

ANNUAL REPORT

ARMENIAN BIOINFORMATICS INSTITUTE

2024

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THE ARMENIAN BIOINFORMATICS INSTITUTE (ABI) IS A NON-PROFIT PRIVATE SCIENTIFIC-EDUCATIONAL FOUNDATION, LAUNCHED IN FEBRUARY OF 2021 TO SUPPORT BIOINFORMATICS CAPACITY BUILDING AND THE DEVELOPMENT OF PRECISION MEDICINE AND MODERN BIOTECHNOLOGIES.

THIS REPORT SUMMARIZES THE FOURTH YEAR OF OUR ACTIVITIES.

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GARIK VANYAN (DESIGN)

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01

INTRODUCTION

INTRODUCTION

The technological revolution in genomics has catalyzed an explosion in genomic data generation. The volume of data deposited in international repositories has surged from 0.01 gigabytes in the late 1980s to around 20 petabytes in the 2020s, doubling every five years. This exponential growth underscores the growing demand for robust infrastructures to store, manage, and share genomic data, essential for sustaining ongoing advancements in research. Equally crucial is the human expertise needed to analyze these vast datasets and derive insights that will help the global community better understand disease mechanisms and identify potential cures. Bioinformatics institutes worldwide are central to these developments, setting standards for genomic data management, providing training, and developing software tools that enhance data analysis capabilities.

In 2021, we established the Armenian Bioinformatics Institute in response to the critical shortage of bioinformatics specialists and the absence of infrastructure for genomic data management in the country. Without these essential resources, progress in life sciences, medicine, and biotechnology in Armenia would be severely limited. Our mission is to equip bioinformatics specialists with both technical expertise and leadership skills, empowering them to drive meaningful change within biotechnology and biomedical sectors. What began as a small, private initiative by a group of scientists has evolved into a dedicated team of over 20 newly trained researchers who are confidently advancing us toward our vision. Our team fosters a culture of knowledge sharing, discipline, and innovation—an environment that will pave the way for new discoveries and contributions to global scientific efforts.

The year 2024 marked several significant milestones, including a partnership with Ritual Dental (US) to explore the oral microbiome for personalized dental treatments. We also continued our collaborations with Vivan Therapeutics (UK) and Agenus (US) on precision cancer therapy research. We published eight papers on topics such as stress responses in grapes, cancer and neurological disorder heterogeneity, and spatial transcriptomics. Additionally, our third OMICSS-24 Summer School in Genome Bioinformatics welcomed 21 students from Armenia and abroad, who worked on projects ranging in topics from cancer treatment resistance, the impact of smoking on the oral microbiome, to grapevine genetics. Several students advanced to internships and research roles with us. Renovations also began on a two-floor space at the Institute of Molecular Biology to house ABI's new Research and Training Center, which will support over 20 researchers upon its completion in 2025.

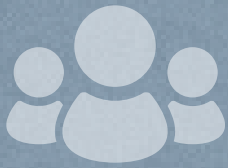
We also recognize the challenges that impede our growth, which we will continue to address in 2025. These include limited resources hindering our efforts to recruit senior scientists from abroad and the lack of international Master's and PhD programs that could foster local talent development and attract specialists to Armenia.

Looking ahead, we remain committed to nurturing talent, advancing innovation, and creating a lasting impact on both local and global scientific communities. Our continued dedication to these goals will help us overcome obstacles and accelerate progress in genomics research.

02

2024 IN NUMBERS

2024 IN NUMBERS



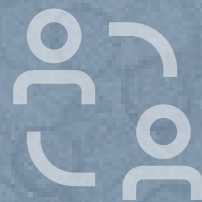
28
RESEARCHERS



7
ALUMNI



8
PUBLICATIONS



3
INDUSTRY
COLLABS



2
COURSES



37
TRAINED
STUDENTS



4
GRANTS



3
RESEARCH
UNITS

03

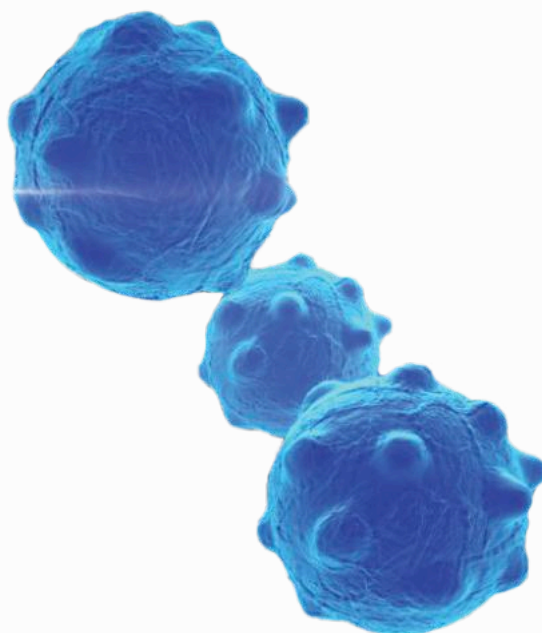
RESEARCH

MOLECULAR MECHANISMS OF LIVER METASTASIS IN COLORECTAL CANCER: ADVANCING PROGNOSTICS FOR ENHANCED IMMUNOTHERAPY

Colorectal cancer (CRC) is the third most prevalent cancer globally and remains one of the leading causes of cancer-related mortality. A considerable proportion of CRC cases are diagnosed at advanced stages, characterized by poor prognosis due to the high propensity for liver metastasis. The advent of immunotherapy has transformed cancer treatment paradigms, introducing promising options for CRC management, especially in metastatic disease. However, the effectiveness of immunotherapy in CRC with liver metastasis is hindered by distinct challenges.

Our collaborator in the United States, Agenus, recently conducted a pivotal clinical trial (published in *Nature Medicine*, 30, 2558–2567, 2024), demonstrating the potential of a novel immunotherapy combination to treat microsatellite-stable metastatic CRC by engaging the immune system against this traditionally immunotherapy-resistant cancer subtype. Despite this breakthrough, treatment failure persists in approximately half of the patients, with mechanisms underlying resistance still largely unclear.

Building on our prior collaboration with Agenus, our team at ABI is undertaking a comprehensive analysis of multi-omics data from the clinical trial to uncover molecular factors driving liver metastasis and treatment resistance. The ultimate aim is to establish an omics-based prognostic framework to predict treatment outcomes in CRC patients with advanced liver metastasis. Our interdisciplinary team, comprising biodata science and bioinformatics researchers, and clinicians, employs a wide array of methodologies, including large-scale machine learning on *omics* data, single-cell analysis, and spatial transcriptomics, to achieve this objective.



GENOME DIVERSITY OF ARMENIAN GRAPEVINE ITS GENETIC HISTORY AND MECHANISMS OF STRESS RESPONSE

Our research addresses two primary objectives: first, characterization of the diversity of Armenian grapevine accessions—both wild and cultivated—through comprehensive whole-genome analysis, and second, investigating the genomic mechanisms underlying stress responses to factors such as temperature fluctuations, drought, and disease. To accomplish this, we utilize DNA and RNA sequencing alongside machine learning techniques for advanced data mining.

These approaches provide insights into the domestication history of grapevines and their associations with phenotypic traits, including cultivar utility and potential resistance to diseases and pests. The outcomes of this work are particularly relevant to overcoming challenges in viticulture, notably those arising from climate change. This project is one of the nine ADVANCE Research Programs funded by the FAST initiative in Armenia.

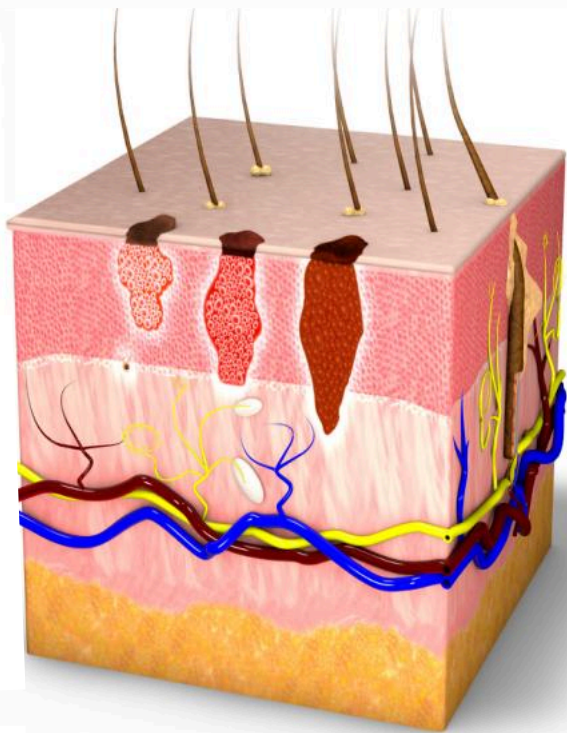
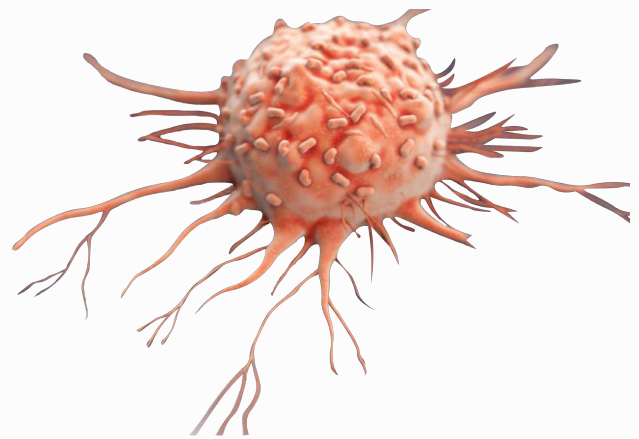


Konecny T, Asatryan A, Nikoghosyan M, Binder H.

