MD Shakhaowat **Hossain**

✉ *mhossain1@tulane.edu*
0000-0003-3366-8720
md-shakhaowat-hossain

Professional Profile

Computational biologist and bioinformatics scientist (PhD Candidate, Biomedical Sciences: Biomedical Informatics & Genomics, anticipated defense August 2026) with 15+ years of post-M.Sc. research experience spanning **classical microbiology and immunology** (M.Sc. Microbiology, University of Dhaka; 7.5-year faculty appointment at Khwaja Yunus Ali University, Bangladesh, teaching Virology, Immunology, Genetic Engineering, and Molecular Genetics), **GCP-regulated vaccine clinical trial coordination** (Rotarix and Japanese encephalitis immunogenicity studies at icddr,b), and computational analysis of **high-dimensional multi-omics data** (bulk/scRNA-Seq, ATAC-Seq, CITE-Seq, spatial transcriptomics), **HLA immunogenetics, and histocompatibility**. Hands-on experimental training across microbiological assays, immunoassays (ELISA), molecular techniques (qPCR, NGS library preparation), flow cytometry (FACS), and transgenic mouse infection models, now applied to **advanced computational and statistical modeling of population-scale biological data**: probabilistic HLA imputation leveraging ∼10M National Marrow Donor Program (NMDP) haplotype frequencies, an individualized Matchability metric validated on over 882K historical transplant candidates against a 2.17M NMDP nine-locus reference panel, transcriptomic and surface-proteomic discovery, and **AI/ML-augmented interpretation of complex biological systems**. **Cross-disciplinary collaboration with pathology (UPenn Kamoun Lab; production clinical HLA typing pipelines), industry (Werfen, Norcross GA; production-grade bioinformatics simulator updates), and statistical-genetics partners (NYU; national allocation simulation).** Programming in **Python** and **R (tidyverse)** with publication-grade **ggplot2** / **plotly** visualization; analysis and deployment on **AWS EC2** and **HPC Linux** environments. Builder of **reproducible, FAIR-aligned production bioinformatics tools** in real-world clinical use.

Education

Spring 2021 – Aug 2026 (Anticipated) **Ph.D. Candidate, Biomedical Sciences**, *Tulane University School of Medicine*, New Orleans, LA.

Center for Biomedical Informatics & Genomics
Dissertation: *Increasing Precision and Prioritization of HLA Matching in U.S. Deceased-Donor Kidney Allocation*.
Advisor: Loren Gragert, PhD
Relevant graduate coursework: Human Molecular Genetics, Human Immunology, Advanced Bioinformatics, Systems Biology, Biomedical Statistics, Graduate Biochemistry, Cell Biology.

2010 **M.Sc. in Microbiology (First Class, CGPA 3.63/4.0)**, *University of Dhaka*, Dhaka, Bangladesh.
Thesis: "Investigation on adenovirus genetic variants causing respiratory infections in Bangladeshi children"

2008 **B.Sc. in Microbiology (First Class, CGPA 3.73/4.0)**, *University of Dhaka*, Dhaka, Bangladesh.
Undergraduate Project: "Chromium (VI) reducing ability of bacteria isolated from tannery effluents"

Technical Skills

Programming & Languages

Languages	Python, R, SQL, Shell Scripting, JavaScript, HTML/CSS, LaTeX
Python Stack	pandas, NumPy, scikit-learn, Matplotlib, Seaborn, Plotly, Django
R Stack	tidyverse, Bioconductor, ggplot2, Seurat, DESeq2, edgeR, survival, lme4

Statistical & Computational Methods

Regression	Linear, logistic, linear discriminant analysis (LDA), generalized additive models (GAM), generalized linear mixed models (lme4); Kaplan–Meier and Cox proportional hazards survival analysis
Regularization & Feature Selection	Ridge, LASSO, elastic net; multivariate analysis, power analysis, hypothesis testing, Bonferroni / Benjamini–Hochberg multiple-comparison control

