

MS. HUMAIRA AMIN

Lecturer

Department of Genomics and Bioinformatics

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PROFILE SUMMARY

Bioinformatics professional and university lecturer with expertise in next-generation sequencing (NGS) data analysis, genomics, transcriptomics, metagenomics, genome-wide association studies (GWAS), and computational biology. Experienced in the analysis and interpretation of high-throughput sequencing datasets, including whole-exome/genome sequencing, RNA-seq, 16S rRNA and ITS-based metagenomic studies, and GWAS, as well as genome assembly, annotation, and phylogenetic analysis. Proficient in Linux-based bioinformatics workflows, statistical analysis, and data visualization using R and Python. Research interests focus on applying computational approaches to investigate disease-associated genes, genetic variants, biological pathways, cancer genomics, viral genomics, microbial diversity, zoonotic pathogens. Author of multiple peer-reviewed publications in the fields of genomics, transcriptomics, infectious diseases, cancer biology, microbial genomics, and computational biology. In addition to research expertise, experienced in university teaching, professional training, academic administration, and student affairs management, with a strong commitment to integrating bioinformatics research and practical data-analysis skills into higher education and interdisciplinary research.

PROFESSIONAL EXPERIENCE

Lecturer — Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Pakistan

April 2024 – Present

Scientific Officer — Alpha Genomics (Pvt.) Limited, Islamabad, Pakistan

August 2021 – March 2024

EDUCATION

MS Bioinformatics — COMSATS University Islamabad, Islamabad | 2018–2020

BS Bioinformatics — COMSATS University Islamabad, Sahiwal | 2014–2018

TECHNICAL SKILLS

- NGS data analysis: Whole exome/genome sequencing, RNA-seq, metagenome sequencing (16S, ITS, whole metagenome)
- Genome assemblies and annotations
- Genome Wide association studies (GWAS)
- Phylogenetics
- Viral genomics
- Computational languages: R, Python, C++, Java
- Platforms: Linux, Windows

STUDY AREAS

- Bioinformatics
- Modern Programming Languages
- Big data analysis
- Structural and Functional Biology
- Bioinformatics Scripting

PROFESSIONAL TRAINING & WORKSHOPS

Trainer — Bioinformatics and Data Analysis

Alpha Genomics (Private) Limited, Islamabad, Pakistan

24–28 August 2026

- Delivered professional training in bioinformatics and data analysis, with emphasis on computational approaches and practical data-analysis techniques.

Co-Trainer — 2-Day Hands-on Workshop on Gene Expression Data Analysis Using Bioinformatics Techniques

IRCBM, COMSATS University Islamabad, Lahore Campus

- Facilitated hands-on training in gene expression data analysis using contemporary bioinformatics approaches and computational techniques.
- Contributed to practical instruction and participant guidance in the analysis and interpretation of gene expression datasets.

PUBLICATIONS

1. **Identification and validation of hub genes involved in papillary thyroid carcinoma progression**

DOI: 10.1186/s12885-026-15841-6

2. **Nanopore sequencing reveals the genomic diversity of the variants of concern of SARS-CoV-2 during 2021 disease outbreak in Pakistan**

DOI: 10.1038/s41598-025-12774-1

3. **Evidence of mutations in tumour suppressor genes among oral cancer in Naswar, smokeless tobacco users**

DOI: 10.2340/aos.v84.43778

4. **Genetic Diversity and Zoonotic Potential of Shiga Toxin-Producing E. coli (STEC) in Cattle and Buffaloes from Islamabad, Pakistan**

DOI: 10.3390/agriculture14091537

5. **The oral microbiome of newly diagnosed tuberculosis patients; a pilot study**

DOI: 10.1016/j.ygeno.2024.110816

6. **Identification and Analysis of Hub Genes and Biological Pathways Involved in Alzheimer's Disease (AD) Using Transcriptomics Dataset**

DOI: 10.32350/cto.32.04

7. **Subtractive Proteomics and Immuno-informatics Approaches for Multi-peptide Vaccine Prediction Against Klebsiella oxytoca and Validation Through In Silico Expression**

DOI: 10.1007/s10989-021-10283-z