Unveiling Iso- and Aniso-Hydric Disparities in Grapevine—A Reanalysis by Transcriptome Portrayal Machine Learning. *Plants* 2024, 13(17):2501.

FROM BRAIN DISORDERS TO WOUND HEALING AND CANCER: DECIPHERING THE GENOMICS OF COMPLEX DISEASES

In a series of collaborations with the Russian-Armenian University and the Institute of Molecular Biology NAS RA, we study the genomics of complex diseases such as Schizophrenia and other neuropsychological disorders, examining their development across the human lifespan as well as mechanisms of genomic regulation that underlie cancer formation and development.



We also collaborate with experimental laboratories at Leipzig University, contributing our bioinformatics expertise to uncover the mechanisms of skin wound healing and the development of melanoma (black skin cancer). This project strengthens our ability to work on collaborative initiatives with experimental partners through weekly discussions, aligning their project goals with state-of-the-art approaches in *omics* data preprocessing, systems biology, and downstream bioinformatics analyses.

Hakobyan M, Binder H, Arakelyan A.

Pan-cancer analysis of telomere maintenance mechanisms. *Journal of Biological Chemistry* 2024;300(6):107392.

Davitavyan S, Martirosyan G, Mkrtychyan G, Chavushyan A, Melkonyan A, Ghazaryan H, Binder H, Arakelyan A.

Integrated analysis of -omic landscapes in breast cancer subtypes. *F1000Research* 2024;13(564).

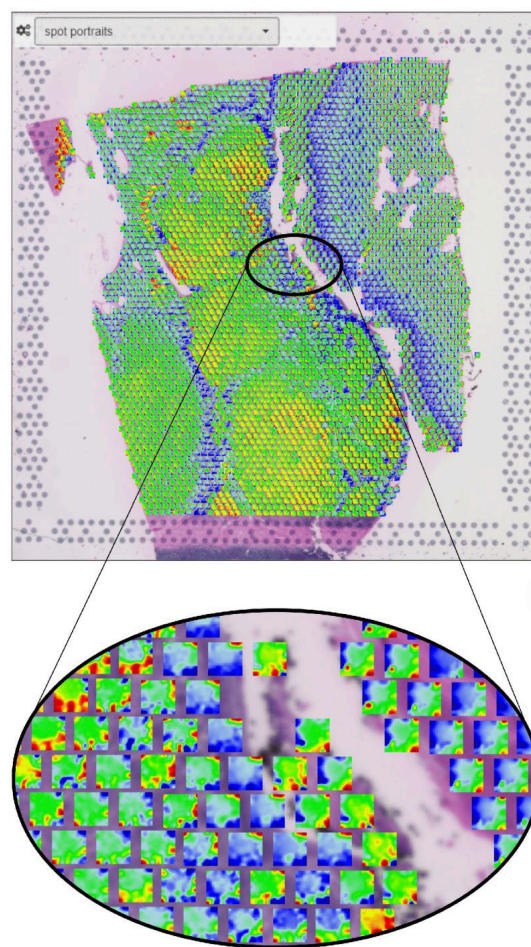
Arakelyan A, Avagyan S, Kurnosov A, Mkrtychyan T, Mkrtychyan G, Zakharyan R, Mayilyan KR, Binder H.

Temporal changes of gene expression in health, schizophrenia, bipolar disorder, and major depressive disorder. *Schizophrenia* 2024;10(1):19.

DISCOVERING GENOME REGULATION IN SPACE AND TIME – SPATIAL AND SINGLE-CELL OMICS

Genomic sequencing methods, alongside essential bioinformatics, are revolutionizing nearly every area of the life sciences, unlocking entirely new perspectives in health research - particularly in genome-based precision and personalized medicine. The latest, state-of-the-art techniques allow for genomic information to be captured with spatial single-cell resolution, providing unprecedented insights into cellular organization within tissue structures and their microenvironments. This includes spatial heterogeneity within tumors, which influences omics-based personalized diagnostics and the development of new immunotherapies and cell-based treatments.

This project focuses on developing bioinformatics methods for comprehensive analysis of single-cell genomics, including spatial gene expression "microscopy". Single-cell and spatial transcriptomics data are central to nearly all current projects in the Binder Lab, enabling both the quantification of microanatomy and tissue heterogeneity at cellular and genomic levels. Through this approach, we aim to elucidate disease development across spatial and temporal scales, identify cell fate mechanisms, and extract disease markers. A key objective is to make these data and their functional interpretations accessible and usable to collaborating experimental labs and clinics via interactive web applications with data browsing functionalities.



Schmidt M, Avagyan S, Reiche K, Binder H, Loeffler-Wirth H.

A Spatial Transcriptomics Browser for Discovering Gene Expression Landscapes across Microscopic Tissue Sections. *Current Issues in Molecular Biology* 2024, 46(5):4701-4720.

M. Torregrossa, S. Avagyan, A. Grigoryan, M. Tamazyan, R. Kandi, J. Simon, H. Binder, Y. Rinkevich, S. Franz.

Identification of cell subsets across anatomical sites in human skin. *EXPERIMENTAL DERMATOLOGY* 33 (3) (Poster)

DIGITALLIFE: LEVERAGING INTERNATIONAL COLLABORATIONS IN HEALTH BIOINFORMATICS

The fields of digital and life sciences are increasingly converging due to the rapid expansion of biological and molecular medical data, which drives a critical need for expertise in data transformation, analysis, and interpretation. The DigitalLife (Sciences) project aims to strategically advance and expand collaboration among the Armenian Bioinformatics Institute, the Interdisciplinary Center for Bioinformatics (IZBI) at Leipzig University, and the Institute of Molecular Biology (IMB) NAS RA in Yerevan. This initiative focuses on genomics bioinformatics, biodata science, and systems medicine to clarify molecular pathomechanisms underlying complex diseases.

DigitalLife was launched in spring 2024 with an kick-off workshop “Genome Bioinformatics for Health” at Leipzig University, where twelve early-career researchers from ABI and the Bioinformatics Group at IMB participated in a week-long program at IZBI. It brought together Armenian and German scientists to present and discuss current cooperative research, covering topics from bioinformatics methods development to applications in plant science, cancer diagnostics, immunology, and skin wound healing. This onsite event established a strong foundation for ongoing and future collaborations.



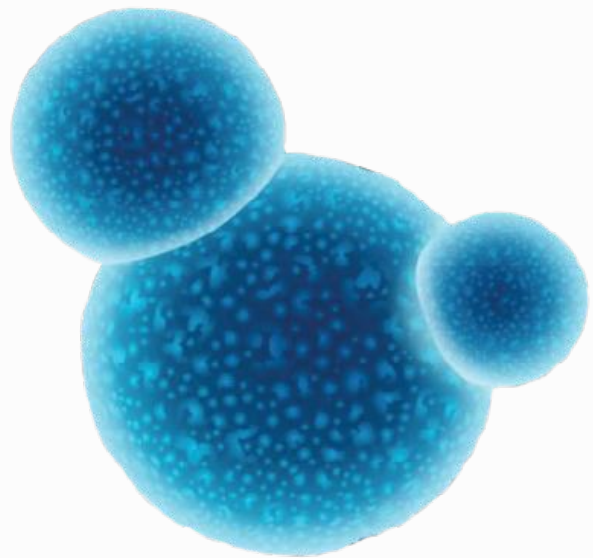
MICROBIOME DYNAMICS: HOW MICROORGANISMS SHAPE OUR HEALTH

Humans and animals host a diverse community of microorganisms, collectively known as the microbiome, that play a crucial role in maintaining health and influencing disease. Each type of microorganism performs specific functions and interacts with others within the ecosystem, through cooperation or competition. These interactions occur across various environments in the body, such as the gut, oral cavity, skin, and sexual organs, where the microbial composition generally remains stable throughout an individual's life. However, external stressors—such as diet, antibiotics, other medications, and disease—can disrupt this balance. While some changes in the microbiome are reversible, others may lead to irreversible shifts, potentially contributing to chronic diseases.