Causal & Quasi-Experimental	Counterfactual causal mediation, inverse-probability-of-treatment weighting (IPTW), DAG-based covariate selection, E-value sensitivity, multiple imputation by chained equations (MICE)
Supervised Learning	Support vector machines (SVM), decision trees, random forests, gradient boosting, neural networks
Unsupervised Learning	Hierarchical clustering, K-means, partitioning around medoids (PAM), model-based clustering (mclust); dimensionality reduction: PCA, canonical correlation analysis (CCA), t-SNE, UMAP
Deep Learning	Convolutional neural networks (CNN), recurrent neural networks (RNN), deep neural networks (DNN), GANs; reinforcement learning. **Hands-on PyTorch CNN image classification**: both built-from-scratch architectures (MNIST, ASL hand-sign datasets) and **ImageNet / VGG16 transfer learning with data augmentation and fine-tuning** (passed NVIDIA Deep Learning workshop final assessment, >92% multi-class validation accuracy; Tulane / LONI HPC, Feb 2025).
Simulation & LLM/AI	Monte Carlo simulation, expectation-maximization (EM), Hardy–Weinberg modeling, organ-allocation simulation (OASIM); retrieval-augmented generation (RAG), vector databases, Model Context Protocol (MCP) server development for LLM-integrated scientific querying

Genomics & Bioinformatics

Multi-Omics NGS Analysis	Bulk RNA-Seq, **single-cell RNA-Seq** (Seurat, Loupe Browser), ATAC-Seq, CITE-Seq; differential expression, gene-set enrichment analysis (GSEA), pathway analysis, signature analysis, and biomarker discovery; therapeutic target prioritization from high-dimensional omics data; high-dimensional single-cell phenotyping; multi-omics integration across transcriptomic, epigenomic, and surface-proteomic layers; **spatial transcriptomics** foundations via 10x Genomics formal training; patient/cohort stratification on high-dimensional omics data
Cellular Readouts & Flow Cytometry	FACS-sorted single-cell RNA-Seq, Bug-FACS, flow cytometry; lung histology and bronchoalveolar lavage (BAL) cellular characterization in pulmonary infection models
Immunogenetics	HLA imputation (haplotype-frequency EM and single-locus); high-resolution HLA typing pipelines; HLA population genetics; GL String; sequence analysis (MEGA, Clustal W).
Calibration & Validation	Brier score, ROC AUC, bin-averaged calibration (MSE and city-block distance), Typing Resolution Score (TRS), Paynter et al. open-source validation framework
Wet-Lab Interface	Single-cell library preparation (scRNA-Seq, ATAC-Seq, CITE-Seq); transgenic mouse line development; qPCR, ELISA; enables effective collaboration with experimental, molecular biology, and pathology teams

Computing Infrastructure

HPC & Linux	Linux HPC clusters: Cypress (Tulane), LONI (LSU), I2C2 (UPenn), BigPurple (NYU Langone Health); shell scripting, SLURM job submission
Cloud & DevOps	AWS EC2 (Bitnami) deployment for production bioinformatics tools; Docker; Git/GitHub for version-controlled collaboration on shared codebases; CI/CD pipelines via GitHub Actions; **LLM-assisted generation of Nextflow and Snakemake workflow orchestration pipelines**
Reproducibility	FAIR-aligned analysis frameworks; reproducible reporting (Quarto, R Markdown, Jupyter, Typst); version-controlled pipelines; technical writing for biomedical and cross-disciplinary audiences
Visualization & BI	ggplot2, Matplotlib, Seaborn, Plotly, Power BI, Tableau
Tools	VS Code, Jupyter, Anaconda, Cursor AI, GitHub Copilot, Claude (Opus), Codex, Gemini, AI-augmented development for rapid prototyping and deployment of analytical pipelines via direct SSH integration with remote HPC clusters (cf. Apr 2025 invited talk, "From Pipettes to Python")

Research Interests

Computational	Multi-omics dissection of immune-cell transcriptional, metabolic, and phenotypic programs; AI/ML-augmented interpretation of high-dimensional cellular and population-scale biological data; biomarker identification and therapeutic target discovery; gene-set enrichment analysis (GSEA) and pathway analysis for target prioritization; population-scale variant interpretation and association analysis; patient/cohort stratification; machine-learning imputation and probabilistic modeling; HLA immunogenetics and population genetics; LLM-integrated scientific querying via RAG and Model Context Protocol.

