

MD Shakhaowat Hossain

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SUMMARY

Computational biologist and Ph.D. candidate (defense anticipated August 2026) who analyzes high-throughput genomic data and builds the pipelines that make it analysis-ready. Works daily in UNIX/Linux, Python, and R, with established-tool workflows for bulk and single-cell RNA-seq, ATAC-seq, and CITE-seq, and sustained hands-on experience acquiring, curating, and querying large public biological repositories (NCBI GenBank, NMDP, OPTN/SRTR). Contributes across the full research cycle: analysis plans and experimental design, figures and tables, computational-methods and results sections, and NIH R01 aims. 15+ years of post-M.Sc. research experience, including 7.5 years in a faculty appointment training and mentoring junior scientists.

TECHNICAL SKILLS

Computing & Scripting	UNIX/Linux (daily driver), Python (pandas, NumPy, scikit-learn, PyTorch), R (tidyverse, Bioconductor), SQL, Shell; Git/GitHub, version-controlled and documented code
High-Throughput Genomics	Bulk RNA-seq (DESeq2, edgeR), single-cell RNA-seq (CellRanger, Seurat, Loupe Browser), ATAC-seq, CITE-seq, spatial transcriptomics (10x Genomics formal training); differential expression, GSEA, pathway and signature analysis, biomarker and target prioritization
Databases & Data Mgmt	Acquisition, curation, QC, and querying of large biological and clinical repositories (NCBI GenBank/RefSeq, NMDP reference panels, OPTN/SRTR); sequence submission (74 GenBank accessions); harmonizing heterogeneous vendor and registry formats into structured, analysis-ready datasets
Statistics & Design	Experimental design and analysis planning; generalized linear/mixed models (lme4), survival analysis (Kaplan–Meier, Cox); multiple-testing correction (Bonferroni, BH); calibration and model evaluation (Brier score, ROC AUC); causal mediation, IPTW, DAG-based covariate selection, MICE
Machine Learning	scikit-learn (SVM, random forests, gradient boosting); clustering and dimensionality reduction (PCA, t-SNE, UMAP); expectation-maximization for latent-variable inference; PyTorch deep learning (CNN, VGG16 transfer learning)
Pipelines & Reproducibility	Production data-processing pipelines from raw instrument output to structured reports; Nextflow, Snakemake; Linux HPC (SLURM, four clusters); AWS EC2, Docker, CI/CD (GitHub Actions); Django; reproducible reporting (Quarto, Jupyter, R Markdown)
Visualization	ggplot2, Matplotlib, Seaborn, Plotly; publication-quality figures and tables; Power BI, Tableau
Wet-Lab Techniques	Single-cell library prep (scRNA-seq, ATAC-seq, CITE-seq); transgenic mouse models; qPCR, ELISA, flow cytometry / FACS, BAL and histology; viral genome sequencing and phylogenetics

PROFESSIONAL EXPERIENCE

Graduate Research Assistant (Dissertation), Tulane University School of Medicine — PI: Loren Gragert, PhD

Oct 2023 – Present

Improving kidney transplant outcomes by using molecular-level HLA matching in allocation (NIH R01 DK139240)

- Developed HLA matchability metrics using a 2.1M+ genotype NMDP reference dataset with high-resolution nine-locus HLA genotypes and population-weighted frequencies.
- Modeled HLA matchability-adjusted allocation points to prioritize candidates with rare HLA genotypes, promoting balanced access in deceased-donor kidney allocation.
- Deployed the HLA Matchability Calculator as a public Django web tool on AWS EC2 (transplanttoolbox.org/matchability), making the metric openly available to the transplant community.
- Collaborated with the Center for Surgical and Transplant Applied Research (CSTAR) at NYU Langone Health to model matchability-adjusted allocation policy in the OASIM organ-allocation simulation.

