



# Palestinian Association of Biotechnology (PAoBio)

## THE SECOND BIOTECHNOLOGY ONLINE SCIENTIFIC DAYS – 2025

**8th, 9th, and 10th of May**

**Theme: Navigating Research Challenges –  
From Obstacles to Breakthroughs.**

**Summary Book!**

# Navigating Research Challenges

*From Obstacles to Breakthroughs*



The Second  
Biotechnology Online  
Scientific Days –2025

Palestinian Association  
of Biotechnology (PAoBio)



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بِسْمِ اللّٰهِ الرَّحْمٰنِ الرَّحِیْمِ

WELCOME TO THE 2025 BIOTECHNOLOGY SCIENTIFIC DAYS  
– MAY 8–10!



Theme: Navigating Research Challenges – From Obstacles to Breakthroughs.

We are pleased to welcome you to the 2025 Biotechnology Scientific Days, organised by the Palestinian Association of Biotechnology (PAoBio). This year’s theme, “Navigating Research Challenges – From Obstacles to Breakthroughs,” highlights the real-world difficulties that researchers face and the innovative solutions that emerge through perseverance.

Over three days, renowned speakers from across the region will share insights into how they’ve tackled scientific, logistical, and ethical hurdles in fields such as molecular biology, genomics, and environmental biotechnology. Their experiences serve not only as inspiration but also as practical guidance for overcoming barriers in research.

Biotechnology continues to evolve rapidly, offering powerful tools to solve global problems—but progress rarely comes without obstacles. By openly discussing the setbacks and breakthroughs behind scientific success, this event encourages transparency, resilience, and mutual learning.

This abstract book reflects the diverse and solution-oriented discussions that define this event. We invite you to engage fully, exchange ideas, and be part of a community where curiosity turns challenges into breakthroughs.

May, 2025

# **Speakers and Organizers of the Event**

## **Speakers**

- Mrs. Raeda Hasan Jalayta (Ph.d. Candidate - China)
- Dr. Saja Ali Shareef (Iraq)
- Mrs. Deena Mohammed Sayes (Palestine)
- Mr. Mohammed Nazzal (Palestine)
- Mr. Bassam AbuBaker (Ph.d. Candidate - Hungary)
- Mrs. Renal Omar Abu Dhair (Palestine)
- Dr. Karim El-Hawary (Egypt)

## **Event Organizers**

- Mr. Mousa Daghamin (Association President)
- Mr. Hamza Othman (Board Member)

## **Book Production & Design**

*Hamza S. Othman*

# Events Timetable

Jerusalem Time : UTC+3

Thursday - 8/5/2025

Title/ Activity	Speaker	start	end
Welcome & Registration	Association Team	08:00 pm	08:15 pm
Environmental drivers of diatom diversity: insights from eDNA metabarcoding.	Mr. Bassam Abubaker	08:15 pm	09:15 pm
A novel Association between ABO-Histo blood group and tumor mutational burden in colorectal cancer patients.	Mrs. Raeda Jalayta	09:25 pm	10:25 pm

Friday - 9/5/2025

Welcome & Registration	Association Team	05:00 pm	05:10 pm
Cytogenetic Analysis Associated with Hashimoto's Thyroiditis in Samples of Iraqi Patients: an in vitro study	Dr. Saja Shareef	05:10 pm	06:10 pm
Identification of Antinuclear Antibodies' Epitopes to be Used in Serodiagnostic Purposes Using M13 Phage Display Libraries	Mrs. Renal Abu Dhair	06:20 pm	07:20 pm

Saturday - 10/5/2025

Welcome & Registration	Association Team	05:00 pm	05:10 pm
Identification of Toxoplasma gondii Epitopes Using Phage Display Libraries for Serodiagnostic Purposes	Mrs. Deena Sayes	05:10 pm	06:10 pm
From Discovery to Disease: Transposable Elements and Their Role in Cancer	Mr. Mohammed Nazzal	06:20 pm	07:20 pm
Chroma: A Diffusion-Based AI Framework for Scalable and Intelligent Protein Design	Dr. Karim ELHawary	07:50 pm	08:50 pm
Closing Activity	Association Team	09:00 pm	09:30 pm

DAY

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# I

Jerusalem Time : UTC+3

Thursday - 8/5/2025

<b>Title/ Activity</b>	<b>Speaker</b>	<b>start</b>	<b>end</b>
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A novel Association between ABO-Histo blood group and tumor mutational burden in colorectal cancer patients.	Mrs. Raeda Jalayta	09:25 pm	10:25 pm

# About The Speaker

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Bassam Abu Baker is a research assistant and PhD candidate at the University of Pannonia & Balaton research institute, Hungary, specialising in environmental sciences. He was awarded a fully funded doctoral scholarship by the Hungarian government.

