أكاديمية كاوست
KAUST ACADEMY

جامعة الملك عبدالله
للعلوم والتقنية
King Abdullah University of
Science and Technology

KAUST ACADEMY 2025 SPECIALIZATION

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KAUST ACADEMY 2025 SPECIALIZATIONS IN NUMBERS

297

Talented university students from **16** nationalities in **16** different training locations.

45%

total **female** student percentage

134

different projects students worked on.

71
Artificial Intelligence

25
Bioinformatics

15
Cybersecurity

23
Energy Transition

94 DIFFERENT **PROJECT MENTORS**

55 DIFFERENT **LOCAL AND INTERNATIONAL UNIVERSITIES** STUDENTS

ABOUT US

The KAUST Academy specializations program represents a strategic response to Saudi Arabia's Vision **2030** objectives, specifically addressing the critical need to develop local talent in emerging technologies that will drive the Kingdom's economic diversification. By offering comprehensive training in artificial intelligence, bioinformatics, cybersecurity, and energy transition, the program directly targets the four key pillars of Vision 2030's research and development priorities: sustainable environment and essential needs, energy and industrial leadership, health and wellness, and economies of the future. This initiative recognizes that Saudi Arabia's transformation from an oil-dependent economy to a knowledge-based one requires a skilled workforce capable of competing in high-tech industries and research sectors.

The program's multi-stage structure creates a natural bridge between undergraduate education in Saudi universities and advanced professional competency in cutting-edge fields. Rather than leaving recent graduates to navigate this transition independently, KAUST Academy provides a systematic pathway that begins with foundational online coursework through Coursera, progresses through intensive in-person training at universities across the Kingdom, and culminates in international summer programs at prestigious institutions like Oxford, Cambridge, Duke, and University of Toronto. This scaffolded approach ensures that students from diverse academic backgrounds can build upon their undergraduate foundation while gaining practical, industry-relevant skills, with the program having successfully trained over 16,000 students across multiple specializations.







This booklet serves as a comprehensive showcase of the remarkable achievements and outcomes that KAUST Academy's 297 graduating students in 2025 have accomplished through their international summer programs at world-renowned universities. These graduates represent more than mere statistics—they demonstrate the tangible impact of Saudi students engaging with cutting-edge research and advanced methodologies at institutions across the globe. Their success validates the program's effectiveness in not only bridging the gap between traditional university education and specialized knowledge required for Saudi Arabia's emerging technology sectors, but also in positioning Saudi graduates as competitive contributors to international research and innovation networks.

OUR SPONSORS

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ALAGIL FOUNDATION

مدينة الملك عبد الله للطاقة الذرية والمتجددة
K.A.CARE

ntdp

الهيئة الوطنية للأمن السيبراني
National Cybersecurity Authority

Site

women & energy

رزم للاستثمار
RZM INVESTMENT

TEAM MEMBERS

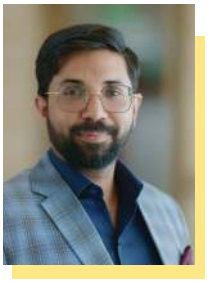


Sultan Albarakati

King Abdullah University of Science and Technology

Doctor of Philosophy in Electrical Engineering

Associate Vice President, Saudi Talent Development

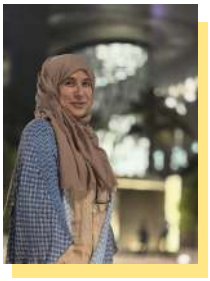


Naeemullah Khan

King Abdullah University of Science and Technology

Doctor of Philosophy in Electrical Engineering

Instruct. Assoc. Professor, Deputy Director KAUST Academy



Oroba Al Nasr

Al Dammam University

Human Research

Promotions & Outreach Specialist

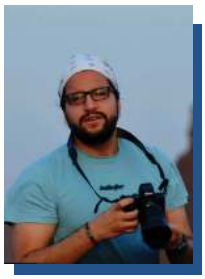


Abdulrahim Alghamdi

Curtin University

Human Research

Master of Commerce, Logistics, Materials, and Supply Chain Management



Abdulaziz Altelmissani

King Abdulaziz University

Medical Laboratory Sciences

Program Coordinator



Ahmed Alhawsawi

Western Kentucky University

Communication Studies and Business Administration

Program Coordinator



Ali Habibullah

King Abdulaziz University

Computer Science

Research Engineer

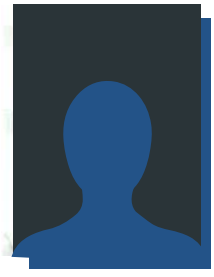


Asim Abdulfattah

Florida Institute

Aeronautical Science, Flight

Program Administrator Pre-University programs



Doa'a Aburayya

King Abdulaziz University

Computer Science

Research Enginner - AI



Emad Surour

Taibah University

Computer Science information systems

Academy Programs Administrator



Farhanaz Beg

National University of Singapore

Computer Science and Engineering

Admissions Lead



Fatma Karabulut Ilter

Istanbul Kültür University

MBA

Program Administrator



Mahmoud Ellouh

King Fahd University of Petroleum and Minerals - KFUPM

Computer Engineering & Cybersecurity

Research Enginner - Cybersecurity

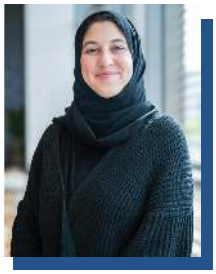


Majed Alghamdi

Beirut Arab University

English Literature

Digital Channels Specialist



Mariam Yaghmour

UC San Diego/KAUST

Chemistry/Molecular Synthesis

Program Administrator, Pre-University programs



Mohamed Nazar O. AlAli

Saudi Electronic University

Business and Finance MSc.

Academy Programs Manager



Saad Alhusainan

Sultan Qaboos University, Sultanate of Oman

Mass and Communication

Development Programs Specialist



Salman Alomari

University of Indianapolis

MBA

Program Coordinator



Tarek Shehata

Tanta University

Mathematics

Manager, Pre-University Programs

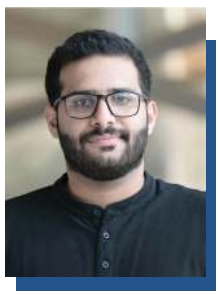


Venu Kas

North Dakota State University

Doctor of Philosophy in Biochemistry

Academic Development Specialist



Yazan Alshuaibi

King Abdulaziz University

Computer Science

Research Enginner - AI



Yubin Huang

Tianjin University

Material Physics and Chemistry

Program Administrator


Raghad Said Algami
ntdp
البرنامج الوطني
لتنمية تقنية المعلومات
National Technology
Development Program
Bioinformatics
Computational
Biology

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King Abdullah University of Science and Technology