Our team is developing bioinformatics algorithms to investigate the sequence of events that result in such irreversible changes. We aim to identify the microorganisms directly impacted by external stressors and track how changes in their abundance influence the broader microbial network, ultimately leading to a stable yet altered composition linked to disease. Understanding these temporal dynamics is critical for designing targeted pro- and pre-biotic treatments to prevent harmful, lasting changes.

This year, we established a joint laboratory with the Institute of Molecular Biology, NAS RA, to complement our computational work with experimental studies. This wet-lab infrastructure enables us to perturb microbial communities using various chemicals and observe time-resolved changes in their composition. Over the next few years, we plan to generate original datasets and apply our bioinformatics tools to develop innovative methodologies for monitoring and understanding the temporal shifts in microbiome composition under different conditions.

This topic was the focus of Lusine Adunts' Bachelor thesis entitled: "Deciphering the Temporal Changes in Microbiome Communities", in the Data Science program at the American University of Armenia.



ENVIRONMENTAL IMPACTS ON BEE GUT MICROBIOME COMPOSITION

Like humans, the honeybee gut is home to a diverse community of microorganisms that play a critical role in health and resilience. In recent years, there has been a concerning decline in honeybee colonies, which threatens global agriculture due to their vital role in pollination. One potential contributor to this decline is agricultural practices, particularly pesticide use, which can directly impact honeybee physiology or indirectly affect their health by altering the gut microbiome.

In collaboration with Yerevan State University, our team conducted a comprehensive meta-analysis of the honeybee gut microbiome, incorporating data from diverse ecosystems. This study evaluates the effects of pesticides and dietary supplements on microbial composition, and expands the current understanding of the bee gut microbiome by including samples from various regions of Armenia alongside reanalyzed datasets from other parts of the world.

To assess pesticide impacts, we employed an innovative graph-based algorithm to identify networks of bacterial species significantly affected by treatments, including glyphosate—the most widely used herbicide—along with various insecticides and sugar-based supplements.



This year, Nelli Vardazaryan presented our study in the SymbNET International Conference on Host-Microbe Symbiosis conference in Portugal.

Nelli Vardazaryan, Lusine Adunts, Chrats Melkonian, Lina Zakharyan, Inga Bazukyan, Lilit Nersisyan.

The effects of geographical and nutrient variation on bee microbiome composition: a meta-analysis.

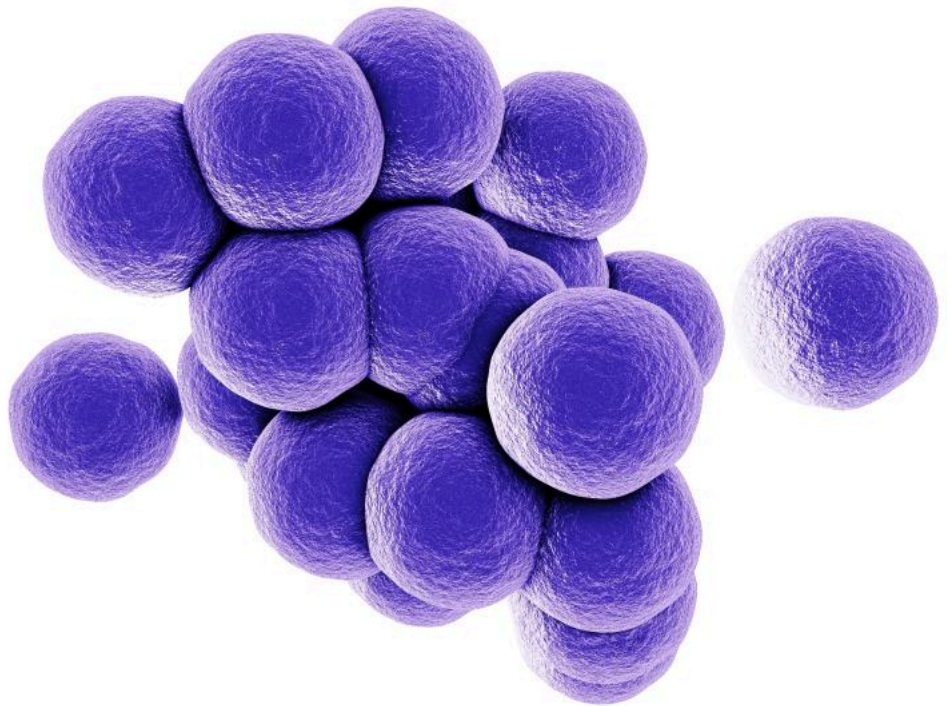
Manuscript in preparation.

ANTIBIOTIC RESPONSE PROFILES OF STAPHYLOCOCCUS AUREUS STRAINS ISOLATED FROM CLINICAL SAMPLES IN ARMENIA

S*taphylococcus aureus* is a significant human pathogen, with antibiotic resistance in its strains posing an increasing global health concern. Methicillin-resistant *S. aureus* (MRSA) is particularly alarming, due to its ability to evade common antibiotics, leading to difficult-to-treat infections and increased mortality rates worldwide.

In collaboration with the Institute of Molecular Biology NAS RA and the Karolinska Institute in Sweden, we are investigating the antibiotic response in methicillin-resistant *S. aureus* strains isolated from clinical samples in Armenia. Utilizing advanced sequencing technologies and innovative bioinformatics approaches, we study changes reflected at the level of RNA in response to treatment with ten distinct antibiotics.

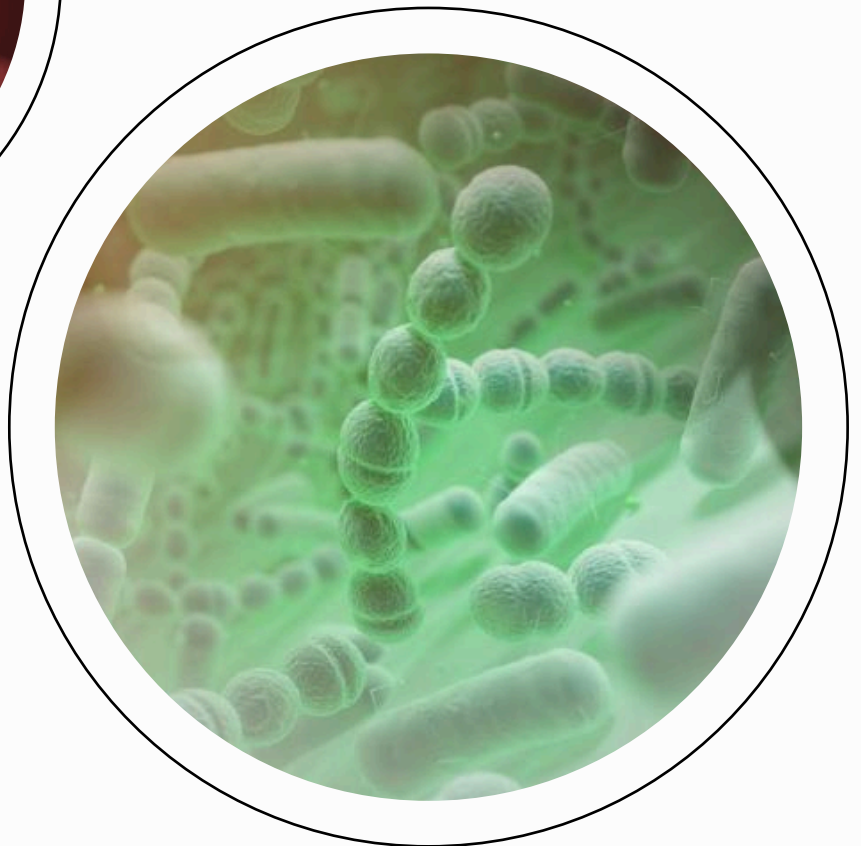
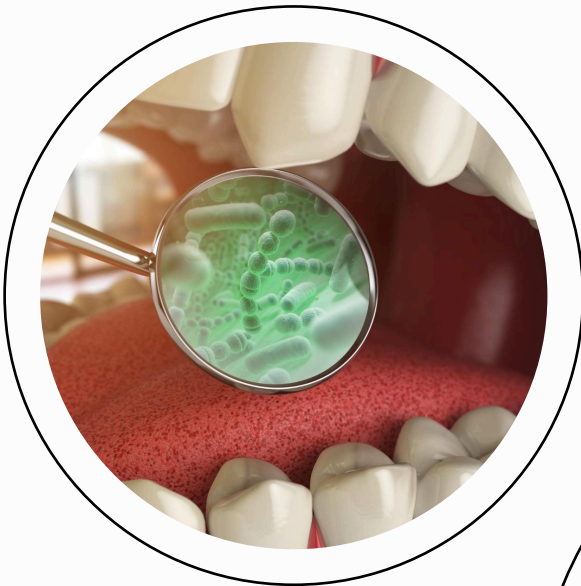
Our goal is to develop methodologies capable of identifying resistance mechanisms without prior knowledge of an antibiotic's mode of action. This research aims to facilitate rapid and precise diagnostics of antibiotic resistance in clinical settings, improving patient outcomes and informing treatment strategies.