He earned his Bachelor's degree in Biotechnology from An-Najah National University in Palestine. He then completed his Master's degree with honours in Environmental Biotechnology at King Fahd University of Petroleum and Minerals, where he studied the effectiveness of thermophilic bacteria in wastewater treatment. His research was published in a Q1-ranked scientific journal.

Bassam has received several scholarships to attend international conferences and training programs in KSA, Serbia, Poland and France, and he has been actively involved in volunteer research activities in both Europe and Palestine. Additionally, he was awarded an EU-funded grant to study the biodiversity in Palestine.

Currently, Bassam's doctoral research focuses on environmental DNA (eDNA) metabarcoding-based community analysis in freshwater ecosystems (rivers and lakes), investigating biodiversity as a key indicator of climate change and pollution.



# Environmental drivers of diatom diversity: insights from eDNA metabarcoding

## Bassam Abubaker

Research Assistant & PhD candidate, University of Pannonia & Balaton research institute, Hungary

### PRESENTATION SUMMARY

Environmental DNA (eDNA) metabarcoding is a powerful technique for identifying aquatic organisms through genetic material present in the environment. This study compares different methods to explore how environmental variables influence benthic algal communities in Hungarian rivers. A total of 130 samples were collected in 2018 and 2019, with environmental data measured both in situ and in the laboratory. Periphyton was sampled from common substrates, then analysed using three approaches: general microscopy for algal groups, diatom-specific microscopy, and DNA metabarcoding targeting a 312 bp *rbcl* gene fragment.

While microscopy offered a broad overview, its taxonomic resolution was limited. Diatom microscopy enabled precise species identification but was time-consuming. DNA metabarcoding revealed fine-scale diversity and ecological insights but relied heavily on complete reference databases.

The study concludes that combining eDNA metabarcoding with microscopy offers a more complete understanding of algal community structures and the environmental factors shaping them in river ecosystems.



# 8:15 PM - 9:15 PM

8 MAY 25

# About The Speaker

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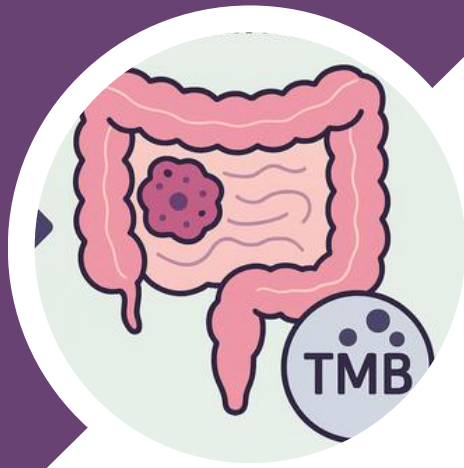
Mrs. Raeda Jalayta is a Palestinian scholar dedicated to advancing cancer genomics and precision medicine.

Currently pursuing her Ph.D. in Pathology and Pathophysiology (Chimeric RNA) at Zhengzhou University, she holds a M.Sc. in Genetics from Dalian Medical University, China. Her groundbreaking work includes identifying the associations between ABO-Histo blood groups and tumour mutational burden in colorectal cancer patients in 2021. She has contributed to critical projects such as developing AFD-based prognostic models for lung cancer.

Mrs. Jalayta is dedicated to advancing cancer research in clinical settings. Her multidisciplinary background bridges molecular biology, cancer genetics science, and radiology, making her a dynamic contributor to the biotechnology field. Enhancing her skills through training in AI-driven scientific research and bioinformatics.

Previously, she contributed to healthcare infrastructure in Palestine, as Head of Radiology department at the Palestinian Health Ministry, and Molecular Genetic Lab Technician at Istishari Arab Hospital. She actively contributes to global scientific communities as a member of the Palestinian Biotechnology Association, the European Society of Human Genetics, and A member of the European Society of Radiology.

Fluent in Arabic and English, with intermediate proficiency in Chinese (HSK4), she champions cross-cultural scientific exchange and ongoing professional development in cancer genetics research. Her ongoing research focuses on prognostic models for colorectal carcinoma and genomic studies to discover novel cancer biomarkers.



## A novel Association between ABO-Histo blood group and tumour mutational burden in colorectal cancer patients

# Raeda Jalayta

Ph.D. Candidate in Pathology and Pathophysiology at Zhengzhou University, China.