Automating the OPTN UNet match run using high-resolution HLA typing imputed from intermediate-level deceased donor HLA typing data

- Developed an HLA typing simulator with Immucor (Werfen) to map high-resolution typing into intermediate-level allele possibilities (IPD-IMGT/HLA Database v3.60).
- Built imputation pipelines within the simulation framework to resolve intermediate-level typing to high resolution across all nine loci, leveraging a 10M+ population high-resolution HLA haplotype-frequency dataset, expectation-maximization, and linkage-disequilibrium patterns; calibrated performance for predicted genotypes and residual ambiguity.
- Developed a Probabilistic Offer Filter across 1M+ simulated offers, automatically comparing each candidate's allele-level antibody profile against the donor's predicted high-resolution typing on a sliding scale of donor-specific antibody tolerance.
- Eliminated the manual review that HLA laboratory directors must perform when donor typing reaches the UNet match run as ambiguous intermediate-level PDF rather than electronically captured data, a bottleneck that prolongs cold ischemia time and increases the risk of organ nonuse.
- Developed automated Python data-extraction pipelines converting raw vendor instrument HLA typing output (PDF reports, RT-PCR SureTyper XML, nine-locus LinkSeq XML) into structured, analysis-ready Genotype List (GL) Strings; deployed by the UPenn Kamoun group to extract intermediate-resolution typing across multiple laboratories for validating the Probabilistic Offer Filter against real clinical data.
- Validating the Offer Filter against historical clinical transplant data in a multicenter study with Dr. Malek Kamoun's group at UPenn.
- Built two retrieval-augmented generation systems, HLA-RAG (immunogenetics) and ILC3-RAG (innate lymphoid cells), over 6,000+ curated articles, exposed to LLMs via Model Context Protocol for rapid, citation-grounded literature review.

- Authored the computational-methods and results sections, prepared tables and figures, and verified numerical accuracy across manuscripts; two first-author and one co-authored manuscript in advisor final review for the *American Journal of Transplantation*.

Graduate Research Assistant, Tulane University School of Medicine — PI: Professor Jay Kolls, MD, CTRII

2021 – 2023

Therapeutic role of LIF-Fc against multidrug-resistant *Klebsiella pneumoniae* ST258 C4 lung infection in a murine model

- Designed and executed a murine pulmonary infection study evaluating LIF-Fc as a host-directed therapeutic against multidrug-resistant *K. pneumoniae* ST258 C4, benchmarked against IL-22-Fc and vehicle controls.
- Compared lung and spleen bacterial burden by CFU across two immunocompromised models, Rag2^{-/-} Il2rg^{-/-} and FK506-treated wild-type C57BL/6 mice.
- Quantified LIF-Fc-mediated innate activation by qPCR, ELISA, and bacterial flow cytometry (BugFACS), measuring hepatic and pulmonary acute-phase responses (SAA1, SAA2, C3) and downstream STAT3 signaling.
- Demonstrated significant reduction in lung infection burden versus controls with marked SAA1/SAA2 induction, more pronounced in liver than lung, supporting LIF-Fc as a host-directed therapeutic candidate.

Isolation, enrichment, and functional characterization of pulmonary ILC3s in murine models

- Developed enrichment and sorting workflows for rare lung-resident ILC3s in wild-type, IL-22 reporter, and Rag2^{-/-} mice.
- Defined ILC3 IL-22 and IL-17A responses to pulmonary infection by integrating flow cytometry, CITE-seq, RNA-seq, qPCR, and ELISA-based cytokine quantification.
- Generated and leveraged a Ccr7-Cre × Icos^{fl/fl} model to interrogate ICOS-dependent regulation of ILC3 biology in the lung.