LEVERAGING ORAL MICROBIOME ANALYSIS FOR PRECISION DENTAL CARE

The oral cavity hosts a diverse community of bacteria and fungi, which typically remain stable despite factors like diet, brushing, and other daily habits. However, influences such as smoking, diet, and chronic health conditions can disrupt this microbial balance, leading to oral diseases such as gingivitis, periodontitis, caries, and halitosis.

In partnership with Ritual Dental, an innovative start-up focused on precision dental care, we are leveraging advanced microbiome analysis to provide data-driven insights into oral health. Ritual Dental specializes in personalizing dental care by using microbiome data to predict the risk of various oral diseases. By analyzing saliva samples, our team is developing bioinformatics methods to estimate the likelihood of oral health disorders and offer customized treatment recommendations. This work aims to transform dental care into a more precise and preventative approach.



TELOMERES IN BLOOD CIRCULATION: UNLOCKING NEW INSIGHTS FOR CANCER DETECTION

Our bodies continuously shed genetic material into the bloodstream, either through secretion or after cell death. This results in fragments of DNA, known as cell-free DNA (cfDNA), circulating freely in the blood. In cancer patients, cfDNA originates not only from healthy cells but also from tumor cells, offering a non-invasive way to detect and monitor cancer through blood sampling—a technique called liquid biopsy. This approach has gained significant attention for its potential in early cancer detection and real-time monitoring of disease progression during treatment.

Our research aims to identify cancer-specific biomarkers within cfDNA to improve diagnostic precision and treatment monitoring. Our team focuses on a specialized subset of cfDNA derived from telomeres.

Telomeres are the protective ends of chromosomes, crucial in maintaining genomic stability, and their length and sequence are often altered in cancer. These changes can differ significantly across cancer types, reflecting the unique telomere dynamics of various tumors. To harness this information, our team is developing advanced bioinformatics algorithms to detect telomeric DNA fragments circulating in the bloodstream of cancer patients. By identifying and analyzing these cancer-associated telomeric alterations, we aim to improve cancer diagnostics and deepen our understanding of tumor biology.

The preliminary results of our team have been presented by Lilit Nersisyan at the EMBO Workshop “Telomere Function and Evolution in Health and Disease” in Rome, Italy.



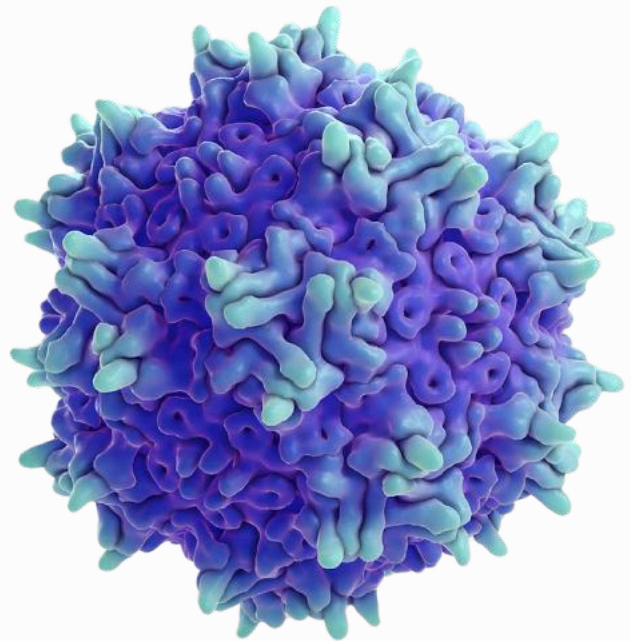
GENE THERAPIES: DESIGNING VEHICLES FOR DISEASE CURE

Certain diseases arise due to the absence of a functional gene in specific tissues, preventing normal biological function. Gene therapies provide a promising treatment by delivering a functional gene copy to the target tissue using viral vectors. However, the high cost of manufacturing these viral vectors significantly impacts the overall expense of gene therapies. For example, the recently approved gene therapy for Haemophilia B, a rare genetic bleeding disorder, has been recognized as the most expensive drug on the market, priced at \$3.5 million per dose. This underscores the urgent need to optimize viral vector production, improve delivery efficiency, and reduce costs.

This year, we concluded a study in collaboration with the Wyss Institute at Harvard University and Rejuvenate Bio, a U.S.-based company, aimed at designing more cost-effective viral vectors for age-related diseases. Through targeted genetic modifications, our collaborators generated a diverse array of modified adeno-associated viral (AAV) vectors and identified the most efficient ones for gene delivery.

Analyzing these vectors remains a challenge. To address this, we developed a computational tool called *hafoe* to assist in the analysis and selection of the most effective chimeric vectors for targeted therapies. Using novel datasets, we applied *hafoe* to identify new AAV variants capable of targeting specific cells in humans and animals, such as immune cells and tissue types like skin and muscle.

We have released the software on GitHub at: <https://github.com/abi-am/hafoe>



Tatevik Jalatyan, Erik Aznauryan, Rokib Hasan, Valeri Vardanyan, Stepan Nersisyan, David Thompson, Noah Davidsohn, Simon van Haren, Jenny Tam, Denitsa Milanova, George Church, Lilit Nersisyan. ***hafoe: an interactive tool for the analysis of chimeric AAV libraries after random mutagenesis.*** *Under review.*

PUBLICATIONS

Turnbull K, Paternoga H, von der Weth E, Egorov AA, Pochopien AA, Zhang Y, *et al.* **The ABCF ATPase New1 resolves translation termination defects associated with specific tRNAArg and tRNALys isoacceptors in the P site.** *Nucleic Acids Res.* 2024;52:12005–20.

Hakobyan A, Meyenberg M, Vardazaryan N, Hancock J, Vulliard L, Loizou JI, *et al.* **Pan-cancer analysis of the interplay between mutational signatures and cellular signaling.** *iScience.* 2024;27:109873.

Konecny T, Asatryan A, Nikoghosyan M, Binder H. **Unveiling Iso- and Aniso-Hydric Disparities in Grapevine—A Reanalysis by Transcriptome Portrayal Machine Learning.** *Plants.* 2024; 13(17):2501.

Hakobyan M, Binder H, Arakelyan A. **Pan-cancer analysis of telomere maintenance mechanisms.** *Journal of Biological Chemistry.* 2024;300(6):107392.

Schmidt M., Avagyan S., Reiche K., Binder B., Loeffler-Wirth H. **A Spatial Transcriptomics Browser for Discovering Gene Expression Landscapes across Microscopic Tissue Sections.** *Current Issues in Molecular Biology.* 2024;46(5):4701-4720.

Arakelyan A, Avagyan S, Kurnosov A, Mkrтчyan T, Mkrтчyan G, Zakharyan R, R Mayilyan K, Binder H. **Temporal changes of gene expression in health, schizophrenia, bipolar disorder, and major depressive disorder.** *Schizophrenia.* 2024;10(19).

Martirosyan A, Ansari R, Pestana F, Hebestreit K, Gasparyan H, Aleksanyan R, *et al.* **Unravelling cell type-specific responses to Parkinson's Disease at single cell resolution.** *Molecular Neurodegeneration.* 2024;19:1–24.

Davitavyan S, Martirosyan G, Mkrтчyan G, Chavushyan A, Melkonyan A, Ghazaryan H, Binder H, Arakelyan A. **Integrated analysis of -omic landscapes in breast cancer subtypes.** *F1000Research.* 2024;13(564).