Bioinformatics Specialization

2025



Lama Khalid Albishri

Umm Al-Qura University

Cambridge - KAUST- Bioinformatics Summer Program



Mohammed Qadi

King Abdulaziz University

University of Toronto - Summer Internship - Bioinformatics



Marwan Mualla Ali Aljohani

King Abdulaziz University

Cambridge - KAUST- Bioinformatics Summer Program



Fatima Abduljabar Alhelal

Imam Abdulrahman bin Faisal University

Cambridge - KAUST- Bioinformatics Summer Program



Fatima Essa Alzahrani

King Abdulaziz University

Cambridge - KAUST- Bioinformatics Summer Program



Atheer Abdullah Alwuthaynani

King Abdulaziz University

University of Toronto - Summer Internship - Bioinformatics



Shaden Abdulaziz Almohawwes

Qassim University

Cambridge - KAUST- Bioinformatics Summer Program



Maha Alsuhaymi

Taibah University

University of Toronto - Summer Internship - Bioinformatics



Amjad Albawardi

King Saud bin Abdulaziz University for Health Sciences

University of Toronto - Summer Internship - Bioinformatics



Balqees Abbas Mohmmed Yamani

Umm Al-Qura University

Cambridge - KAUST- Bioinformatics Summer Program



Khalid Mohammed Alnashri

King Abdulaziz University

Cambridge - KAUST- Bioinformatics Summer Program



Rahaf Hashim Kassar

Umm Al-Qura University

Cambridge - KAUST- Bioinformatics Summer Program



Raghad Said Algarni

King Fahd University of Petroleum and Minerals

Cambridge - KAUST- Bioinformatics Summer Program



Suhaib Amer Alghamdi

King Abdulaziz University

Cambridge - KAUST- Bioinformatics Summer Program



Wateen Ali Alshawi

King Saud bin Abdulaziz University for Health Sciences

Cambridge - KAUST- Bioinformatics Summer Program



Afnan Abdullah Abdulwahab

Jeddah International College

Cambridge - KAUST- Bioinformatics Summer Program



Abdullah Mohammed R. Alahmadi

King Abdulaziz University

Cambridge - KAUST- Bioinformatics Summer Program



Mohammed Khaled Shafeey

King Abdulaziz University

University of Toronto - Summer Internship - Bioinformatics



Lamis Saeed Alghamdi

King Abdulaziz University

Cambridge - KAUST- Bioinformatics Summer Program



Saad Khalid A Aldawsari

University of Tabuk

Cambridge - KAUST- Bioinformatics Summer Program



Aljori Ahmed Alsheraimi

King Saud University

Cambridge - KAUST- Bioinformatics Summer Program



Ali Hani Alsaad

King Fahd University of Petroleum and Minerals

University of Toronto - Summer Internship - Bioinformatics



Taif Bandr Alharbi

University of Jeddah

University of Toronto - Summer Internship - Bioinformatics



Rahaf Ahmed Alsahafi

King Abdulaziz University

Cambridge - KAUST- Bioinformatics Summer Program



Khulud Theyab Alharbi

University of Jeddah

Cambridge - KAUST- Bioinformatics Summer Program



Shouq Esam Kaaki

King Abdulaziz University

Cambridge - KAUST- Bioinformatics Summer Program

BEYOND SWABS: A MORTALITY-ANCHORED METHOD TO ESTIMATE TRUE COVID-19 INFECTIONS

This project estimates how many coronavirus disease 2019 (COVID-19) infections were missed by relying on deaths rather than reported cases. I combine age-specific infection fatality risk (IFR) estimates from Ward et al. with each country's age structure to create age-standardized, era-specific IFRs.Weekly case fatality rate (CFR) values are computed from reported deaths and cases (no lag). I then infer a detection fraction (≈ IFR ÷ CFR) and implied infections (deaths ÷ IFR) for the United Kingdom, Italy, South Korea, and Saudi Arabia. Results show low detection early, but improving over time, with clear uncertainty.

PROJECT MENTOR: N/A

PROJECT MEMBERS: Lamis Saeed Alghamdi

CO-HOUSING ACCELERATES EXCHANGE OF AGE-LINKED GUT MICROBIOTA WITH SYNCHRONIZED GENUS-LEVEL RESPONSES

This project investigated the exchange of gut microbiota between young and aged mice through co-housing. By analyzing microbial composition at the genus level, we observed that specific taxa were transferred in both directions (young-to-aged and aged-to-young), including beneficial bacteria and taxa with context-dependent effects. These findings highlight how co-housing accelerates age-linked microbiota exchange and may provide insights into microbiome-based strategies for improving health across generations.

PROJECT MENTOR: Lajos Kalmar, Puspendu Sardar

PROJECT MEMBERS: Fatima Abduljabar Alhelal

CORRELATION BETWEEN EMBRYO DEVELOPMENT OF C. ELEGABS AND TIME USING BULK AND SINGLE CELL RNA SEQ

Looking into two RNA-Seq datasets for the C. Elegans to find if there is a relationship between the stages of embryo development found in the bulk dataset. And clusters of cells categorized by time and anatomy found in the Single Cell dataset

PROJECT MENTOR: Hugo Tavares, Andries

PROJECT MEMBERS: Suhaib Amer Alghamdi, Khalid Mohammed Alnashri

DIFFERENTIALLY ENRICHED NEURAL BIOLOGICAL PROCESSES BETWEEN L1 AND L4 IN CAENORHABDITIS ELEGANS

Variation in gene expression underpins variation in organismal traits and diversity. Therefore, understanding how gene expression evolves will allow us to better understand the mechanisms of evolutionary change. The strength and form of selection on gene expression and its role in evolution is difficult to estimate, however, because of the high dimensional and highly correlated nature of gene expression data. In this project the SUDS scholar will estimate selection on gene expression traits and compare the results from different methods that are commonly used to study selection on gene expression.

PROJECT MENTOR: Thomas Krueger

PROJECT MEMBERS: Balqees Abbas Mohmmed Yamani

DOES CROSS-BORDER TRANSMISSION CONTRIBUTE TO THE DEVELOPMENT OF DRUG RESISTANCE IN TUBERCULOSIS (TB) IN SOUTHERN AFRICA?

This project investigated the transmission of drug-resistant tuberculosis between Botswana and Namibia using whole-genome sequencing. By analyzing genomic data from over 300 bacterial isolates, we identified clear evidence of cross-border transmission events involving multidrug-resistant strains. The key biological finding is that while drug resistance has emerged multiple times independently (polyphyletic), it is also potentially spread through cross-border chains.

PROJECT MENTOR: Dr. Andries Van Tonder

PROJECT MEMBERS: Lama Khalid Albishri

EPIGENETIC AGE ACCELERATION AS A MARKER OF CYSTIC FIBROSIS SEVERITY

Investigate association of epigenetic age acceleration (epigenetic age - chronological age) with cystic fibrosis severity including CFTR genotype, measures of pancreatic function, age of chronic infection with Pseudomonas aeruginosa, age of diabetes onset, sweat chloride levels and lung function.

PROJECT MENTOR: Lisa Strug

PROJECT MEMBERS: Amjad Albawardi

ESTIMATING SELECTION ON GENE EXPRESSION

The research aims to gain a deeper understanding of the stages of nervous system development in C. elegans through protein expression analysis and to elucidate the differences between the first and fourth stages. Proteins were normalized, clustered, and examined for differential expression. Gene Ontology enrichment revealed that nervous system biological processes are highly enriched at L1, consistent with the early waves of neurogenesis. These findings offer a proteomic viewpoint on C. elegans nervous system development.

PROJECT MENTOR: Jacqueline Sztepanacz

PROJECT MEMBERS: Mohammed Khaled Shafeey

ESTIMATING THE INCIDENCE AND SEVERITY OF OVARIAN HYPERSTIMULATION SYNDROME (OHSS) AFTER SOLITARY GONADOTROPIN-RELEASING HORMONE AGONIST (GNRH-A) TRIGGER

Assisted reproductive technology (ART) refers to any fertility treatment in which oocytes (eggs) or embryos (fertilized eggs) are manipulated in a laboratory. The first step of ART is controlled ovarian stimulation (COS), which involves daily injections that stimulate the growth of multiple ovarian follicles. Eggs are then retrieved from these follicles. Predicting a patient's response to COS is challenging. Ovarian reserve markers such as antral follicle count (AFC) and serum antimüllerian hormone (AMH) are good, but not perfect, predictors of oocyte yield. For example, a patient with a high AFC or AMH may have poor COS response, whereas a different patient with the same AFC or AMH might have a robust COS response. Follicular Output RaTe (FORT) has been proposed as a solution to this problem. The FORT score is calcuated by dividing the preovulatory follicular count (follicles measuring 16-22 mm) by AFC and multiplying by 100. Previous studies have demonstrated an association between FORT and mature oocyte yield; however, these data have been generated from young egg donors or patients undergoing in vitro fertilization. The current project aims to investigate the utility of FORT scores in women undergoing COS for urgent fertility preservation due cancer or other medical indications.