### PRESENTATION SUMMARY

**Background:** ABO blood group considers important genetic factors that can be associated with colorectal cancer. However, the association between the ABO Histo-Blood group and Tumor Mutation Burden (TMB) in the colorectal cancers has not been rigorously evaluated. Therefore we, sought to examine whether the ABO blood group associated with higher tumor mutation burden in colorectal cancer patients. **Methods:** In this study, possible association between ABO Histo-blood group and tumor mutational burden in 19 colorectal cancer patients were detected using DNA targeted sequencing Technology. **Results:** the results of DNA targeted sequencing indicated that a novel preliminary association between ABO-blood group and TMB in colorectal cancer, and the results revealed that the average number of mutations in A-blood type patients was significantly higher compared with non-A blood types (blood types B, O, and AB) patients, while the mutations count with O-blood type was significantly lower compared with A-blood type ( $P \leq 0.05$ ). Furthermore, a new promising finding is tumor size with A-blood type was significantly smaller compared with the O-blood type and B-blood type tumor size ( $P \leq 0.05$ ). **Conclusion:** A-Blood type associated with higher TMB in colorectal cancer patients.

**2** 9:25 PM - 10:25 PM  
8 MAY 25

DAY

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# II

Jerusalem Time : UTC+3

Friday - 9/5/2025

<b>Title/ Activity</b>	<b>Speaker</b>	<b>start</b>	<b>end</b>
Welcome & Registration	Association Team	05:00 pm	05:10 pm
Cytogenetic Analysis Associated with Hashimoto's Thyroiditis in Samples of Iraqi Patients: an in vitro study	Dr. Saja Shareef	05:10 pm	06:10 pm
Identification of Antinuclear Antibodies' Epitopes to be Used in Serodiagnostic Purposes Using M13 Phage Display Libraries	Mrs. Renal Abu Dhair	06:20 pm	07:20 pm

# About The Speaker

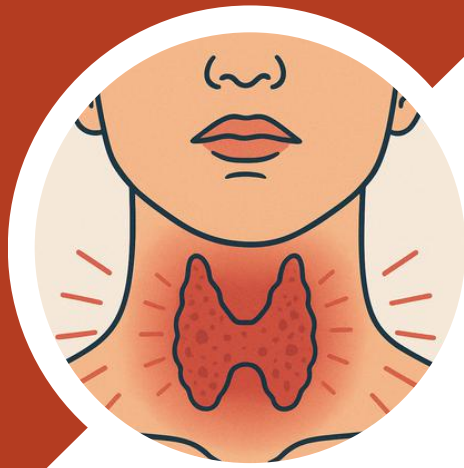
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Dr. Saja Ali Shareef Hamam Al-Juboori is a lecturer in the Department of Biomedical Technologies at the College of Biotechnology, Al-Nahrain University, Iraq. She holds a Ph.D. in Biotechnology from Al-Nahrain University, where she also earned her Bachelor's (2014–2015) and Master's (2017–2018) degrees in the same field.

Dr. Al-Juboori began her academic career as an Assistant Lecturer at Al-Farabi University College in the Department of Medical Laboratory Technology from 2018 to 2023. She then joined Al-Nahrain University in April 2023 as an Assistant Lecturer and was promoted to the position of Lecturer in June 2024.

Her research interests focus on immunogenetics, infectious diseases, and molecular diagnostics, particularly in relation to autoimmune disorders such as Hashimoto's thyroiditis, and pathogenic bacteria such as *Staphylococcus aureus*. She has authored and co-authored several publications in peer-reviewed journals, exploring topics such as cytokine gene polymorphisms, cytogenetics, microbial biofilms, and anti-inflammatory effects of medicinal plants.

Dr. Al-Juboori is an active member of the academic research community, with profiles on major scientific platforms including [Google Scholar](#), [Scopus](#), [Web of Science](#), [ResearchGate](#), and [ORCID](#).