RESEARCH: PARTNERS AND FUNDING

COLLABORATIONS



Institute of Molecular Biology
National Academy of Sciences of Armenia



YEREVAN
STATE
UNIVERSITY



Universiteit
Utrecht



University of Nevada, Reno



Karolinska
Institutet



Universitätsklinikum
Leipzig
Anstalt öffentlichen Rechts

FUNDING



Ritual Dental

agenus

04

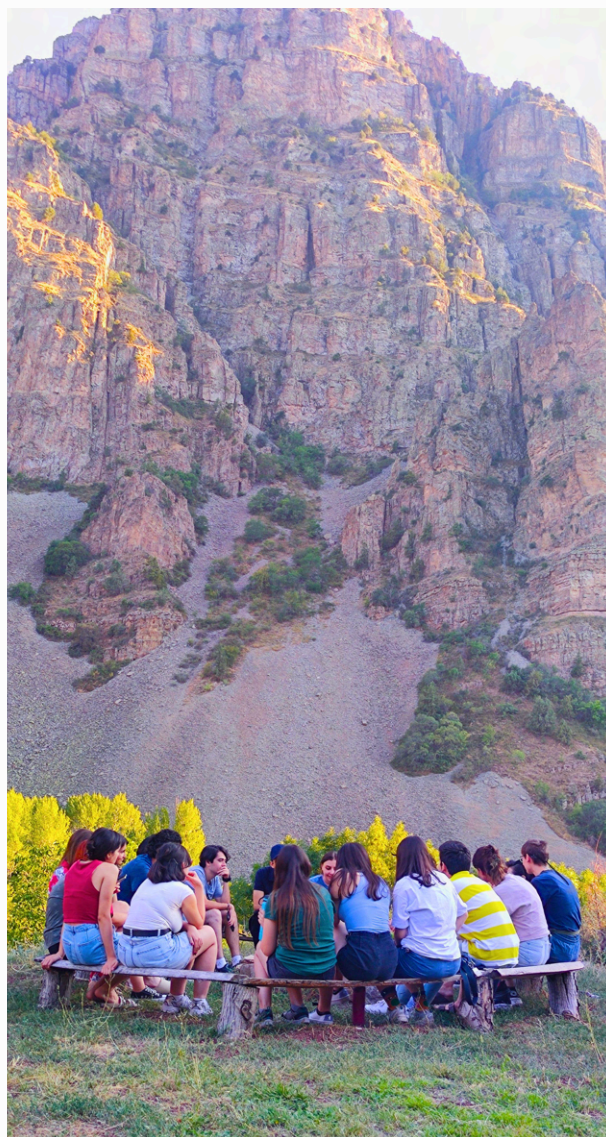
TRAINING

OMICSS-24 SUMMER SCHOOL IN GENOME BIOINFORMATICS

The third edition of the OMICSS summer schools, focused on introducing newcomers to bioinformatics, took place from June 21 to August 24, 2024. The program covered basic topics in molecular biology, programming, statistics, sequencing technologies, and genomics data analysis. A total of 21 students were enrolled, including 2 students from Russia, 1 from Germany and 1 from Sweden and 11 completed the full course. The students who applied came from universities such as the National Polytechnic University of Armenia (NPUA), American University of Armenia (AUA), Yerevan State Medical University (YSMU), Russian-Armenian University (RAU), Yerevan State University (YSU), University of French-Armenian Relations (UFAR), and other institutions. The students were guided by 5 lecturers, 19 guest lecturers, and 9 mentors from institutions such as ABI (Armenia), the University of Copenhagen (Denmark), Stanford University (USA), Janssen PRD (USA), the Medical University of Vienna (Austria), the University of Southern California (USA), Harvard Wyss Institute (USA), Thomas Jefferson University (USA), KU Leuven (Belgium), Flagship Pioneering (Armenia), Stanford Burnham (USA), IMB (Armenia), Johns Hopkins University (USA), Harvard Medical School (USA), and the University of Pennsylvania (USA), Penn State University (USA), Utrecht University (Netherlands), YerevaNN (Armenia) and Ayb School (Armenia).

This summer school provides an important opportunity for students to gain practical knowledge and skills in bioinformatics, preparing them for careers in the growing fields of data science and biotechnology. Throughout the course, the ABI team provided mentorship, offering hands-on guidance and continuous support through stand-up meetings, one-on-one sessions, office hours, and peer-to-peer discussions.

The school concluded with a bootcamp where students applied what they had learned by working on their first bioinformatics projects titled “Exploring Treatment Resistance in Colorectal Cancer at the Single-Cell Level”, “Cell-free DNA and telomeres as cancer biomarkers”, “Finding loci associated with resistance to downy and powdery mildew in grapevine” and “The effects of smoking on the composition of oral microbiome”.



TRAINING

We also had a Career Day closer to the end of the program, where representatives from ABI, IMB, and BostonGene presented their work, discussed ongoing projects and labs, and talked about potential internship opportunities. After the bootcamp, DeepOrigin invited the participants to their office for a tour, giving them a closer look at their work and facilities.

Partners and Sponsors of the program included:



Institute of Molecular Biology
National Academy of Sciences of Armenia

DigitalLife

Project funded by BMBF (Germany) &
Higher Education & Science Committee RA

BostonGene

 **DeepOrigin**



Following the successful completion of the course, five students pursued internships, and three of them later secured positions at ABI.

MENTORS:

1. Maria Nikoghosyan (ABI, Armenia)
2. Siras Hakobyan (ABI, Armenia)
3. Susanna Avagyan (Stanford, Newman Lab, USA)
4. Lilit Nersisyan (ABI, Armenia)
5. Razmik Sargsyan (ABI, Armenia)
6. Emma Hovhannisyan (ABI, Armenia)
7. Nelli Vardazaryan (ABI, Armenia)
8. Arik Avagyan (YerPhy, Armenia)
9. Arpine Grigoryan (ABI, Armenia)
10. Meline Mkrtychyan (ABI, Armenia)
11. Davit Tarverdyan (ABI, Armenia)
12. Melina Tamazyan (ABI, Armenia)

LECTURERS:

1. Aleksey Kurnosov, PhD (RAU, Armenia)
2. Pesho Ivanov, PhD (Penn State University, USA)
3. Vahan Huroyan, PhD (YerevaNN, Armenia)
4. Chrats Melkonian (Utrecht University, The Netherlands)
5. Meri Hovsepyan (Ayb School, Armenia)
6. Lusine Adunts (ABI, Armenia)
7. Gayane Aydinyan (ABI, Armenia)

GUEST SPEAKERS:

1. Arsen Arakelyan, PhD (ABI, IMB NAS RA, Armenia)
2. Roza Selimyan (Johns Hopkins University, USA)
3. Antranig Wardanean (ABI, Armenia)
4. Araks Martirosyan (KU Leuven, Belgium)
5. Aram Adourian (Flagship Pioneering, USA)
6. Andrei Osterman (Sanford Burnham, USA)
7. Ashot Margaryan (University of Copenhagen, Denmark)
8. Stepan Nersisyan (Thomas Jefferson University, USA)
9. Anna Hakobyan (Medical University of Vienna, Austria)
10. Vardges Tserunyan (University of Southern California, USA)
11. Haig Eskandarian (Harvard Medical School, USA)
12. Lilit Grigoryan (Stanford University, USA)
13. Jonathan Schug (University of Pennsylvania, USA)
14. Erik Aznauryan (Wyss Institute, Harvard, USA)
15. Chiara Sabatti (Stanford University, USA)
16. Aaron Newman (Stanford University, USA)
17. Davit Sargsyan (Janssen PRD (J&J), USA)
18. Alexandre Persat (EPFL, Switzerland)

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3. Tamara Sirunyan (IMB, Armenia)
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5. Luiza Stepanyan (ABI, Armenia)
6. Sveta Mnatsakanyan (ABI, Armenia)

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1. Lilit Nersisyan (Founding Director of ABI, Armenia)
2. Maria Nikoghosyan (IMB NAS, ABI, Armenia)
3. Araz Chiloyan (ABI, Armenia)
4. Karine Shahgaldyan (ABI, Armenia)
5. Tatev Grigoryan (ABI, Armenia)

BIOINFORMATICS GUIDE 2024

On December 13, the ABI Bioinformatics Guide 2024 was made available online for public use. This comprehensive resource offers essential knowledge and practical skills in bioinformatics and genomics, specifically designed for beginners. Drawing from materials and expertise shared at ABI's annual summer schools (OMICSS-21, 22, and 24), the guide provides a solid foundation for individuals from both biology and data science backgrounds to start their first bioinformatics projects.