PROJECT MENTOR: Pereira Nigel

PROJECT MEMBERS: Taif Bandr Alharbi



GENE EXPRESSION DYNAMICS REVEAL DEVELOPMENTAL PROCESSES

Embryogenesis in C. elegans is driven by stage-specific changes in gene expression over time. This project aims to explore how transcriptional programs shift during development using time-course bulk RNA-seq. Through differential expression testing and clustering, we identified over 8,000 genes with dynamic expression patterns. Gene Ontology analysis showed that each gene cluster is enriched in distinct biological processes—such as cell division, differentiation, and tissue development—highlighting how coordinated gene programs drive the embryo through successive developmental stages.

PROJECT MENTOR: Hugo Tavares

PROJECT MEMBERS: Afnan Abdullah Abdulwahab

GENE MAPPING OF PROTEINS ASSOCIATED WITH RECESSIVE DYSTROPHIC EPIDERMOLYSIS BULLOSA (RDEB) IN THE CONTEXT OF CUTANEOUS SQUAMOUS CELL CARCINOMA

Multi-omics approach integrating proteomics with single-cell gene expression

PROJECT MENTOR: N/A

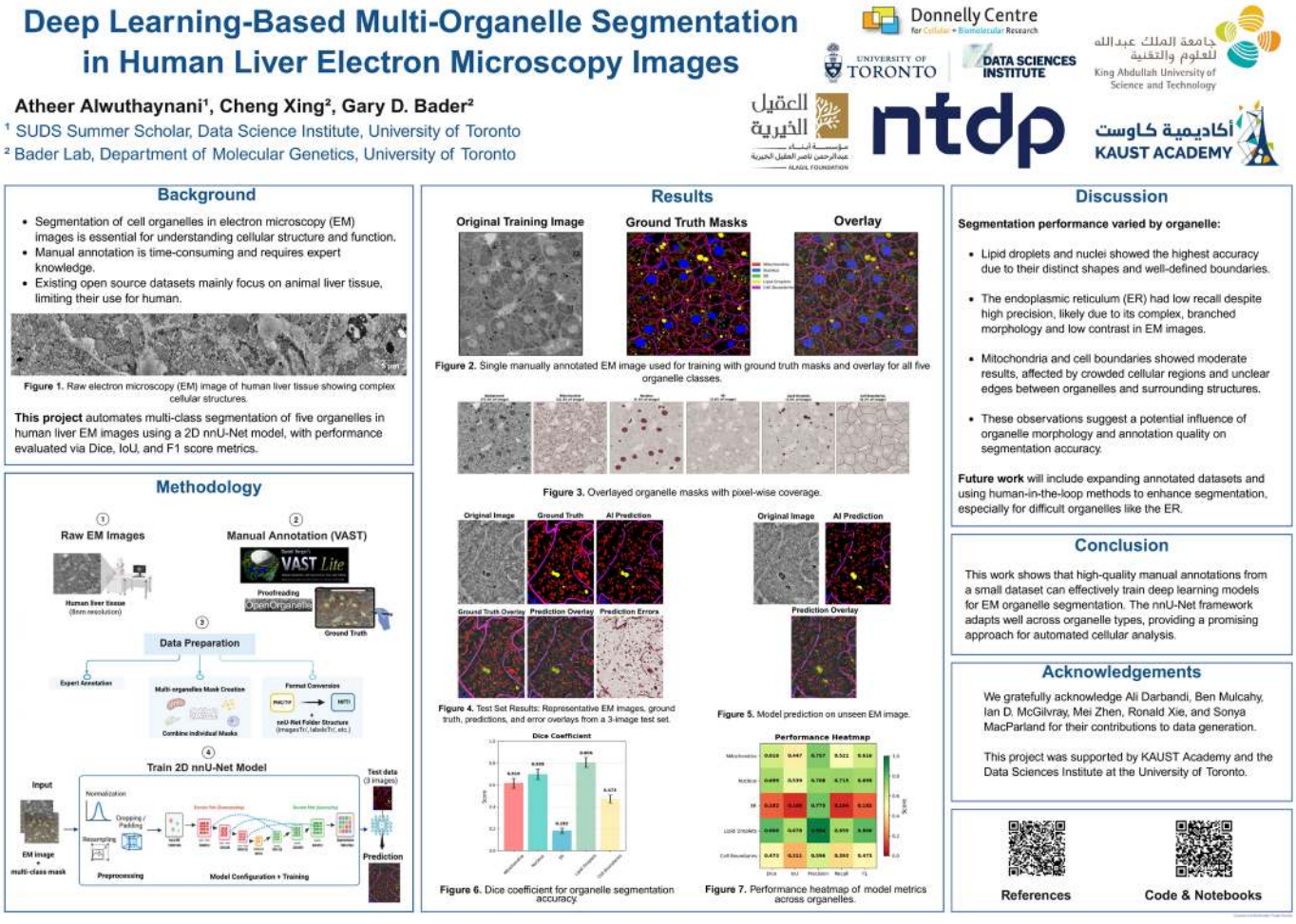
PROJECT MEMBERS: Aljori Ahmed Alsheraimi

DEEP LEARNING-BASED MULTI-ORGANELLE SEGMENTATION IN HUMAN LIVER ELECTRON MICROSCOPY IMAGES

Electron microscopy (EM) enables the high-resolution visualization of liver hepatocyte organelles; however, manual segmentation is time-consuming and requires specialized expertise. This project developed a deep learning pipeline using a 2D nnU-Net for multi-organelle segmentation of mitochondria, nuclei, endoplasmic reticulum (ER), lipid droplets, and cell boundaries, based on manually annotated datasets prepared with expert guidance. Evaluation across independent test images revealed organelle-specific performance: lipid droplets achieved the highest accuracy (Dice ≈ 0.81), nuclei moderate (≈ 0.70), mitochondria variable (≈ 0.62), and the ER the lowest (≈ 0.18), due to its structural complexity. These results demonstrate that limited high-quality annotations can effectively train deep learning models, establishing a scalable workflow for large-scale EM analysis and future 3D organelle modeling.

PROJECT MENTOR: Gary Bader

PROJECT MEMBERS: Atheer Abdullah Alwuthaynani



HOW DOES GENE EXPRESSION IN DIFFERENT BRAIN CELL TYPES RELATE TO PROXIMITY TO AMYLOID PLAQUES IN ALZHEIMER'S MOUSE MODEL?

Widespread deposition of extracellular amyloid-β (Aβ) plaques are the neuropathologic hallmarks of Alzheimer's disease . Studying different cells surrounding Aβ plaques can reveal molecular pathways driving their reactive states and provide insights into how histopathological hallmarks contribute to neurodegeneration. The aim of this project is to understand the cells interactions and whether specific genes are differently expressed near Aβ plaques.

PROJECT MENTOR: Lajos Kalmar

PROJECT MEMBERS: Rahaf Ahmed Alsahafi

IAQ DATA ANALYSIS USING PHYSICS BASED MACHINE LEARNING

People spend nearly 90% of their time indoors, where they are exposed to various airborne contaminants. Indoor air quality (IAQ) has a substantial impact on human health and comfort. However, understanding and analyzing IAQ in diverse indoor environments remains challenging despite the well-established principles of mass transfer and fluid dynamics and various low-cost sensing technologies. This is due to the difficulty of collecting key information, such as contaminant generation rate, degree of air mixing, airflow patterns between spaces, etc.This project aims to develop a method for analyzing time series IAQ data using physics-informed machine learning (ML). The method will incorporate mass balance equations, represented by ordinary differential equations, as physical knowledge. A set of probabilistic ML models, regulated by domain knowledge, will adess the imperfection of the mass balance equations and the impact of missing key information. Probabilistic programming will serve as the overarching framework to integrate all the model components. The student will work with Jeffrey Siegel (CIVMIN, IAQ expert) and Seungjae Lee (CIVMIN, ML expert in building science). Indoor air quality data collected from multiple homes and other indoor environments will be used to test the developed method.