Translational Clinical translation of multi-omics findings for patient stratification and outcome prediction; clinical informatics for transplant histocompatibility; allocation-policy simulation for population-scale outcomes; equity-aware analytic frameworks; production deployment of bioinformatics tools for routine clinical use.

Methodological Causal inference and quasi-experimental design; simulation-based validation frameworks; multi-source data integration across heterogeneous clinical-genomic inputs; production-grade bioinformatics tooling for clinical deployment.

Software & Computational Tools Developed

– **HLA Matchability Calculator**: public Django web application on AWS EC2 (transplanttoolbox.org/matchability/); real-time individualized HLA matching-opportunity assessment against 2.17M NMDP nine-locus reference genotypes; PDF/CSV/spreadsheet export.

– **HaploFreqImpute**: a high-resolution HLA imputation model leveraging expectation-maximization, ∼10M NMDP haplotype frequencies, and linkage-disequilibrium patterns to resolve intermediate-resolution typing ambiguity into calibrated allele-level posterior probabilities at HLA-A, -B, -C, -DRB1, -DRB3/4/5, -DQA1, -DQB1, -DPA1, -DPB1.

– **AlleleFreqImpute**: single-locus baseline imputation pipeline (comparator to HaploFreqImpute).

– **Probabilistic Offer Filter**: reference implementation demonstrating automation of the UNet match-run via imputed allele-level HLA typing at the 1% DSA-probability threshold; simulation demonstrates reduction in manual histocompatibility review and expansion of the compatible donor pool. Brier / TRS calibration via the Paynter et al. open-source framework.

– **Clinical Typing Parsers**: three production-grade ingestion pipelines that convert heterogeneous vendor-specific histocompatibility-laboratory typing outputs into structured GL Strings consumable by the imputation pipeline: PDF-to-structured-data extractor; RT-PCR SureTyper XML-to-GL-String parser; nine-locus LinkSeq XML-to-GL-String parser. Deployed by the UPenn / Kamoun group for multi-laboratory deceased-donor typing extraction.

– **HLA-RAG**: domain-specific retrieval-augmented generation system over ∼3,500 curated HLA articles; exposed to LLMs via Model Context Protocol for citation-grounded scientific querying.

Primary Research Experience

Oct 2023 – Present **Graduate Research Assistant (Dissertation)**, *Tulane University School of Medicine*, New Orleans, LA.

PI: Loren Gragert, PhD, Center for Biomedical Informatics & Genomics

–**Developed and validated a probabilistic HLA Molecular Typing model to automate manual histocompatibility review in donor-recipient HLA matching.** Built dual large-scale imputation models: *HaploFreqImpute* (a high-resolution HLA imputation model leveraging expectation-maximization, ∼10M NMDP haplotype frequencies, and linkage-disequilibrium patterns to resolve typing ambiguity into calibrated allele-level posteriors) and *AlleleFreqImpute* (single-locus baseline comparator), converting intermediate-resolution donor typing into calibrated allele-level posteriors. Engineered a four-step **simulated allocation framework**: (i) realistic SSO ambiguities via AlleleAmbiguityUtility v2.0; (ii) per-allele uncertainty estimation; (iii) UNet allocation simulation under imputed typing; (iv) benchmarking against ground-truth high-resolution typing. Calibrated on a multi-population OPTN cohort using Brier scores and the Paynter et al. open-source framework.

–**Built the first U.S. individualized HLA matching-opportunity metric (HLA Matchability)**, analogous to CPRA on the matching-likelihood side. Public Django web tool deployed on AWS EC2 (transplanttoolbox.org/matchability/); validated against the national SRTR transplant-candidate cohort using a large NMDP nine-locus reference panel.