The Guide

ADVANCED MOLECULAR BIOLOGY COURSE



Dr. Aleksey Kurnosov

The second round of the six-month Advanced Molecular Biology course covered core concepts such as molecular and cellular biology, genomes, and genetic mechanisms. Topics included DNA replication, membrane structure, cell communication, and more. Dr. Aleksey Kurnosov, a Molecular Biologist with expertise in bioinformatics and genetics, led the course. The course kicked off on February 16th with a vibrant group of approximately 20 students. Dr. Kurnosov's guidance provided students with a deep understanding of the molecular principles that underpin life.

CAPSTONES

In 2024, several ABI researchers graduated from their university programs, defending theses based on the projects they worked on at ABI:



Lusine Adunts



Bachelor's degree in Data Science,
American University of Armenia (AUA)



Project: "Deciphering the Temporal Changes in
Microbiome Communities"



Supervised by Dr. Lilit Nersisyan



Arpine Grigoryan



Bachelor's degree in Biophysics and Bioinformatics,
Yerevan State University (YSU)



Project: "Roles of Piezo and Thy-1 Genes in
Transcriptomic Regulation of Cell Mechanics"



Supervised by Dr. Hans Binder



Lilit Galstyan



Master's degree in Bioinformatics,
Russian-Armenian University



Project: "RNA Expression
Regulated by RNA Degradation"



Supervised by Dr. Lilit Nersisyan

05

INDUSTRY COLLABORATIONS

RITUAL DENTAL



In 2024, ABI entered into a collaboration with Ritual Dental, a US-based company focused on enhancing oral health care. This partnership aims to integrate ABI's bioinformatics expertise with Ritual Dental's patient-centered approach to create more personalized and effective dental care. By focusing on the role of the oral microbiome, the collaboration seeks to improve both dental health and overall well-being through better understanding of how oral bacteria contribute to disease. The primary objective of the partnership is to develop new bioinformatics tools to analyze the oral microbiome. This research will help link the composition of oral microbes to dental diseases and other health conditions, improving diagnostic accuracy and enabling more tailored treatment plans. The collaboration is expected to result in better preventative care, allowing for earlier detection of potential issues and more personalized interventions for patients.

AGENUS



Since 2022, ABI has been collaborating with AGENUS, a leading US-based biotech company specializing in immuno-oncology, to advance cancer treatment research. AGENUS is developing novel immunotherapies, targeting various cancers, including metastatic colorectal cancer (CRC). Despite promising clinical trial results, certain CRC patients remain unresponsive to these therapies, necessitating deeper investigation into resistance mechanisms. To support these efforts, ABI has established a dedicated team of researchers and students to explore the genomic and transcriptomic heterogeneity of cancer metastases. Utilizing cutting-edge bioinformatics and machine-learning techniques, the team analyzes large-scale omics data—including single-cell and spatial transcriptomics—to identify biomarkers and potential therapeutic targets.

VIVAN THERAPEUTICS



In 2024, ABI has continued its active partnership with Vivan Therapeutics, a UK-based startup specializing in precision medicine, which began in 2022. Vivan employs an innovative approach by using patient-specific tumor models in fruit flies. This enables high-throughput, unbiased drug screening to identify the most effective treatment combinations tailored to individual patients. These efforts focus on improving outcomes for various cancers by addressing the unique genetic makeup of each tumor. Dr. N. Borisov's group at ABI supports this groundbreaking work by providing bioinformatics and data science expertise. We use machine learning to identify optimal matches between mutational patterns and effective drug combinations. This collaboration plays a vital role in advancing personalized oncology and accelerating the discovery of novel cancer therapies.

06

**CONFERENCES,
EVENTS AND
MEDIA PRESENCE**

CONFERENCES, EVENTS AND MEDIA PRESENCE



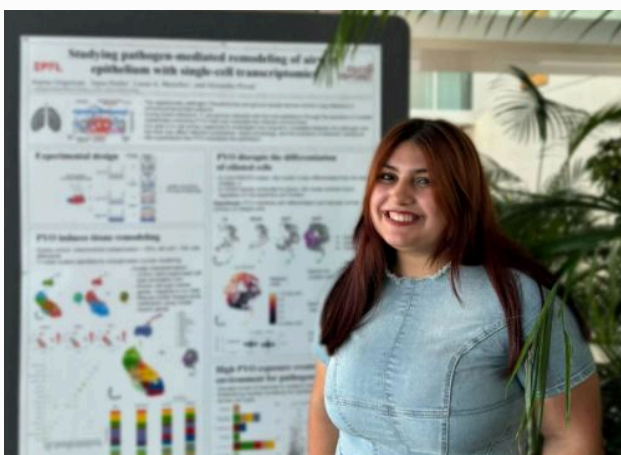
EXPLORING BACTERIAL DYNAMICS: NELLI VARDAZARYAN AT UTRECHT UNIVERSITY

In early 2024, Nelli Vardazaryan joined the Bioinformatics Lab at the Biology Department of Utrecht University, under the supervision of Dr. Chrats Melkonian. During her three-month internship, she focused on studying bacterial community dynamics in health and disease. The project was funded by the Young Scientists Support Program.



LILIT NERSISYAN AT THE TELOMERE FUNCTION CONFERENCE IN ROME

In May (6th-11th), 2024, Lilit Nersisyan participated in the *Telomere Function and Evolution in Health and Disease* conference in Rome, Italy. She presented her team's research on finding telomere-related biomarkers of cancer from blood plasma samples. This research is primarily carried out by Meline Mkrtychyan, Davit Tarverdyan and Anahit Yeghiazaryan.



INVESTIGATING AIRWAY EPITHELIUM: ARPINE GRIGORYAN AT EPFL

Arpine Grigoryan, ABI researcher, completed an 8-week Summer Research Program at EPFL in Switzerland, where she investigated pathogen-mediated remodeling of airway epithelium using single-cell transcriptomics in Persat Lab and presented her research at the final symposium.

CONFERENCES, EVENTS AND MEDIA PRESENCE



NELLI VARDAZARYAN PRESENTS BEE MICROBIOME RESEARCH AT SYMBNET CONFERENCE

Nelli Vardazaryan (PhD) from the ABI Nersisyan Lab presented her research at the 'SymbNET International Conference on Host-Microbe Symbiosis' in Olhão, Portugal. Her study, titled "The Effects of Geographical and Nutrient Variation on Bee Microbiome Composition: A Meta-analysis," conducted in collaboration with YSU, IMB, and Utrecht University, explored regional variations in bee gut bacteria and the impact of pesticides, herbicides, and supplements on bee health. The work was supported by Lusine Adunts (ABI) and other team members.



ABI AND IMB RESEARCHERS AT "GENOME BIOINFORMATICS FOR HEALTH" WORKSHOP

From June 12th to 14th, researchers from the ABI and the IMB attended the "Genome Bioinformatics for Health" workshop at the University of Leipzig's Interdisciplinary Centre for Bioinformatics (IZBI). The event, marking the launch of the DigitalLife project, focused on precision medicine, single-cell transcriptomics, and Armenian grapevine genetics. It was supported by the German Federal Ministry of Education and Research and the Foundation for Armenian Science and Technology (FAST).



ABI'S STORY PRESENTED AT HORIZONS IN MOLECULAR BIOLOGY SYMPOSIUM IN GERMANY

ABI Director Lilit Nersisyan spoke at the Horizons in Molecular Biology 2024 Symposium, held by the International Max Planck Research School at the Georg-August-Universität Göttingen from September 9–12. In her presentation, she shared ABI's journey with the international community, detailing its establishment, strategies for building bioinformatics research capacity in Armenia, securing funding, assembling a talented team, and leading impactful research and training initiatives.

CONFERENCES, EVENTS AND MEDIA PRESENCE



ABI AT SCIENCE WEEK: BIOINFORMATICS AND AI

At Science Week, ABI director Dr. Lilit Nersisyan discussed the impact of bioinformatics on research and innovation in Armenia. Anush Baloyan and Emma Hovhannisyan from the ABI team highlighted the role of AI in the field and presented the FAST ADVANCE research program on grapevine genomics.



HANS BINDER DISCUSSES SPATIAL SINGLE-CELL TRANSCRIPTOMICS AT ABI

On October 15, Dr. Hans Binder, a lab leader and Chairman at ABI, discussed Spatial Single-Cell Transcriptomics, named Method of the Year in 2020. He highlighted its impact on fields like precision oncology and developmental biology, focusing on challenges related to data complexity and its applications in studying cancer heterogeneity and treatment resistance.



LUSINE ADUNTS TALKS SCIENCE AND BIOINFORMATICS ON BOON TV

Lusine Adunts, an ABI researcher, was interviewed by Boon TV, where she discussed her passion for science and bioinformatics. She shared details of her current projects and highlighted the impact of bioinformatics on modern research.