PROJECT MENTOR: Seungjae Lee

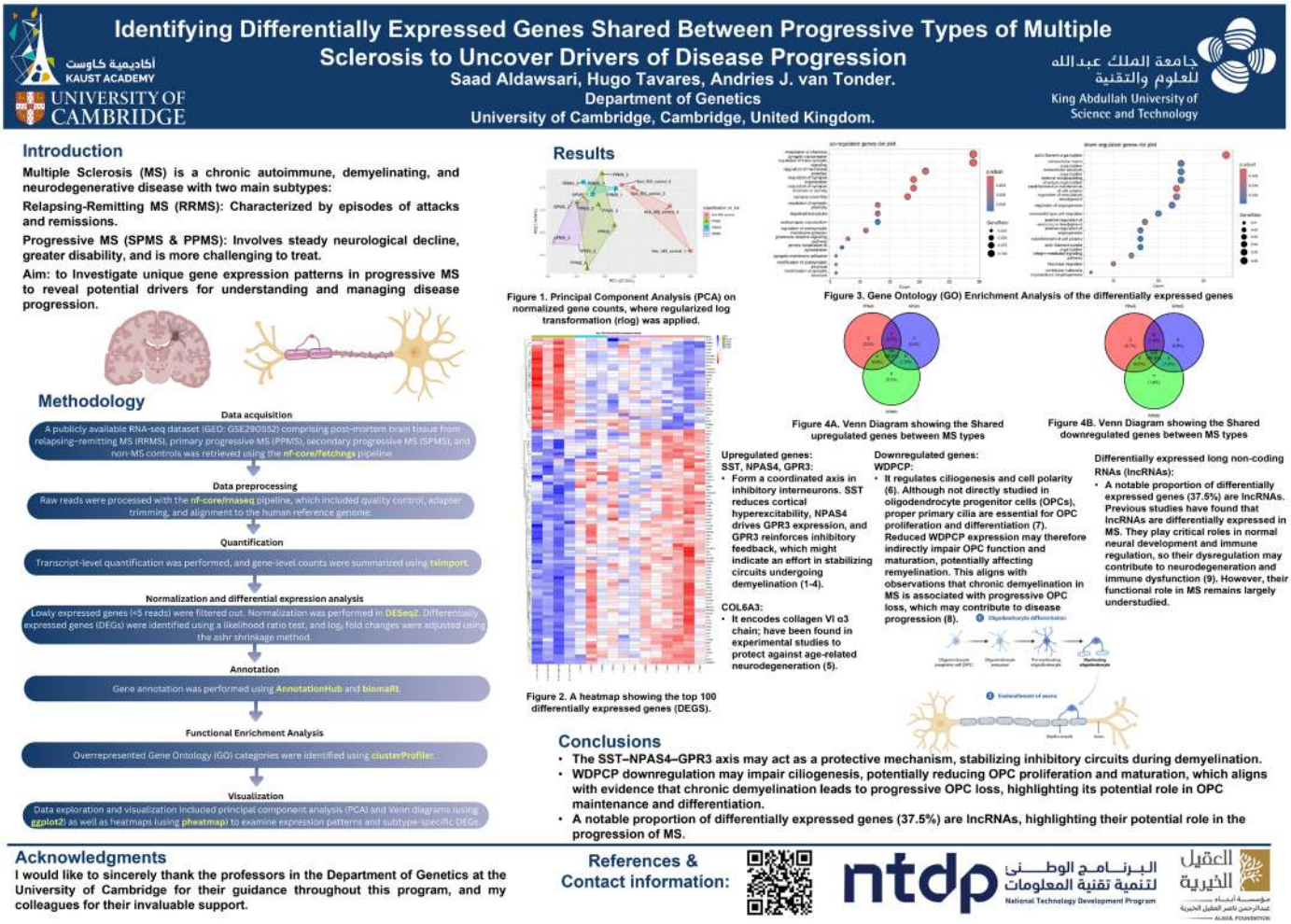
PROJECT MEMBERS: Mohammed Qadi

IDENTIFYING DIFFERENTIALLY EXPRESSED GENES SHARED BETWEEN PROGRESSIVE TYPES OF MULTIPLE SCLEROSIS TO UNCOVER DRIVERS OF DISEASE PROGRESSION

This project aims to identify differentially expressed genes shared between the progressive forms of Multiple Sclerosis (MS); Primary Progressive MS (PPMS) and Secondary Progressive MS (SPMS) to better understand the molecular mechanisms driving disease progression. A bulk RNA-seq transcriptomic analysis was conducted using publicly available brain tissue data (GEO accession: GSE290552). The data were analyzed using DESeq2, with pairwise comparisons between MS subtypes. Venn diagrams were used to identify and visualize genes uniquely shared between the progressive types. To further interpret the biological relevance of these findings, a literature review was conducted to investigate the potential roles of the identified genes in the context of Multiple Sclerosis.