# Cytogenetic Analysis Associated with Hashimoto's Thyroiditis in Samples of Iraqi Patients: an in vitro study

## Dr. Saja A. Shareef

Lecturer at Department of Biomedical technologies, College of Biotechnology, Al-Nahrain University, Iraq

### PRESENTATION SUMMARY

**Background:** One of the most prevalent autoimmune diseases is Hashimoto's thyroiditis (HT), which is characterized by autoantibodies specific to the thyroid but whose precise cause is still unknown. **Objective:** By comparing a sample of Iraqi patients with healthy controls using the comet assay, chromosomal abnormalities, micronucleus production, and mitotic index, the current study aims to clarify the cytogenetic impact of Hashimoto's thyroiditis. **Methodology:** The study included ten Iraqi patients with HT (six males and four females), ages 20 to 75 years old, compared with ten healthy control groups (six males and four females). **Results:** The results showed that only cells in metaphase /1000 were being assessed, and the patient group ( $9.82 \pm 0.0153$ ) was more affected than the healthy control group ( $5.94 \pm 0.170$ ). The micronucleus formation result compared to the proportion of healthy controls was ( $0.004 \pm 0.0018$  Mn/cell), while the frequency of Mn formation in HT was higher ( $0.0068 \pm 0.00132$  Mn/cell). Three parameters were employed in the comet assay to indicate DNA damage in HT patients and healthy controls: tail length ( $9.2 \pm 6.016$  and  $25.5 \pm 10.607$  px), tail moment ( $2.047 \pm 2.687$  and  $11.32 \pm 15.058$ ), and DNA damage in the tail ( $20.892 \pm 11.225$  and  $35.153 \pm 44.429\%$ ). **Conclusion:** The percentage of mitotic index, micronucleus formation, and DNA damage detected by the comet assay in HT patients was higher than in healthy control.

**3** 5:10 PM - 6:10 PM  
9 MAY 25

# About The Speaker

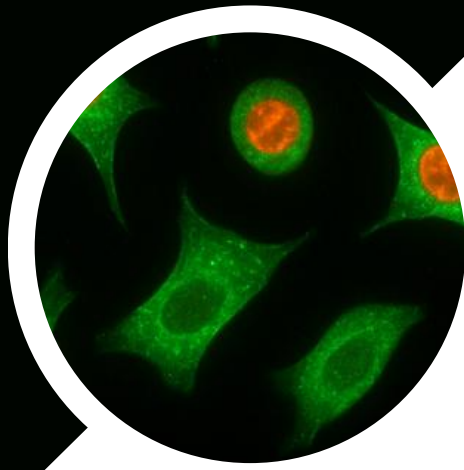
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Renal Abu Dhair is an aspiring molecular geneticist from Bethlehem, currently pursuing a B.Sc. in Molecular Genetics at Al-Quds Bard College. She broadened her academic horizons during a semester abroad at Bard College in New York, funded by the Open Society University Network (OSUN) scholarship. Her education has been complemented by rigorous coursework in functional genomics, molecular diagnostics, and bioinformatics.

Renal has engaged in several hands-on research and training experiences. Her senior project focused on identifying antinuclear antibody epitopes for serodiagnostic use using M13 phage display libraries, integrating immunological techniques like ELISA and advanced bioinformatics tools. She also trained at Bethlehem University's Hereditary Research Laboratory, gaining practical experience in PCR, DNA extraction, gel electrophoresis, and Sanger sequencing. Additional training in whole genome sequencing further solidified her technical skillset.

Her research interests lie at the intersection of immunogenetics and molecular diagnostics, particularly in applying genomic tools to medical diagnostics. She is proficient with a range of software and bioinformatics platforms including MegaX, Galaxy, Primer3, IGV, and BLAST. Renal has also explored functional genomics, emphasizing DNA, RNA, and epigenetic marker analysis—an area she aims to develop further in graduate studies or research-based roles.

Beyond the lab, Renal is passionate about continuous learning and scientific outreach. She completed a research fundamentals course tailored for early-stage Arab researchers and is currently enrolled in Udacity's Programming for Data Science with Python nanodegree. She has also attended global scientific lectures, including topics on telomerase in cancer and the biology of aging. Renal aspires to contribute meaningfully to genetic research and precision medicine.



# Identification of Antinuclear Antibodies' Epitopes to be Used in Serodiagnostic Purposes Using M13 Phage Display Libraries

## Renal Abu Dhair

B.Sc. in Molecular Genetics at Al-Quds Bard College

### PRESENTATION SUMMARY

Antinuclear antibodies (ANAs) are specific autoantibodies that target components of the cell nucleus, including DNA, RNA, histones, and other proteins. They serve as well-established serological markers in various systemic autoimmune diseases (SADs) and play a crucial role in diagnosis and treatment strategies. While molecular diagnostic techniques are highly sensitive and specific but highly expensive, serodiagnostic approaches remain widely used for ANA detection. This study employed a phage display library, a serological approach, to identify specific ANA epitopes using human serum samples positive for ANAs. Next-generation sequencing and bioinformatics tools were used to analyze the phage sequences, and the results were validated using an ELISA test. Three main epitopes, including “CLRCGR”, “VLRVR,” and “RLMVL” were identified as specific epitopes against ANAs, highlighting their potential utility in developing more efficient and targeted serodiagnostic tests for autoimmune diseases. These findings could contribute to improved diagnostic accuracy and patient management.