CONFERENCES, EVENTS AND MEDIA PRESENCE



RAZMIK SARGSYAN TALKS ABOUT HIS JOURNEY INTO SCIENCE AND RESEARCH

Razmik Sargsyan, ABI researcher, talked about his journey into science during an interview. He shared his early interests, why he chose the Faculty of Biology, and the path that led him to his career in science. Razmik also spoke about the areas he has worked on and the impact of his studies.



LUSINE ADUNTS DISCUSSES MATHEMATICS AND SCIENTIFIC CURIOSITY

Lusine Adunts, ABI researcher, was interviewed about her work in applied mathematics and her collaboration with young science enthusiasts like Levon. She shared insights into her research and discussed the importance of curiosity in solving complex scientific problems.



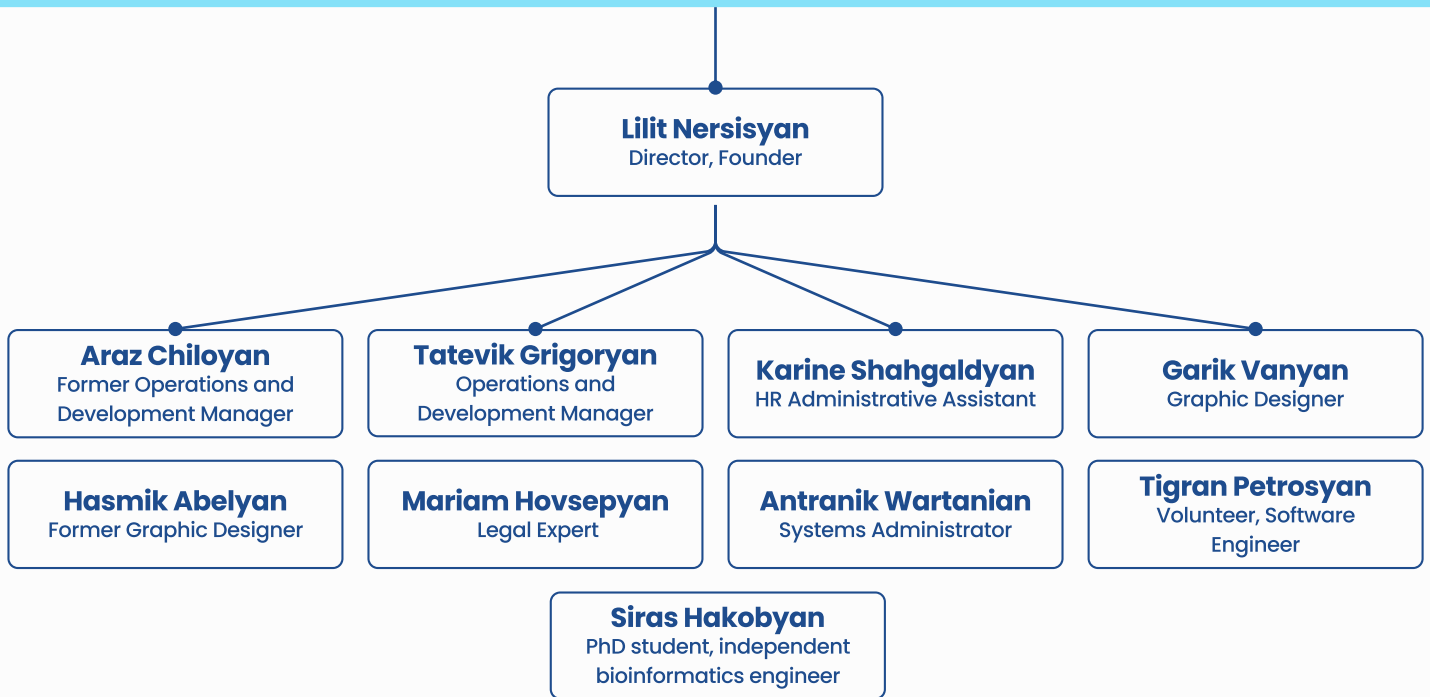
BIOINFORMATICS JOURNEY: INSIGHTS FROM LILIT NERSISYAN

Lilit Nersisyan, Director of ABI, shared insights in an interview on the Nzhar Podcast about her journey into bioinformatics, discussing how she arrived at the decision and the challenges involved. She talked about how bioinformatics is supporting science in Armenia and offered advice on choosing a career, emphasizing key indicators to determine if bioinformatics is the right path.