Assistant Professor and Chair, Department of Microbiology, Khwaja Yunus Ali University, Bangladesh

2017 – 2021

- Supervised undergraduate research projects, advising students on experimental design, data interpretation, and scientific writing.
- Taught Virology, Immunology I and II, Genetic Engineering, and Microbial & Molecular Genetics (lecture and laboratory practical); designed and moderated course examinations.
- Led a newly established department as Chair, providing its academic and operational leadership; served on curriculum and examination committees.
- Directed an independent research line alongside a full teaching load: antibiotic-resistance surveillance of clinical isolates (MRSA, *E. coli*) at a rural tertiary-care hospital, yielding several peer-reviewed publications.

Senior Lecturer, Department of Microbiology, Khwaja Yunus Ali University, Bangladesh

2014 – 2017

- Mentored junior teaching staff joining the department; supervised laboratory instruction and student assessment.
- Taught General Microbiology, Basic Biochemistry, Microbial & Molecular Genetics, and Immunology II; set and moderated examinations.

Lecturer, Department of Microbiology, Khwaja Yunus Ali University, Bangladesh

2013 – 2014

- Taught Microbial Ecology, Basic Techniques in Microbiology, Bacteriology, and Environmental Microbiology.
- Built lecture content, laboratory protocols, and assessments for the department's new BS microbiology program, introducing students to aseptic technique, culture and identification methods, and antimicrobial susceptibility testing.

Research Officer, icddr,b (Matlab Health Research Centre & Virology Lab), Bangladesh

2010 – 2012

- Coordinated GCP vaccine-immunogenicity clinical trials (Rotarix, JE).
- Conducted norovirus and adenovirus molecular surveillance; performed viral genome sequencing, alignment, and phylogenetics.
- Co-authored a *Journal of Medical Virology* publication.

EDUCATION

Ph.D. in Biomedical Sciences, Tulane University School of Medicine — Center for Biomedical Informatics & Genomics

2021 – 2026 (expected)

Dissertation: *Increasing Precision and Prioritization of HLA Matching in U.S. Deceased-Donor Kidney Allocation*. Advisor: Loren Gragert, PhD.

M.Sc. in Microbiology (First Class, 3.63/4.0), University of Dhaka, Bangladesh

2010

B.Sc. in Microbiology (First Class, 3.73/4.0), University of Dhaka, Bangladesh

2008

SELECTED PUBLICATIONS & SCIENTIFIC COMMUNICATION

- Nordham KD, ..., Gragert L, **Hossain MS**, et al. "Hormone Replacement Before Brain Death Increases Organ Donation Rate After Catastrophic Brain Injury: An EAST Multicenter Trial." *J. Trauma and Acute Care Surgery*, 2026 (published online ahead of print).
- **Hossain MS**, et al. "Antibiotic Susceptibility Pattern of Clinical Isolates of *E. coli* at a Tertiary Care Hospital." *KYAMC Journal* 7(1), 2017.
- Rahman M, ..., **Hossain MS**, et al. "Norovirus Diarrhea in Bangladesh, 2010–2014." *Journal of Medical Virology* 88, 2016.
- Six peer-reviewed articles and five published or accepted conference abstracts; first-author abstracts in *American Journal of Transplantation* 26(7):S636 (2026) and *Human Immunology* 85(Suppl) (2024).
- Presenter, American Transplant Congress 2026 and ASHI 50th Annual Meeting; invited speaker, "From Pipettes to Python: My Unexpected Journey with AI-Assisted Coding," Tulane University School of Medicine (2025); technical volunteer and instructor, ASHI Clinical Informatics Workshop (2025–2026).

AWARDS, CERTIFICATIONS & AFFILIATIONS

Awards	Tulane Biomedical Sciences PhD Scholarship & Fellowship (2020); Dean's Award, University of Dhaka (2011)
Certifications	NVIDIA Fundamentals of Deep Learning (2025); 10x Genomics Spatial Training (2021); LA CaTS Research Coordinator Levels I–III, SOCRA (2025); CITI (RCR, GCP, Human Research, IACUC)
Affiliations	American Society of Transplantation (AST); American Society for Histocompatibility and Immunogenetics (ASHI)
Languages	English (fluent, professional); Bengali (native)