PROJECT MENTOR: Hugo Tavares, Andries J. van Tonder

PROJECT MEMBERS: Saad Khalid A Aldawsari

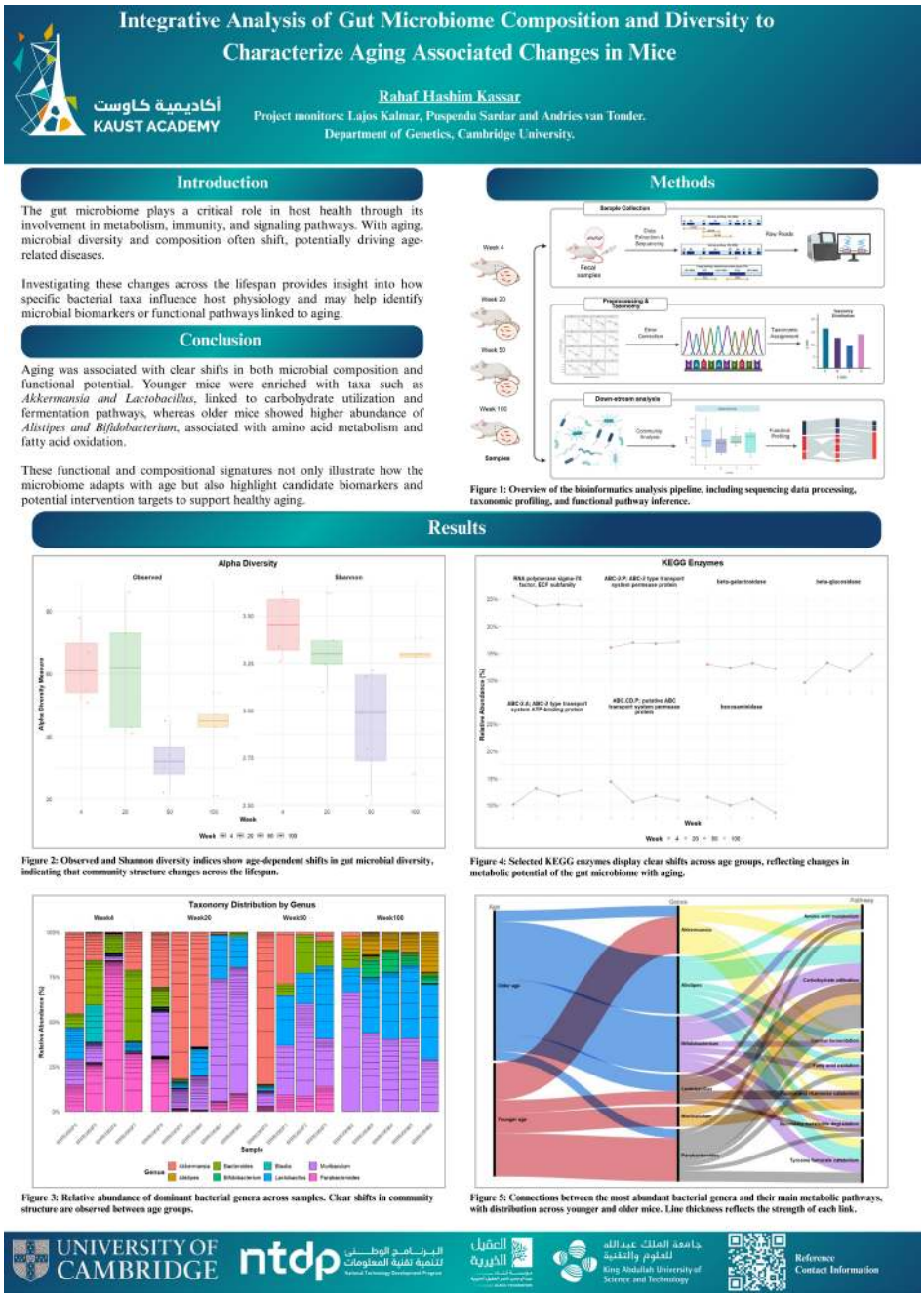


INTEGRATIVE ANALYSIS OF GUT MICROBIOME COMPOSITION AND DIVERSITY TO CHARACTERIZE AGING-ASSOCIATED CHANGES IN MICE

This project aim to investigate how aging shapes the gut microbiome in mice. By comparing microbial communities across different life stages, we observed clear shifts in both composition and functional potential. Predicted functional analyses further revealed age-related patterns in metabolic pathways, highlighting how microbial diversity and functions are linked to host health during aging.

PROJECT MENTOR: Lajos Kalmar

PROJECT MEMBERS: Rahaf Hashim Kassar



INVESTIGATING TRANSPORT, MECHANOTRANSDUCTION, AND ANGIOGENESIS PATHWAYS IN SYNCYTIOTROPHOBLAST CELLS: A LITERATURE-BASED NETWORK ANALYSIS OF BIOMARKERS.

We are conducting a literature-based network analysis to investigate key biomarkers involved in mechanotransduction, transport, and angiogenesis in syncytiotrophoblast cells, with a particular focus on the BeWo cell line. Studies published between 2015 and 2025 were reviewed to compile a comprehensive list of relevant biomarkers. A pathway enrichment analysis is currently being performed to identify shared biological pathways associated with the identified biomarkers and their genes. These results will be visualized through an enrichment map, highlighting functional relationships across the three biological processes and enabling the identification of cross-category pathway overlaps. All biomarkers are being integrated into a protein-protein interaction (PPI) network. Mechanotransduction pathways are categorized into differential pressure, shear stress, and tensile stress. Additional interactions between biomarkers related to angiogenesis and transport are also being analyzed. The complete network will be visualized in a 2D graph, with key metrics such as degree, centrality, and clustering coefficient calculated to assess biomarker significance. This project provides a comprehensive, up-to-date network-level summary of mechanotransduction, transport, and angiogenesis biomarkers in syncytiotrophoblast cells and offers insights into the interconnectivity of findings across recent studies.

PROJECT MENTOR: Hagar Labouta

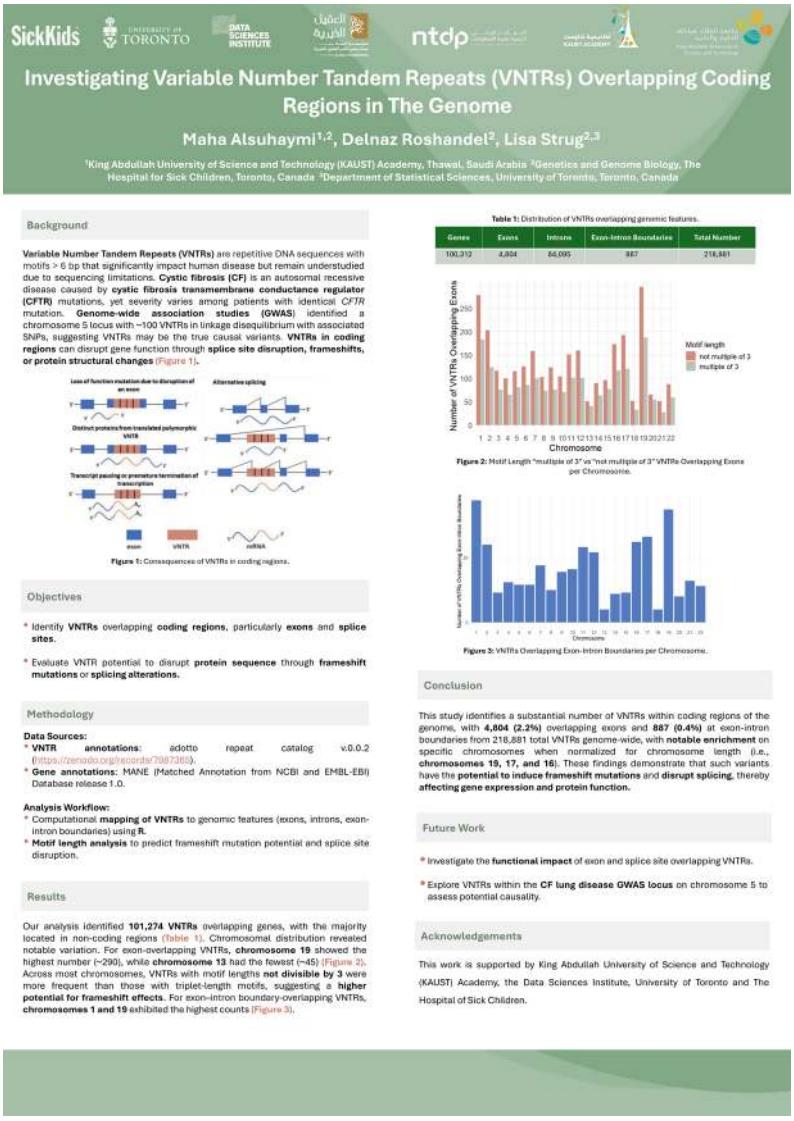
PROJECT MEMBERS: Ali Hani Alsaad

INVESTIGATING VARIABLE NUMBER TANDEM REPEATS (VNTRS) OVERLAPPING CODING REGIONS IN THE GENOME

This project will identify Variable Number Tandem Repeats (VNTRs) that overlap protein-coding regions of the genome, with a focus on a region of chromosome 5 linked to cystic fibrosis (CF) lung disease. Using the adotto repeat catalog (v0.0.2) and the MANE release 1.0 (Matched Annotation from NCBI and EMBL-EBI) database, we aim to find VNTRs that may disrupt splicing or protein sequences. The goal is to discover VNTRs that could explain genetic signals seen in CF GWAS studies and improve our understanding of variation in disease severity.