07

PEOPLE

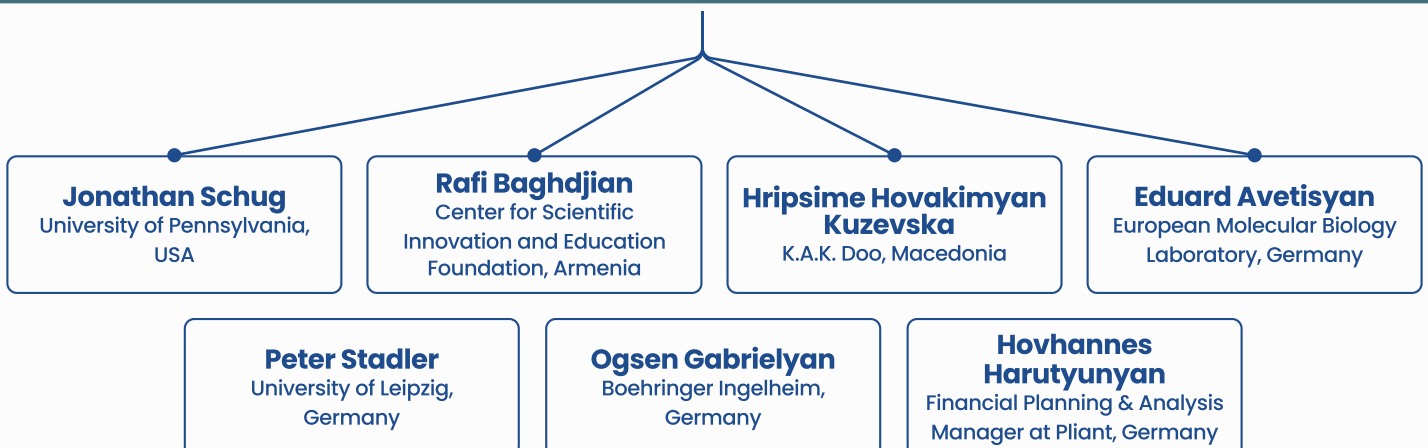
OPERATIONS



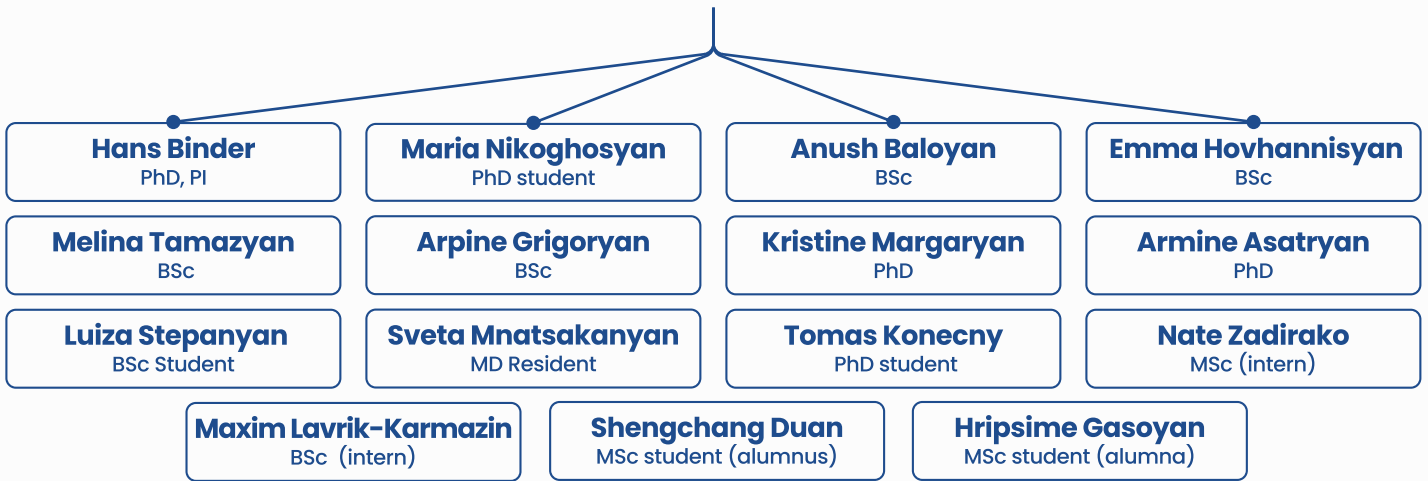
BOARD OF TRUSTEES



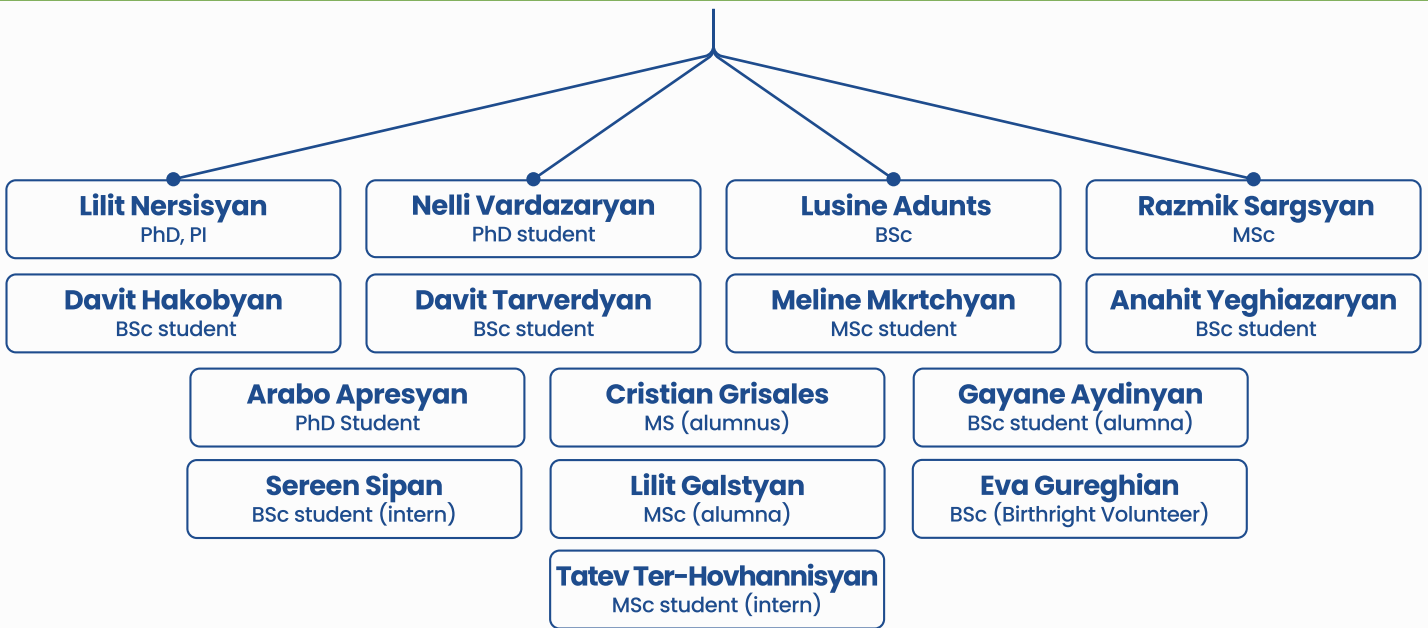
ADVISORS



RESEARCH STAFF: HANS BINDER LAB



RESEARCH STAFF: LILIT NERSISYAN LAB



VIVAN THERAPEUTICS LAB



08

NEW RESEARCH & TRAINING CENTER

NEW RESEARCH & TRAINING CENTER

In 2024, ABI secured \$70,000 in grants and donations to support the creation of a modern research and training facility at the Institute of Molecular Biology (IMB). These contributions include \$40,000 from the H. Hovnanian Family Foundation, \$20,000 from the Adobe Employee Community Fund, and \$10,000 from an anonymous donor. This initiative marks a significant step in ABI's expansion, enabling it to meet the needs of its growing team of over 20 researchers and staff.

The new facility, spanning two-floors and featuring nine rooms, including offices for lab leaders, meeting spaces, open workspaces, and areas for rest, is designed to promote collaboration and innovation, enhance ABI's training programs and bilateral collaborations with IMB. It will also serve as a welcoming space for international guests, partners, and interns.

The renovation is anticipated to conclude in 2025.



\$40,000

H. Hovnanian
Family Foundation



\$20,000

Adobe Employee
Community Fund



\$10,000

Anonymous donor

09

BUDGET

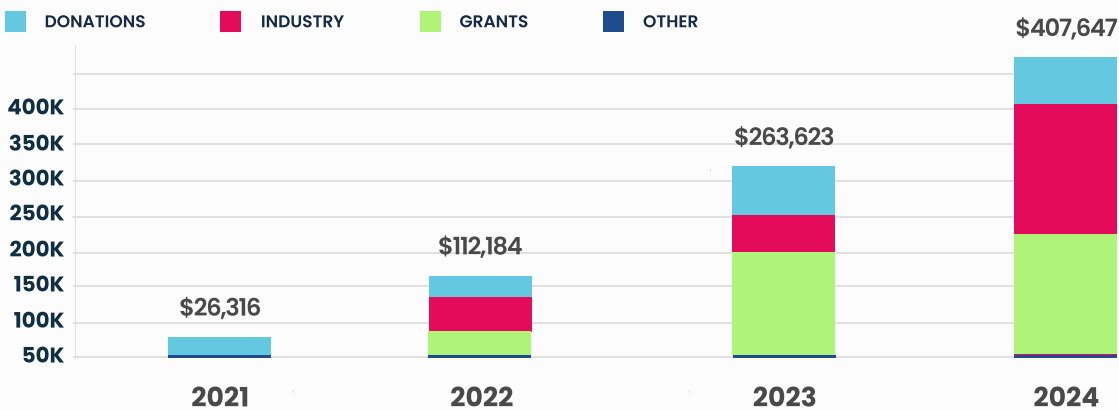
BUDGET

Our expanding budget supports the growth of our team and broadens the scope of our initiatives. As a private organization, we strive to diversify our funding streams to ensure the sustainability of our mission. Our work is made possible through the support of organizations that provide research and general support grants and donations, the financial backing of our industry partners, and generous contributions from individual supporters, some matched by tech companies. Invaluable support also comes from the in-kind contributions of individuals who voluntarily engage in research, training, and technical support. These efforts, though not reflected in our financial charts, are crucial for our activities, particularly during these foundational stages.

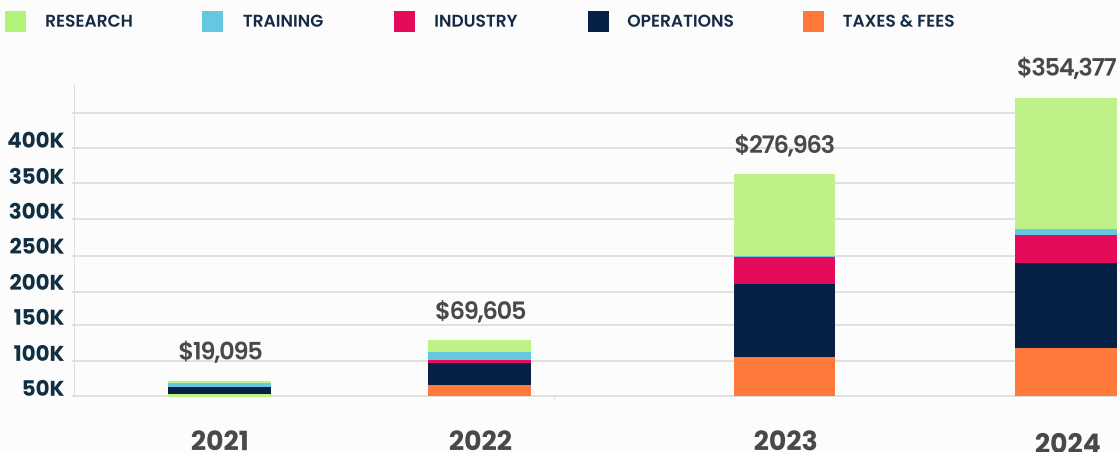
In 2024, our expenses primarily supported research activities and training initiatives. Notably, the training efforts, including the OMICSS-24 summer school, were largely made possible through voluntary contributions from ABI team members and the local and international community of researchers. Additionally, we allocated a significant portion of our expenses to operational tasks such as daily administration, system management of our compute node, and the renovation of our new research and training facility.

Looking ahead, we are committed to sustaining this momentum through strategic fundraising, strengthening industry collaborations, and securing international research grants.

INCOME (USD)



EXPENSES (USD)



BUDGET

COLLABS IN INDUSTRY



GRANTS



DONOR ORGANIZATIONS



MATCHED INDIVIDUAL DONATIONS THROUGH BENEVITY





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