–**Demonstrated that the longstanding matching-vs-equity tradeoff can be resolved** in U.S. kidney allocation via the Personalized Immunologic Compatibility Likelihood (PICL) framework, a frequency-weighted HLA-match priority for candidates with rare HLA genotypes (disproportionately Black, Asian, and Pacific Islander). National simulation via the NYU OASIM platform shows that allocation can be made more equitable across racial groups while preserving HLA matching gains and without significantly changing overall transplant rates. Race is not used as a scoring variable; Matchability is applied as a continuous individual percentile.

–Built HLA-RAG (∼3,500 articles) and ILC3-RAG (∼2,600 articles) retrieval systems via Model Context Protocol for citation-grounded LLM querying; modernized the Transplant Toolbox platform (transplant-toolbox.org).

–Industry partnership with Werfen (Norcross, GA): contributed to AlleleAmbiguityUtility v2.0 updates supporting realistic SSO ambiguity simulation.

– **Two first-author manuscripts in advisor final review**, targeted for the *American Journal of Transplantation*; co-author on companion NYU OASIM manuscript.

Jan 2022 – Sep 2023 **Graduate Research Assistant**, *Tulane University School of Medicine*, New Orleans, LA.

PI: Professor Jay Kolls, MD, Center for Translational Research in Infection and Inflammation (CTRII)

– **Identified and validated LIF-Fc as a candidate host-directed therapeutic** against multidrug-resistant *Klebsiella pneumoniae* ST258 pulmonary infection; computationally delineated the hepatocyte STAT3 / acute-phase response (Saa1/Saa2, complement C3) / pulmonary IL-22 & IL-17A signaling axis as the actionable pathway driving efficacy across $Rag2^{-/-}Il2rg^{-/-}$ double-knockout and FK506-pretreated WT C57BL/6 models, establishing a mechanistic framework for target-based optimization of LIF-receptor pathway agonists.

– **Integrated and analyzed high-dimensional multi-omics data: bulk RNA-Seq, single-cell RNA-Seq, ATAC-Seq, and CITE-Seq**; characterized T-cell and ILC3 immune-cell transcriptional, metabolic, and phenotypic programs; gene-set enrichment analysis (GSEA) and pathway analysis for mechanistic target identification; differential-expression and signature-based biomarker discovery and target prioritization; hands-on across library preparation, QC, and downstream computational analysis (Seurat) on Linux HPC infrastructure.

– **Established novel CCR7-Cre $Icosl^{fl/fl}$ transgenic mouse line**; characterized lung ILC3 populations ($Rag2^{-/-}$ IL22-eGFP and Thy1.2 reporter strains); FACS-sorted scRNA-Seq, Bug-FACS, qPCR, lung histology (tissue imaging and microscopy readouts), and bronchoalveolar lavage (BAL) fluid analysis.

Mar – Dec 2021 **Graduate Rotations (Three Labs)**, *Tulane University School of Medicine*, New Orleans, LA.

– **Hong-Wen Deng Lab**: machine learning for biomedical data.
– **Yi-Ping Li Lab**: scRNA-Seq analysis with Seurat and VISION.
– **Jay Kolls Lab**: T-cell metabolism via scRNA-Seq of immunized mice.

Sep 2010 – May 2012 **Research Officer**, *icddr,b, Matlab Health Research Centre*, Bangladesh.

– Conducted clinical trials for oral live human rotavirus vaccine (Rotarix) and JE vaccine immunogenicity study.
– Performed norovirus surveillance, virus isolation, immunogenicity data analysis, and reporting.
– Co-authored peer-reviewed publication in *Journal of Medical Virology*.

Jul 2009 – Jun 2010 **Graduate Research Student**, *Virology Laboratory, icddr,b*, Bangladesh.

Supervisor: Md. Mustafizur Rahman, PhD, Senior Director, Infectious Diseases

– Characterized human adenovirus through viral genome extraction, qPCR, and phylogenetic analysis.
– Published sequences on NCBI GenBank (Accession KP268083–KP268156).