PROJECT MENTOR: Lisa Strug

PROJECT MEMBERS: Maha Alsuhaymi



IS GENE EXPRESSION IN GLIAL CELL ALTERED IN AUTISM SPECTRUM DISORDER

Its a single rna sequence from postpartum brain tissue, i uses R studio to analyze the data of 95 thousands of cells total of autism and control

PROJECT MENTOR: Hugo and chandra

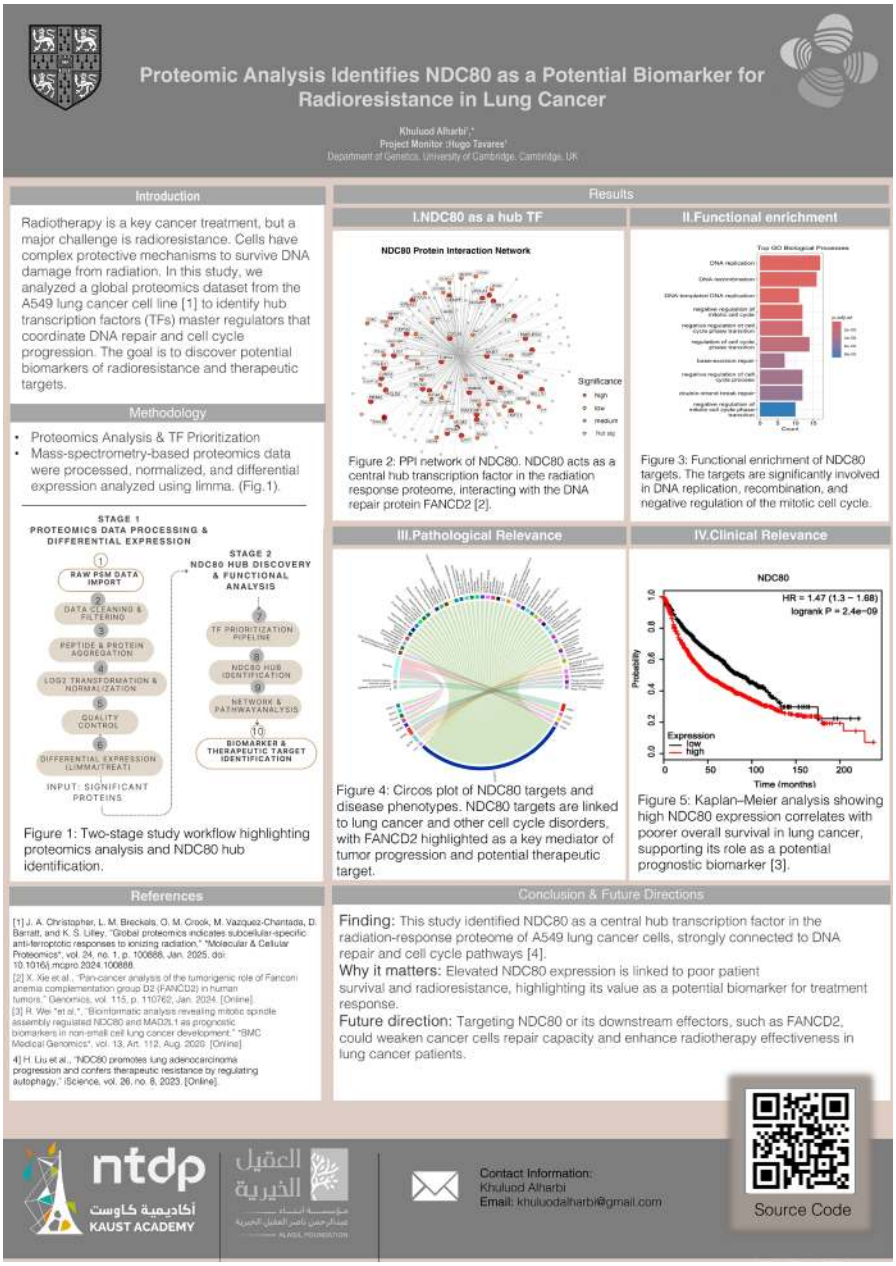
PROJECT MEMBERS: Wateen Ali Alshawi

PRIORITIZATION OF TRANSCRIPTION FACTORS IDENTIFIES BIOMARKERS OF RADIORESISTANCE ACROSS MULTIPLE CANCERS

Radioresistance is a major challenge in cancer therapy, reducing the effectiveness of radiation treatment across diverse tumor types. To uncover key regulators of this process, I analyzed proteomic data from radiation exposed cells and prioritized transcription factors based on their significant target networks. Using statistical ranking and functional enrichment, I identified potential biomarkers of radioresistance that may guide personalized therapeutic strategies across multiple cancers.

PROJECT MENTOR: Hugo

PROJECT MEMBERS: Khulud Theyab Alharbi

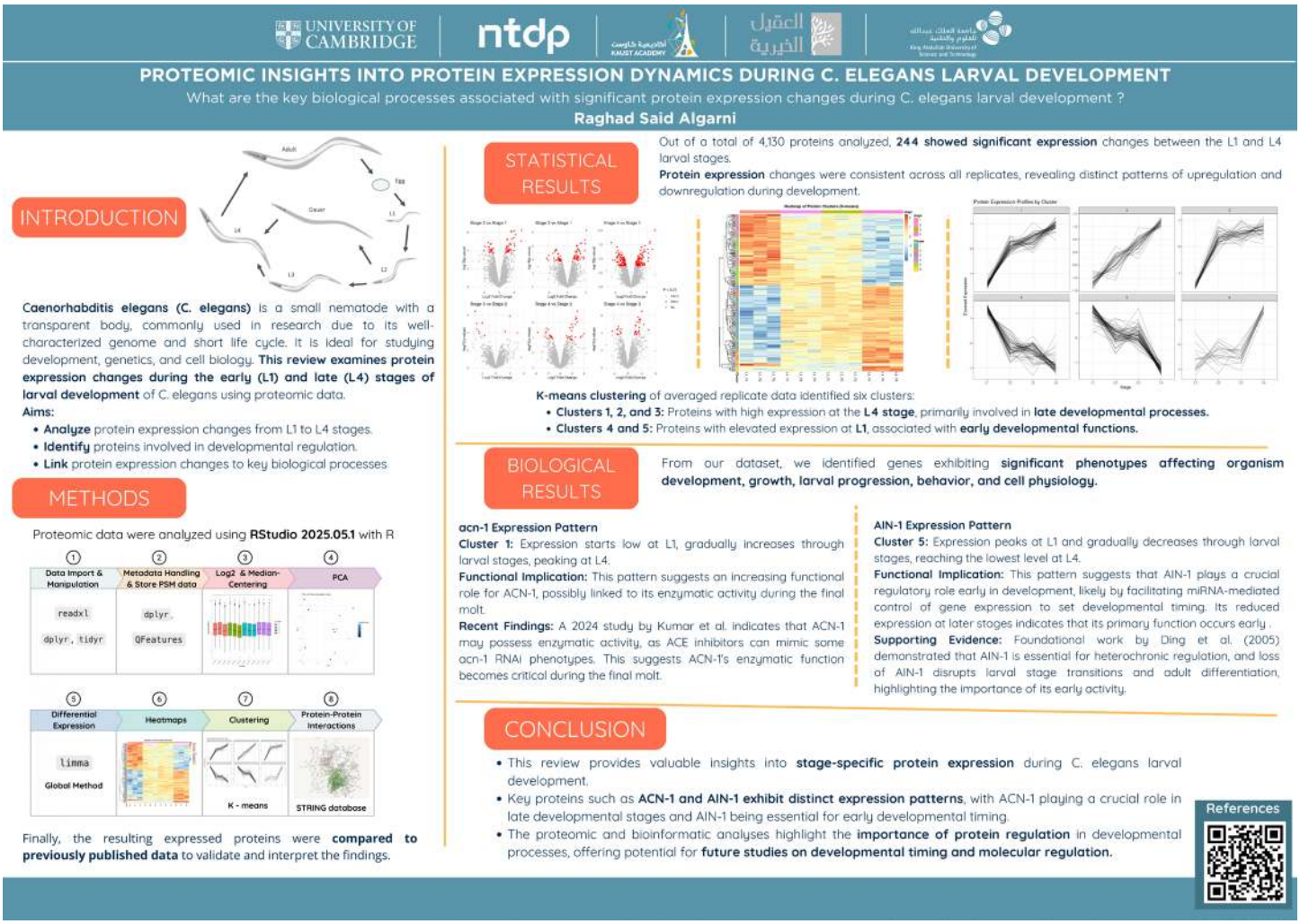


PROTEOMIC INSIGHTS INTO PROTEIN EXPRESSION DYNAMICS DURING C. ELEGANS LARVAL DEVELOPMENT

This study investigates protein expression dynamics in Caenorhabditis elegans during larval development, focusing on early (L1) and late (L4) stages. Proteomic analysis identified 244 proteins with significant expression changes out of 4,130 analyzed, revealing distinct patterns of upregulation and downregulation. Bioinformatics analyses, including clustering and protein interaction networks, highlighted stage-specific proteins: ACN-1, which peaks at L4 and is linked to enzymatic activity and molting, and AIN-1, which peaks at L1 and plays a key role in developmental timing and regulation. These findings provide insights into the biological processes underlying larval growth and differentiation.