**4** **6:20 PM - 7:20 PM**  
9 MAY 25

DAY

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# III

Jerusalem Time : UTC+3

Saturday - 10/5/2025

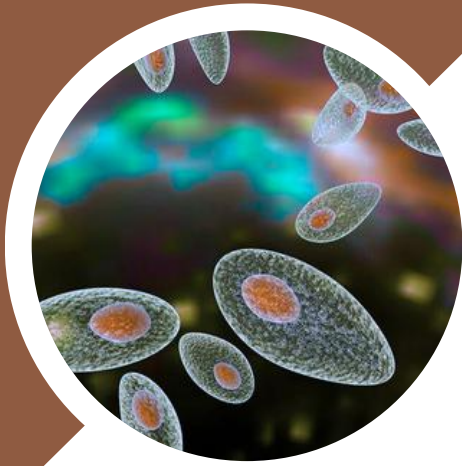
<b>Title/ Activity</b>	<b>Speaker</b>	<b>start</b>	<b>end</b>
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# About The Speaker

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Deena Sayes is a molecular genetics graduate from Al-Quds Bard College with a strong academic record and hands-on experience in genetic research and diagnostic techniques. With consistent placement on the Honor List throughout her studies, she has demonstrated both academic excellence and a deep commitment to the life sciences. Deena earned first place in the biomedical research category at the 6th Palestinian Undergraduate Research Conference for her work on identifying *Toxoplasma gondii* epitopes using phage display libraries for serodiagnostic applications.

Her technical skills include DNA, RNA, and protein extraction, PCR, gel electrophoresis, and cell and microbial culture. Deena is passionate about genetic research and contributing to public health initiatives.



## Identification of *Toxoplasma gondii* Epitopes Using Phage Display Libraries for Serodiagnostic Purposes

# Deena Sayes

B.Sc. in Molecular Genetics at Al-Quds Bard College

### **PRESENTATION SUMMARY**

Toxoplasmosis, caused by *Toxoplasma gondii*, is diagnosed mainly through serological tests, which detect interactions between parasite-specific epitopes and host antibodies. Improving diagnostic accuracy relies on identifying highly specific epitopes, enhancing both sensitivity and specificity of detection methods.

Phage display libraries are powerful, low-cost, and safe tools for epitope identification in infectious diseases. They enable the discovery of highly specific peptide sequences that can be used in developing targeted diagnostic approaches.

This study used the M13 phage display library to identify novel *T. gondii* epitopes. Key steps included phage amplification, biopanning, clone selection, PCR, NGS, and bioinformatics. ELISA validation with positive sera confirmed selected phages displayed *T. gondii*-specific peptides, supporting their diagnostic relevance.

Two novel *T. gondii* epitopes were identified: "ASGS," part of the chorion TM protein, and "VESCL," linked to the activating signal cointegrator 1 complex. These short sequences show promise for improving diagnostic tools targeting *T. gondii* infections.

**5** 5:10 PM - 6:10 PM  
10 MAY 25

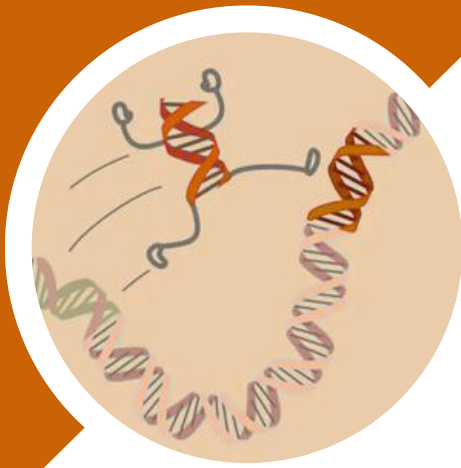
# About The Speaker

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Mohammed Nazzal holds a bachelor's degree in biotechnology from An-Najah National University, where he graduated with a very good average. In 2020, he completed a higher diploma in Pathogenomics at the Wellcome Sanger Institute in the United Kingdom. He has worked in various fields of biotechnology, focusing on the molecular diagnosis of genetic, infectious, and cancer-related diseases. In 2022 he worked as a molecular and histopathology assistant in Medicare Central lab – Ramallah.