Collaborative Research

Jul 2025 – Present **Research Collaborator**, *Harbor-UCLA Medical Center*, Los Angeles, CA.

Collaborator: Kristen Nordham, MD, Department of Surgery

– Performed post-review statistical revision for an EAST multicenter trial (*Journal of Trauma and Acute Care Surgery*, accepted).
– Methods: generalized linear mixed models with center random intercept, DAG-based covariate selection, counterfactual causal mediation, IPTW, MICE, E-value sensitivity, and nine prespecified sensitivity analyses.

Aug 2024 – Present **Research Collaborator**, *NYU Langone Health*, New York, NY.

PI: Michal A. Mankowski, PhD, Department of Surgery, NYU Grossman School of Medicine

– Provided HLA matchability metrics and the Monte Carlo policy-mechanism foundation for the PICL-based deceased-donor kidney allocation framework.
– Simulated via SRTR Organ Allocation Simulator (OASIM) using evolutionary graph algorithms; balances medical urgency and population-informed organ access without compromising HLA compatibility.
– Co-author on resulting national-scale allocation manuscript in advisor final review for the *American Journal of Transplantation*.

Nov 2023 – Present **Research Collaborator**, *University of Pennsylvania*, Philadelphia, PA.

PI: Professor Malek Kamoun, MD, PhD, Department of Pathology and Laboratory Medicine, Perelman School of Medicine

– Built three production-grade clinical HLA typing ingestion pipelines: PDF-to-structured-data extractor; RT-PCR SureTyper XML-to-GL-String parser; nine-locus LinkSeq XML-to-GL-String parser.

–Pipelines bridge simulated and real-world validation of the Probabilistic Offer Filter.
–Now in production use by the Kamoun group for multi-laboratory deceased-donor typing extraction.

Teaching Experience

2021 – 2022 **Graduate Teaching Assistant**, *Tulane University School of Medicine*, New Orleans, LA.
Facilitated small-group discussions, prepared review materials, managed programming assignments, and administered exams.

Jul 2013 – Jan 2021 **Faculty (Lecturer → Senior Lecturer → Assistant Professor)**, *Department of Microbiology, Khwaja Yunus Ali University*, Bangladesh.
Taught core microbiology and immunology curriculum (Virology, Immunology I/II, Genetic Engineering, Microbial & Molecular Genetics) across BS programs; mentored undergraduate research projects.

Publications

First-Author Manuscripts in Advisor Final Review

2026 **Hossain MS**, Frangus C, DeConinck M, Ray B, Gragert L. "Use of Intermediate-Resolution Deceased Donor Molecular Typing in Organ Allocation Systems Could Increase the Fraction of HLA-Compatible Donor Offers." Target: *American Journal of Transplantation*.

2026 **Hossain MS**, Liyanage L, Akizhanov D, Massie A, Mankowski M, Gragert L. "A Web-based Matchability Calculator Based on Comprehensive HLA Population Reference Data, A New Metric for Optimizing US Organ Allocation Policy." Target: *American Journal of Transplantation*.

Co-Authored Manuscripts in Advisors Final Review

2026 Liyanage L, Akizhanov D, Mukatay K, Gragert L, **Hossain MS**, Gentry SE, Massie A, Segev D, Mankowski M. "More HLA-Matched Transplants at 'Zero' Cost, Personalizing HLA Allocation Priority." Target: *American Journal of Transplantation*.

Peer-Reviewed Articles

2025 Nordham KD, Tatum D, Patel MB, Paramesh A, Gragert L, **Hossain MS**, Duchesne JC, Nahmias J, Keeley JA, et al. (2025). "Hormone Replacement Before Brain Death Increases Organ Donation Rate After Catastrophic Brain Injury: An EAST Multicenter Trial". In: *Journal of Trauma and Acute Care Surgery*. In press

