Conference Abstract

2026 16th International Conference on Bioscience, Biochemistry and Bioinformatics (ICBBB 2026)

Kobe, Japan | January 16-19, 2026

Co-Organized by

Technical Supported by

www.icbbb.org

Table of Contents

Welcome Letter

Welcome to the 2026 16th International Conference on Bioscience, Biochemistry and Bioinformatics (ICBBB 2026)! We are delighted to welcome you to this distinguished event, which will be held in Kobe, Japan, during January 16–19, 2026.

ICBBB 2026 is co-organized by Kobe University and the Biology and Bioinformatics Society, and is technically supported by Chulalongkorn University, Khon Kaen University, Tokai University, Faculty of Pharmacy, Chiang Mai University, and Faculty of Allied Health Sciences, Chulalongkorn University. The conference aims to bring together researchers, scholars, and professionals to share cutting-edge advances, exchange innovative ideas, and discuss emerging challenges and technological developments shaping the future of life science research and biomedical applications.

ICBBB 2026 has received over 200 submissions from researchers across 18 countries and regions, including China, Chile, Colombia, Egypt, Hong Kong, India, Italy, Japan, Kazakhstan, Malaysia, the Philippines, Poland, the Republic of Korea, Saudi Arabia, South Africa, Taiwan, Thailand, and the United Kingdom, highlighting the strong international participation of the conference.

With a successful history spanning 15 years, the ICBBB conference series has been held annually to provide an interactive international forum for the presentation and discussion of research in bioscience, biochemistry, bioinformatics, and related interdisciplinary fields. ICBBB warmly welcomes participants from around the world who are interested in building professional ties and exploring collaboration and career opportunities across Japan and beyond. The conference also serves as an ideal platform to foster long-term relationships among researchers and practitioners from Japan and other regions worldwide.

We sincerely hope that the discussions and outcomes of ICBBB 2026 will contribute meaningfully to scientific progress and strengthen international cooperation among academic and industrial partners worldwide.

Once again, welcome to ICBBB 2026. We wish you a productive, inspiring, and memorable conference experience in Kobe.

Local Organizing Chair

Assoc. Prof. Shuhei Noda, Kobe University

Conference Venue

Integrated Research Center of Kobe University, Kobe, Japan

Web: http://www.ircpi.kobe-u.ac.jp/index.html

Addr: 7 Chome-1-48 Minatojima Minamimachi, Chuo Ward, Kobe, Hyogo 650-0047 Japan

Note: The registration fee does not cover the accommodation. The organizing group won't book hotels for participants. Please do not share your personal credit card information with unrelated persons.

➢ **Getting to the Venue (Integrated Research Center of Kobe University, Port Island)**

Nearest station: *Port Liner Keisan Kagaku Center (P08) (also shown as "K Computer Mae" on some maps)*
From South Exit, walk about 1 minute to the venue.

1. From Kobe Airport (UKB)

Take Port Liner (toward Sannomiya)→Get off at Keisan Kagaku Center (P08) (~5 min) → Walk ~1 min to the venue

2. From Kansai International Airport (KIX)

1. Option A (easy, fewer transfers):

Bay Shuttle (high-speed ferry) KIX → Kobe Airport (~30 min) →Then follow UKB route above

2. Option B (rail):

Train to Kobe-Sannomiya→Transfer to Port Liner (toward Kobe Airport) → Keisan Kagaku Center (P08) (~15 min from Sannomiya) →Walk ~1 min

3. From Osaka Itami Airport (ITM)

Airport limousine bus to Kobe-Sannomiya →(~40 min)Port Liner (toward Kobe Airport) → Keisan Kagaku Center (P08) (~15 min) →Walk ~1 min

➢ **Recommended Hotel:**

1. Kobe Portopia Hotel (4-star hotel)
   Addr.: 6 Chome-10-1 Minatojima Nakamachi, Chuo Ward, Kobe, Hyogo 650-0046, Japan
   Web.: https://www.portopia.co.jp/

2. Hotel Pearl City Kobe (3-star hotel)
   7 Chome-5-1 Minatojima Nakamachi, Chuo Ward, Kobe, Hyogo 650-0046, Japan
   Web.: https://go-hmihotelgroup.reservation.jp/en/hotels/pearlcity-kobe/plans

3. Ariston Hotel Kobe (3-star hotel)
   Addr.: 6 Chome-1 Minatojima Nakamachi, Chuo Ward, Kobe, Hyogo 650-0046, Japan
   Web.: https://www.ariston.jp/kobe/en/

4. Kobe Sannomiya Tokyu REI Hotel (3-star hotel)
   Addr.: 6 Chome-1-5 Kumoidori, Chuo Ward, Kobe, Hyogo 651-0096, Japan
   Web.: https://www.tokyuhotels.co.jp/kobesannomiya-r/index.html