PROJECT MENTOR: Dr. Hugo Tavares

PROJECT MEMBERS: Raghad Said Algarni



PUBERTY-DRIVEN GENE EXPRESSION SHIFTS IN AUTISM

This research explores how puberty influences gene expression in children with Autism Spectrum Disorder (ASD), with a focus on the roles of steroid hormones and immune pathways. Using RNA-seq expression data (GSE221645) from whole blood samples, the study compares ASD children to their unaffected siblings both before and after puberty.

PROJECT MENTOR: Dr. Hugo Tavares

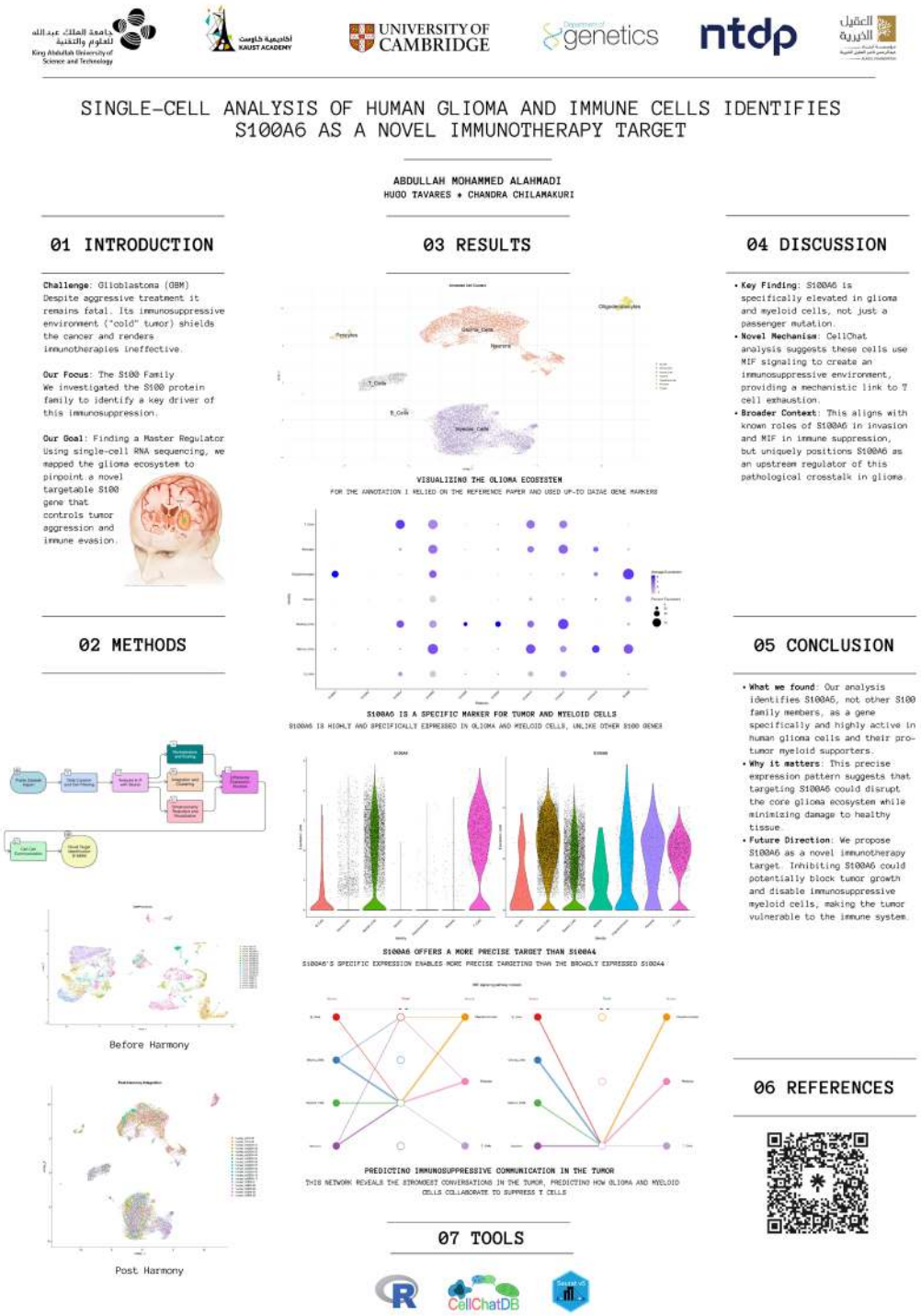
PROJECT MEMBERS: Fatima Essa Alzahrani

SINGLE-CELL ANALYSIS OF HUMAN GLIOMA AND IMMUNE CELLS IDENTIFIES S100A6 AS A NOVEL IMMUNOTHERAPY TARGET

Looking through S100 genes family for an immune therapy target to Glioblastoma

PROJECT MENTOR: Dr. Hugo Tavares

PROJECT MEMBERS: Abdullah Mohammed R. Alahmadi

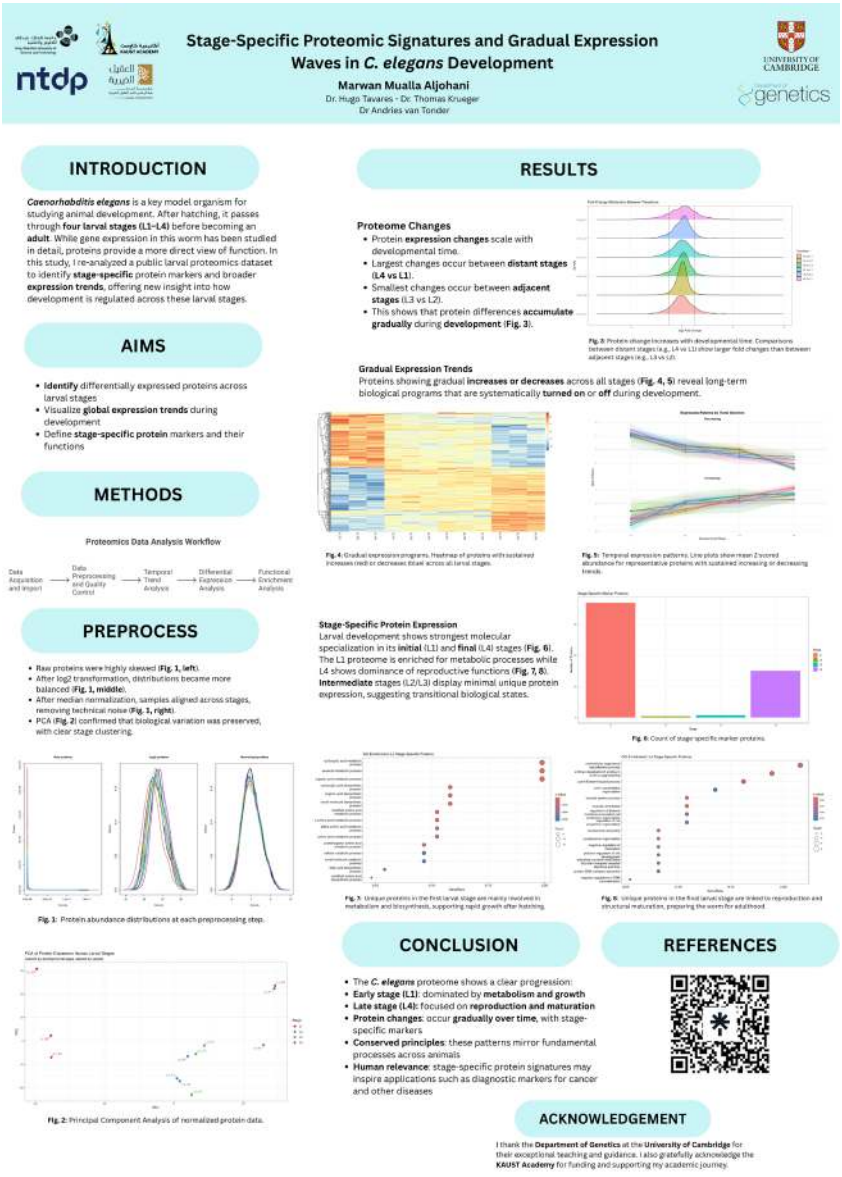


STAGE-SPECIFIC PROTEOMIC SIGNATURES AND GRADUAL EXPRESSION WAVES IN C. ELEGANS DEVELOPMENT

This project involved a comprehensive bioinformatic re-analysis of a public proteomics dataset to characterize protein expression dynamics across C. elegans larval stages (L1-L4). Key findings include the identification of stage-specific protein markers, with L1 enriched for metabolic processes and L4 for reproductive functions, and the discovery of gradual temporal expression trends. The study provides a high-resolution proteomic map and a reproducible workflow for investigating developmental biology. Understanding these protein expression patterns in C. elegans provides a model for studying similar processes in humans, offering potential insights into diseases like cancer where disrupted protein expression plays a critical role.

PROJECT MENTOR: Dr. Hugo Tavares - Dr. Thomas Krueger Dr Andries van Tonder

PROJECT MEMBERS: Marwan Mualla Ali Aljohani



THERAPEUTIC TARGETS IN OVARIAN CANCER: PROLIFERATIVE (C1) VS DIFFERENTIATED (C4) SUBTYPES