2020 Abedin MZ, Ahmed AA, **Hossain MS**, Aktar MB (2020). "Laboratory Based Diagnosis of Bacteremia among Inpatients and Outpatients with Acute Febrile Illness at Khwaja Yunus Ali Medical College and Hospital in Bangladesh". In: *European Journal of Medical and Health Sciences* 2.3, pp. 46–51. DOI: 10.34104/ejmhs.020.046051

2018 Ahmed AA, Salam MA, **Hossain MS**, Aktar MB, Juyee NA, Hasan SA (2018). "Trends in Antibiotic Resistance Patterns of Methicillin Resistant and Methicillin Sensitive *Staphylococcus aureus* in Khwaja Yunus Ali Medical College Hospital". In: *KYAMC Journal* 9.1, pp. 6–10. DOI: 10.3329/kyamcj.v9i1.36596

2017 Ahmed AA, **Hossain MS**, Aktar B, Juyee NA, Hasan SA (2017). "Prevalence of Methicillin Resistant *Staphylococcus aureus* in Khwaja Yunus Ali Medical College Hospital". In: *KYAMC Journal* 7.1, pp. 673–677. DOI: 10.3329/kyamcj.v7i1.33756

2017 **Hossain MS**, Khatun R, Solayman M, Aktar B, Ahmed AA (2017). "Antibiotic Susceptibility Pattern of Clinical Isolates of *Escherichia coli* at a Tertiary Care Hospital". In: *KYAMC Journal* 7.1, pp. 681–686. DOI: 10.3329/kyamcj.v7i1.33758

2016 Rahman M, Rahman R, Nahar S, **Hossain MS**, Ahmed S, Golam Faruque AS, Azim T (2016). "Norovirus Diarrhea in Bangladesh, 2010–2014: Prevalence, Clinical Features, and Genotypes". In: *Journal of Medical Virology* 88, pp. 1742–1750. DOI: 10.1002/jmv.24530

Conference Abstracts & Proceedings

2026 **Hossain MS**, Liyanage L, Akizhanov D, Mankowski M, Gragert L (2026). *A Web-based Matchability Calculator Based on Comprehensive HLA Population Reference Data—A New Metric for Optimizing US Organ Allocation Policy*. American Transplant Congress, Boston, MA, USA. Accepted Abstract

2026 Nordham KD, Tatum D, Patel MB, Paramesh A, Gragert L, **Hossain MS**, Duchesne JC, Nahmias J, Keeley JA, et al. (2026). *Hormone Replacement Before Brain Death Increases Organ Donation Rate After Catastrophic Brain Injury: An EAST Multicenter Trial*. Eastern Association for the Surgery of Trauma 39th Annual Scientific Assembly, Atlanta, GA, USA. Accepted Abstract

2025 Gragert L, Liyanage L, Akizhanov D, **Hossain MS**, Massie A, Stewart D, Gentry S, Segev D, Mankowski M (2025). "A Novel Strategy for Prioritizing Closer HLA Matching in Kidney Allocation Policy Would Avoid a Tradeoff of Increased Ethnic Disparity". In: *American Journal of Transplantation* 25.8, Supplement 1. World Transplant Congress, San Francisco, CA, USA. Published Abstract, S113

2024 **Hossain MS**, Frangus C, DeConinck M, Ray B, Gragert L (2024). "Use of Intermediate-Resolution Deceased Donor Molecular Typing in Organ Allocation Systems Could Increase the Fraction of HLA-Compatible Donor Offers". In: *Human Immunology* 85.Supplement. ASHI 50th Annual Meeting, Anaheim, CA, USA. Published Abstract, p. 110923. DOI: 10.1016/j.humimm.2024.110923

Selected Presentations

Jun 2026 **"A Web-based Matchability Calculator Based On Comprehensive HLA Population Reference Data"**, *American Transplant Congress*, Boston, MA, USA, (Accepted Poster).

Oct 2025 **"Probabilistic Offer Filters Using Imputed High-Resolution HLA Typing from Intermediate-Resolution Data Expand the Compatible Donor Pool in Deceased-Donor Organ Allocation"**, *BMS Graduate Program Fall Retreat, Tulane University*, New Orleans, LA, (Oral Presentation).

