.

SELECTED PUBLICATIONS

74 citations, h-index 5 (Google Scholar) • 3 manuscripts in preparation

- **Huda, N.**, Yasmin, T., & Nabi, A.H.M.N. (2021). MNS16A VNTR polymorphism of human telomerase gene: gender-specific allele associated with type 2 diabetes. *J. Diabetes Complications*, 35(10), 108018.
- **Huda, N.**, Hosen, M.I., Yasmin, T., et al. (2018). GATA3 transcription factor variant associated with type 2 diabetes risk. *PLOS ONE*, 13(7), e0198507.
- Goswami, A., **Huda, N.**, et al. (2021). Leukocyte telomere length and hTERT promoter polymorphism with type 2 diabetes. *Mol. Biol. Reports*, 48(1), 285–295.
- Saha, S.K., Akther, J., **Huda, N.**, et al. (2019). Association of mitochondrial DNA variants C5178A and G10398A with type 2 diabetes. *Meta Gene*, 19, 23–31.

AWARDS, MEMBERSHIPS & SERVICE

Awards & Affiliations: COSAM Travel Grant (2023); NST Master's Fellowship, Bangladesh (2016); Genetics Society of America (2019–Present); SMBE (2022–Present); Judge, Alabama Science & Engineering Fair (2024); Volunteer, Auburn Summer Science Institute (2022–2024).