This project explored proteomic differences between the proliferative (C1) and differentiated (C4) subtypes of high-grade serous ovarian carcinoma using CPTAC datasets. By applying PCA, heatmaps, and differential expression analysis with limma, we identified subtype-specific proteins and pathways. Enrichment analysis revealed that C1 tumors are enriched in ribosomal and DNA replication proteins, while C4 tumors show detoxification and immune-related processes. Finally, drug–target mapping highlighted potential therapeutic opportunities, suggesting that C1 and C4 may require different treatment strategies. This work emphasizes the importance of proteomics in guiding personalized therapy for ovarian cancer

PROJECT MENTOR: Dr. Lajos Kalma

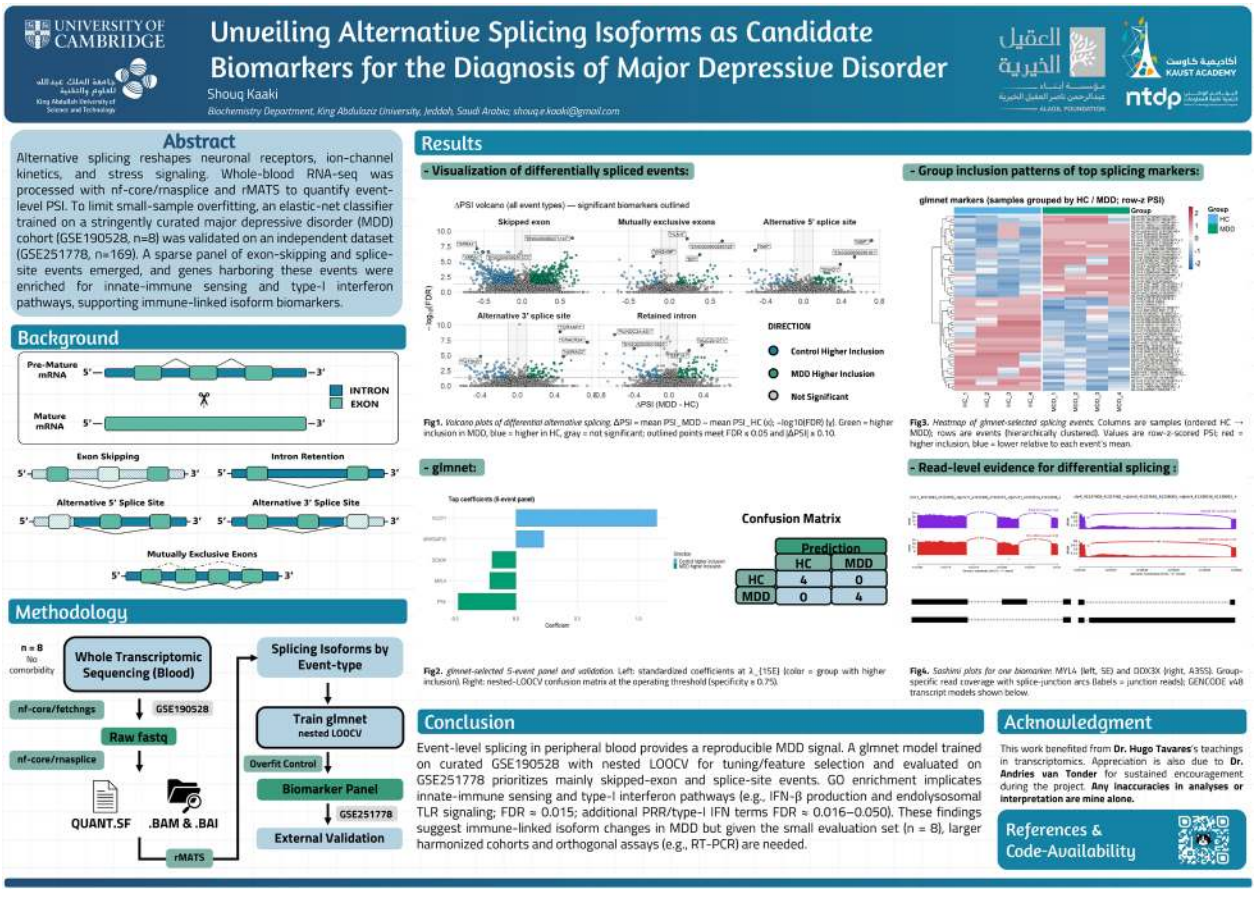
PROJECT MEMBERS: Shaden Abdulaziz Almohawwes

UNVEILING ALTERNATIVE SPLICING ISOFORMS AS CANDIDATE BIOMARKERS FOR THE DIAGNOSIS OF MAJOR DEPRESSIVE DISORDER

This project investigated alternative splicing isoforms as candidate biomarkers for Major Depressive Disorder (MDD). Peripheral blood RNA from MDD patients and controls was analyzed using the nf-core/rnasplice pipeline, with splicing events quantified by rMATS v2.10. Isoforms were first filtered based on false discovery rate (FDR) and percent spliced-in (PSI), using read counts only as a minimum threshold to ensure reliability. Differential analysis revealed that skipped exons were the most abundant significant events, while retained introns were enriched in DNA repair–related genes.Since no single isoform fully separated cases from controls, a LASSO-regularized logistic regression model (glmnet) was applied to identify a diagnostic multi-isoform panel. Enrichment of glmnet-selected features highlighted pathways involved in apoptosis, telomere maintenance, synaptic development and plasticity, cell cycle regulation, and neuronal survival, all processes previously implicated in MDD pathophysiology.The purpose of this trial is to establish whether splicing-derived isoform panels can serve as objective biomarkers for MDD diagnosis, to be used alongside the DSM-IV framework after confirmation in clinical trials. By improving diagnostic accuracy, this approach also aims to address the likelihood that depression represents a spectrum of molecular subtypes, an idea supported by contradictory findings in the literature on disease mechanisms.

PROJECT MENTOR: Hugo Tavares, Andries van Tonder

PROJECT MEMBERS: Shouq Esam Kaaki



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