Oct 2024 **"Use of intermediate-resolution deceased donor molecular typing in organ allocation systems could increase the fraction of HLA-compatible donor offers"**, *ASHI 50th Annual Meeting*, Anaheim, CA, USA, (Poster).

Apr 2025 **"Use of intermediate-resolution deceased donor molecular typing in organ allocation systems could increase the fraction of HLA-compatible donor offers"**, *Tulane Research Innovation and Creativity Summit*, New Orleans, LA, (Poster).

Apr 2025 **"From Pipettes to Python: My Unexpected Journey with AI-Assisted Coding"**, *AI-Assisted Coding Workshop, Rudolph Matas Library, Tulane University School of Medicine*, New Orleans, LA, (Oral Presentation).

Research Funding

2024 – Present **NIH R01 DK139240** (NIDDK; Mankowski MA & Gragert L, MPIs). "Improving Kidney Transplant Outcomes by Using Molecular-Level HLA Matching in Allocation." NYU School of Medicine / Tulane University. Active (Year 3; FY2026 total $693,985; $469,219 direct costs). Aims 2 & 3 of dissertation conducted within this award; graduate research effort supported by this grant.

2024 – 2026 **Lavin-Bernick Faculty Development Grants** ($3\times$ $15,000 to L. Gragert, PI) inspired by Aim 1 imputation framework, Aim 2 Matchability tooling, and dissertation AI-assisted coding methodology.

Awards and Distinctions

Fall 2020 Tulane Biomedical Sciences PhD Scholarship and Fellowship Awards, Tulane University School of Medicine

Oct 2011 Dean's Award, Faculty of Biological Sciences, University of Dhaka, recognized for outstanding academic performance

2009 Hall Provost Award, Shahidullah Hall, University of Dhaka

Selected Training and Certifications

Feb 2025 NVIDIA *Fundamentals of Deep Learning* Workshop, Tulane University (LONI HPC): hands-on PyTorch CNN image classification; built-from-scratch architectures (MNIST, ASL hand-sign), ImageNet / VGG16 transfer learning with data augmentation and fine-tuning; final assessment passed with >92% multi-class validation accuracy.

2021 10x Genomics Spring Spatial Training Series Certification (spatial transcriptomics foundations)

2025 LA CaTS Research Coordinator Training Program – Levels I, II, & III (SOCRA-accredited), Tulane University Health Sciences Center

2024 OpenAI API: Working with Files, LinkedIn Learning Certification

2024 Werfen HLA Antibody Workshop & Virtual HLA Global Scientific Symposium

2024 Regulatory Training and CITI Program Certifications, NYU Langone Health

2020 CITI Program Certifications (RCR, GCP, Human Research, IACUC), Tulane University

Leadership and Professional Engagement

2025 – 2026 Technical Volunteer (two consecutive annual sessions), ASHI Clinical Informatics Workshop (ACIW), New Orleans, LA; provided coding environment setup and troubleshooting support for workshop attendees.

2013 – 2020 **Founding Chair, Department of Microbiology**, Khwaja Yunus Ali University (KYAU), Bangladesh; established and led the new department at this newly-founded private university: faculty coordination, examinations workflow, BS Microbiology curriculum update, and departmental operations.

2016 – 2020 Organizer, departmental excursions, field trips, and industry visits, Department of Microbiology, Khwaja Yunus Ali University.

2016 – 2020 University and departmental committee service, Khwaja Yunus Ali University: University Journal Committee (2016–2020); Distinguished Speaker Invitation Committee (2017–2020); Central Task Force of the Exam Committee (2017–2020); Departmental Curriculum Committee (2017–2019); Central Routine Committee (2018–2020); National & International Days Celebration Committee (2018–2020).

Professional Affiliations

Since 2026 Student Member, American Society of Transplantation (AST)

Since 2024 Member, American Society for Histocompatibility and Immunogenetics (ASHI)

Languages

Bengali Native

English Fluent (academic, professional, and conversational)

Full contact details, reference letters, and detailed methodology summaries available upon request.