BASEERAT HAMZA

Ph.D. | Proteomics and Mass Spectrometry | Cancer and Infection Biology
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EDUCATION

Ph.D., Chemistry | International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi, India
Dissertation: SWATH-based human proteome library development using the THP-1 cell line; mechanistic investigation of disease progression in cancer, tuberculosis, and diabetes through data-independent acquisition (DIA) and data-dependent acquisition (DDA) proteomics.

M.Sc., Organic Chemistry | Jamia Hamdard, New Delhi, India

B.Sc., Biochemistry | University of Kashmir, Kashmir, India

RESEARCH EXPERIENCE

Assistant Professor | Department of Applied Sciences and Chemistry, University of Kashmir, India **|** March 2021 to Present
Conducting proteomics-based investigations of cancer biology and molecular pathology using both experimental and clinical sample cohorts. Responsibilities include large-scale proteomic and molecular dataset analysis, identification of disease-associated biomarkers, and integration of laboratory findings with clinically relevant outcomes. Also engaged in scientific writing, data compilation, and contributions to collaborative academic research.

Senior Research Associate | CSIR, Indian Institute of Integrative Medicine, Srinagar, India
Investigated proteomic and metabolic alterations in aggressive and therapeutically resistant breast cancer subtypes using high-throughput mass spectrometry. Work encompassed large-scale molecular profiling, identification of disease-associated protein and metabolite signatures, and evaluation of candidate therapeutic targets. Conducted parallel proteomics-based studies of depression using experimental mouse models and human clinical samples to delineate molecular pathways and neurobiological biomarkers associated with neuropsychiatric disease mechanisms.

Doctoral Researcher | International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi, India
Developed a SWATH-based human proteome reference library from THP-1 macrophage-like cells to support disease-focused proteomic investigations in cancer, tuberculosis, and diabetes. Applied DIA and DDA acquisition strategies across clinical and experimental samples to generate reproducible, large-scale quantitative proteomic datasets.

Contributed to a genome-wide siRNA screen of human proteins in Mycobacterium tuberculosis-infected macrophages to identify host factors essential for pathogen intracellular survival, with subsequent validation in multidrug-resistant clinical strains to define candidate therapeutic targets.

Gained extensive experience in LC-MS/MS, GC-MS/MS, and HPLC-based analytical workflows for biomolecular and pharmacological investigations, alongside mammalian cell culture, patient-derived biological sample processing, and downstream bioinformatic data interpretation.

PEER-REVIEWED PUBLICATIONS

1. Kumar A, Sofi AH, **Hamza B**, Rubab S, Shah MA. Eco-friendly synthesis of antibacterial CuO nanoparticles using garlic bulb extract. Green Materials. 2024.

2. Khan SU, **Hamza B,** Mir RH, Fatima K, Malik F. Lavender plant: farming and health benefits. Current Molecular Medicine. 2023.

3. Khan SU, Pathania AS, Wani A, Fatima K, Minto MJ, **Hamza B**, et al. Activation of lysosomal-mediated cell death in autophagy by m-TOR inhibitor. Scientific Reports. 2022.

4. Khan SU, Fatima K, Aisha S, Hamza B, Malik F. Redox balance and autophagy regulation in cancer progression. Medical Oncology. 2022.

5**. Hamza B.** Survey of analytical methods used in pharmaceutical analysis. Design Engineering. 2022.

6. Hamza **B**, Kumar A, Midha M, Sharma A, Sharma B, Rao KVS. THP-1 cell proteome library generation using SWATH analysis. International Journal of Life Sciences. 2018.

7. Kumar A, Jamwal S, Midha MK**, Hamza B**, et al. Dataset generated using hyperplexing and click chemistry for macrophage secretome analysis. Data in Brief. 2016.

8. Bhat G, Masood A, Ganai BA, **Hamza B**, et al. Gracilone, a new sesquiterpene lactone from Tanacetum gracile. Natural Product Research. 2016.

TECHNICAL SKILLS AND EXPERTISE

Mass Spectrometry and Proteomics

- LC-MS/MS-based proteomic analysis and quantitative experimental workflows
- SWATH/DIA and DDA data acquisition strategy design and implementation
- Nano-LC 5600 TripleTOF (SCIEX) instrument operation and sample processing
- MALDI-TOF/TOF analysis for peptide and protein identification
- Quantitative peptide labeling including iTRAQ
- ZipTip-based sample purification for high-resolution mass spectrometry
- Targeted and untargeted proteomic experimental design and data interpretation

Cell Biology and Molecular Techniques

- Mammalian cell culture including macrophage and cancer cell line maintenance
- SDS-PAGE, Western blotting, and protein expression analysis
- Flow cytometry-based cellular characterization
- RT-PCR, ELISA, and molecular biomarker assessment
- Handling and processing of patient-derived clinical samples and tissue specimens

Metabolomics and Analytical Chemistry

- GC-MS/MS and HPLC-based metabolite and drug analysis
- Biomolecular extraction, purification, and quality control workflows
- Experimental design for biochemical and pharmacological studies

Bioinformatics and Data Analysis

- Proteomic data processing and biological pathway interpretation
- STRING database analysis, KEGG pathway mapping, and protein interaction network analysis
- Basic R programming for statistical and biological data analysis
- Scientific data visualization, interpretation, and reporting

REFERENCES

Available upon request.