

NABIL AHMED

Postdoctoral Fellow | Molecular & Computational Biology

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SUMMARY

Motivated molecular and cellular biologist with a Ph.D. in biochemistry and molecular immunology, focused on cellular homeostasis and unfolded protein response in mast cell leukemia. Skilled in immunology, cancer biology, and biochemistry, with advanced training in bioinformatics, biostatistics, and data analysis. Experienced in leading research projects and communicating complex scientific concepts to diverse audiences. Eager to apply expertise in molecular and computational biology in a postdoctoral role dedicated to advancing research and producing high-quality publications.

WORK EXPERIENCE

Postdoctoral fellowship
Goethe University Frankfurt, University Hospital Frankfurt, Hematology Department

- 📅 10/2024 – 04/2025 📍 Frankfurt, Germany
- Six-month fellowship combining wet-lab and computational work:
- Three months in wet lab to establish a base editing system screen (cytosine and adenine deaminase base editors) system using CROP-seq system for single cell analysis.
 - Three months of training in analyzing proteomic data from TMT labeling measured by mass spectrometry.

Medical Technical Assistant
University Ulm, University Hospital Ulm, Institute of Immunology

- 📅 03/2018 – 06/2019 📍 Ulm, Germany
- To complete the project initiated during my master’s thesis, I was employed as a technical assistant. My responsibilities included:
- Characterizing cells by flow cytometry (BD FACSCanto and LSRFortessa).
 - Breeding mice for blood collection and isolating bone marrow and spleen cells from genetically modified mouse models to obtain B cells.
 - Extracting DNA and performing genotyping PCR.

EDUCATION

Ph.D. (Dr. rer. nat.) in Biology
RWTH Aachen University, Institute of Molecular Immunology and Biochemistry

- 📅 07/2019 – 10/2024 📍 Germany
- Thesis: Comprehensive analysis of the IRE1 interactome using TurboID in the human mast cell leukemia line HMC-1.2.
 - Participated in the RWTH start grant-funded Research Training Group.
 - Supervised undergraduate students; conducted research using cancer and immune cell lines.

M.Sc. in Molecular Bioscience
Ulm University, Institute of Neurobiology

- 📅 10/2015 – 12/2017 📍 Germany
- Thesis: Immunophenotype and downstream signaling of suppressive CD39 and CD73 in glioblastoma primary cells.
 - Performed analyses on tumor tissues and flow cytometry-based characterization.

B.Sc. in Biochemistry and Microbiology

- MNF University
- 📅 09/2009 – 05/2013 📍 Egypt
- Thesis: The role of *Pseudomonas aeruginosa* proteases in degrading IL-2 and modulating host immune responses.
 - Worked with bacterial culture and ELISA assays.

FURTHER TRAINING

- Applied Bioinformatics and Biostatistics
CQ, Mplus Academy
- 📅 08/2025 - Present 📍 Berlin, Germany
- Introduction to programming and Python (including Shell (BASH), programming methodology, object-oriented programming in Python)
 - Bioinformatics and databases (including NCBI, Biopython, web services, and database management, SQL)
 - Applied bioinformatics (including sequence analysis and strategies, structural bioinformatics, software for structure visualization, NGS analysis using Galaxy & Snakemake)
 - Applied biostatistics (including statistical analysis using R, descriptive and multivariate statistics, ANOVA, PCA, HCA, workflows using R/Bioconductor, Markov chain implementation)

SKILLS

Selected Technical Expertise

Cloning

Protein pulldown/analysis

Cell Culture 2D/3D

Flow Cytometry

Gene Editing: CRISPR/Cas9 - Base Editing

Viral Transduction

ELISA

In vivo mouse models (FELASA B License)

Data analysis and visualization

GraphPad Prism

Rstudio

ImageJ

Benchling

FlowJo

Programming

R (Advanced)

Python (Intermediate)

Bash & Git (Intermediate)

LANGUAGES

English

Proficient

German

Proficient

PUBLICATIONS

KIRA6 is an effective and versatile mast cell inhibitor of IgE-mediated activation. *European Journal of Immunology*

European Journal of Immunology

Wunderle, V., Wilhelm, T., Boukeileh, S., Goßen, J., Margreiter, M. A., Sakurov, R., Capellmann, S., Schwoerer, M., Ahmed, N., Bronneberg, G., Arock, M., Martin, C., Schubert, T., Levi-Schaffer, F., Rossetti, G., Tirosh, B., & Huber, M

12/2024 DOI: [10.1002/eji.202451348](https://doi.org/10.1002/eji.202451348)

My Contribution:

Cultured murine bone marrow-derived mast cells (BMMCs), performed inhibitor treatments, and analyzed gene expression by RT-qPCR.

TurboID-Based IRE1 Interactome Reveals Participants of the Endoplasmic Reticulum-Associated Protein Degradation Machinery in the Human Mast Cell Leukemia Cell Line HMC-1.2

MDPI Cells

Ahmed, N., Preisinger, C., Wilhelm, T., & Huber, M

04/2024 DOI: [10.3390/cells13090747](https://doi.org/10.3390/cells13090747)

My Contribution:

Responsible for all experiments and data generation, except mass spectrometry measurements. Wrote the first manuscript draft and collaborated with supervisors on revisions and final editing.

B-cell antigen receptor expression and phosphatidylinositol 3-kinase signaling regulate genesis and maintenance of mouse chronic lymphocytic leukemia

Haematologica

Schmid, V. K., Khadour, A., Ahmed, N., Brandl, C., Nitschke, L., Rajewsky, K., Jumaa, H., & Hobelka, E.

08/2022 DOI: [10.3324/haematol.2021.279924](https://doi.org/10.3324/haematol.2021.279924)

My Contribution:

Performed *in vivo* work supporting the generation and analysis of Cre/loxP-based mouse models to study BCR signaling in CLL, including tissue collection and flow cytometric analysis. This work introduced me to cancer modeling by handling mouse models and therapeutic targeting of B-cell malignancies, an area central to my academic development.

RESEARCH SOFTWARE AND RESOURCES

Disease-Level Signature Explorer “REEF” (R, Shiny). Open tool that pools cell lines for a single disease and identifies shared gene signatures: commonly and selectively essential genes from CRISPR screen data, and consensus up- and down-regulated genes from expression data. Scoring combines effect size with cross-line consistency. Developed with Dr. Burak Demircan at the Department of Hematology and Oncology, University Hospital Frankfurt; manuscript in preparation.

Application (in preparation): <https://nnahmed9-REEF.hf.space/>

SOFTWARE & CODE

 flowGateR

Scripted gating workflow for flow cytometry in R, written to make gating decisions explicit and repeatable.

 mtDNA workflow

Snakemake workflow for mitochondrial DNA sequencing from blood samples, read processing through variant calling.

 TurboID pipeline

Analysis pipeline for TurboID proximity-labeling proteomics; underlies the IRE1 interactome published in *Cells*.