Additionally, he is a member of the Scientific Committee of the Palestinian Association of Biotechnology, where he gives lectures about biotechnology and its roles in medicine and disease.

Through these roles, he has gained valuable experience in tissue, cell, and genetic analysis of diseases within the Palestinian community and is passionate about leveraging genomic technology to combat diseases. He is also dedicated to raising awareness about health issues through public health communication.



## From Discovery to Disease: Transposable Elements and Their Role in Cancer

# Mohammad Nazza

Molecular Pathologist , with a higher diploma in Pathogenomics, Wellcome Sanger Institute , United Kingdom.

### **PRESENTATION SUMMARY**

Transposable elements (TEs), or transposons, are mobile DNA sequences that can move within the genome. Discovered by Barbara McClintock in maize, they make up nearly half of the human genome. TEs are classified into two types: Class I (retrotransposons), which use a “copy-and-paste” RNA-based mechanism, and Class II (DNA transposons), which move via a “cut-and-paste” method using transposase enzymes.

Once considered “junk DNA,” transposons are now recognized for their roles in genome evolution, gene regulation, and generating genetic diversity. Their insertions can influence gene expression, create mutations, or even be repurposed for beneficial functions such as development and immune defense. However, they can also destabilize the genome and contribute to diseases like cancer, prompting organisms to evolve defense mechanisms like DNA methylation and RNA interference.

With advances in genome sequencing, scientists better understand TE diversity and function. Transposons have also become valuable tools in gene editing and gene therapy.

In this presentation, McClintock’s groundbreaking discovery and the impact of transposons on human health, particularly their role in cancer will be discussed.

**6** 6:20 PM - 7:20 PM  
10 MAY 25

# About The Speaker

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Dr. Karim El-Hawary is a seasoned bioinformatician and biotechnology expert with experience spanning academia, industry, and freelance consultancy. At EIB Corporation in London, he contributes to drug development using computational biology and cheminformatics. As Head of IT at the Oncology Center, Mansoura University, he leads data analysis and bioinformatics solutions that support advanced cancer research.

In academia, Dr. El-Hawary serves as an Assistant Lecturer at Galala University's Faculty of Engineering and Artificial Intelligence. He also conducts bioinformatics workshops and training, simplifying complex topics for students and professionals. His educational efforts focus on empowering learners to apply computational methods to solve problems in healthcare and engineering.

Dr. El-Hawary's research spans diverse fields. In bioinformatics, he explores genetic mutations in cancer and neurological disorders, nanoparticle-based gene targeting, and epigenetic biomarkers in livestock. His work in genomics and proteomics includes RAPD banding, PCR primer design, and motor protein analysis. He is also skilled in drug docking using PyRx and PyMOL, particularly on compounds like tramiprosate.

He develops machine learning models for diagnostics, such as KNN classifiers for medical datasets, using Python and R. His projects include NGS data analysis, miRNA biomarker discovery, and molecular dynamics simulations for drug design. His interdisciplinary research, including genetic studies on radiation in plants, reflects his commitment to innovation in healthcare and agriculture.



# Chroma: A Diffusion-Based AI Framework for Scalable and Intelligent Protein Design

## Karim EL-Hawary

Teaching Assistant, Faculty of Engineering and Artificial Intelligence, Galala University, Galala Plateau, Attaka, Suez.  
Bioinformatician (Drug Development) for EIB Corp.

### PRESENTATION SUMMARY

In this talk, I introduce the Chroma Diffusion Model, an AI-driven system I developed to address core limitations in protein design. Traditional approaches I encountered were slow, rigid, and prone to failure—constrained by limited diversity, low scalability, and a heavy reliance on trial-and-error. Chroma was my response: a diffusion-based generative model that reframes protein folding as a guided noise-removal process, enabling intelligent and efficient structure generation.

I will walk through the major challenges that led to this work, including poor experimental translation, design bottlenecks, and model generalizability issues. Chroma's architecture offers a solution by combining deep learning precision with structural creativity—allowing for the rapid design of protein candidates across a range of functions. This presentation is not just about an algorithm—it's about rethinking how we build proteins using machine learning, and what happens when design finally becomes scalable, flexible, and data-driven.

**7** 7:50 PM - 8:50 PM  
10 MAY 25

# Navigating Research Challenges

*From Obstacles to Breakthroughs*



التسجيل من خلال  
تعبئة النموذج  
المرفق والإنضمام  
إلى مجموعة  
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