Conference Committee

Assoc. Prof. Zeti A. M. Hussein, National University Of Malaysia (UKM)
Assoc. Prof. Yun-Ju Chuang, Ming Chuan University
Asst. Prof. Dr. Sirikalaya Brimson, Chulalongkorn University
Assoc. Prof. Young-Won Choi, Dongguk University
Assoc. Prof. Jayantha Gunaratne, A*STAR
Assoc. Prof. Xin Gao, King Abdullah University of Science and Technology
Assoc. Prof. Toni Anwar, Universiti Teknologi Malaysia
Prof. Xiaodan Fan, The Chinese University of Hong Kong
Assoc. Prof. Max Alekseyev, George Washington University
Assoc. Prof. Zurinahni Zainol, Universiti Sains Malaysia
Assoc. Prof. Tzu-Hao Chang, Taipei Medical University
Assoc. Prof. Wen-Ling Chan, Asia University
Assoc. Prof. Chia-Ling Lee, Ming Chuan University
Assoc. Prof. Jie Yang, Dalian University of Technology
Assoc. Prof. Zhifu Sun, Mayo Clinic (Rochester, MN)
Assoc. Prof. Ahmad M. Syarhabil, Universiti Malaysia Perlis
Asst.Prof.Dr. Kamonlak Leecharoenkiat, Chulalongkorn University
Dr. Chandana Tennakoon, The Pirbright Institute
Dr. Woo Chiat Tei, Universiti Malaysia Terengganu
Dr. Nuttachat Wisittipanit, Mae Fah Luang University
Dr. Murat Gok, Yalova University
Dr. Xiaochuan Liu, Rutgers University
Asst. Prof. Dr. Anchalee Techasen, Khon Kaen University
Dr. Monalisha Saikia Borah, Asian Institute of Management & Technology
Dr. Neelabh Srivastava, Banaras Hindu University (BHU)
Dr. Lili Jiang, Dalian University of Technology
Dr. Tongyi Dou, Dalian University of Technology
Dr. Asaad Gaber, Mansoura University
Dr. Suresh Kumar, Management and Science University
Dr. Lu Bingxin, Genome Institute of Singapore
Dr. Anand Duraiswamy, Hexacara Laboratories
Prof. Dulani Meedeniya, University of Moratuwa
Dr. Aarti Jajoo, Baylor College of Medicine
Assoc. Prof. Ziyan Wang, University of Electronic Science and Technology of China
Assist. Prof. Hemant Sharma, National Institute of Technology Rourkela
Dr. Kah Keng Wong, Universiti Sains Malaysia
Assist. Prof. Brajesh Kumar Jha, Pandit Deendayal Petroleum University
Assist. Prof. Amrita Jha, Indus University
Prof. Koen Bertels, Delft University of Technology

Assoc. Prof. Hiroshi Yamaguchi, Tokai University
Prof. Qingyu He, Jinan University
Dr. Renmin Han, King Abdullah University of Science and Technology
Prof. Balasundaram Padmanabhan, National Institute of Mental Health and Neuro sciences
Assoc. Prof. Junpeng Bao, Xi'an Jiaotong University
Prof. Junfeng Xia, Anhui University
Prof. Hung-Yi Lin, National Taichung University of Science and Technology
Assoc. Prof. Liang Gong, Shanghai Jiao Tong University
Assoc. Prof. Chuan Chen, Meiho University
Assist. Prof. Aleksandar Shurbevski, Kyoto University
Assoc. Prof. Pensak Jantrawut, Chiang Mai University
Assist. Prof. Willy Hugo, University of California
Assoc. Prof. Malinee Sriariyanun, King Mongkut's University of Technology North Kobe
Assoc. Prof. Emrah Caylak, Cankiri Karatekin University
Assist. Prof. Joel P. Arrais, University of Coimbra
Dr. Mohammad Moneruzzaman Khandaker, University Sultan Zainal Abidin
Prof. Hideo Matsuda, Osaka University
Assist. Prof. Anuraj Singh, India Institute and Information Technology and Management
Prof. Huai-Kuang Tsai, Academia Sinica
Dr. Nazanin Zounemat Kermani, Imperial College London
Assist. Prof. Panchika Prangkio, Chiang Mai University
Prof. Yangli Jia, Liaocheng University
Prof. Leon Canseco Carlos, Universidad Carlos III de Madrid
Prof. Shyh Ming Kuo, I-Shou University
Assoc. Prof. Supakit Khacha-ananda, Chiang Mai University
Prof. Lemmuel L. Tayo, Mapua University
Prof. A. Velayudham, Jansons Institute of Technology
Prof. Tzu-Ching Shih, China Medical University
Dr. Xueyan Mei, Icahn School of Medicine at Mount Sinai
Assoc. Prof. An-Chi Wei, NTU
Prof. Hsiuying Wang, National Yang Ming Chiao Tung University
Assist. Prof. Apaporn Menakongka, Navamindradhiraj University
Dr. Wen-chang Lin, Case Western Reserve University
Dr. Peize Zhao, Hong Kong University of Science and Technology
Dr. Bongkoch Turathum, Mahidol University
Prof. Chih-En Kuo, National Chung Hsing University
Assoc. Prof. Rui Camacho, FEUP & INESC-TEC
Prof. Max Leong, National Dong Hwa University
Assoc. Prof. Asita Elengoe, Lincoln University College

Assist. Prof. Yongmin Jeon, Gachon Univeristy
Assoc. Prof. Asita Elengoe, Lincoln University College
Assoc. Prof. Heherson S. Cabrera, Mapua University
Dr. Kefei Li, Cornell University
Assoc. Prof. Jin-Ku Lee, Seoul National University
Assist. Prof. Alicia Lai Yee Ho, Tunku Abdul Rahman University
Prof. Kyoung-Yong Chun, Korea University
Dr. Siti Azma Jusoh, Universiti Teknologi MARA
Assist. Prof. Rainier Ulrich D. Velasco, University of the City of Manila
Dr. Fatahiya Mohamed Tap, University of Technology Malaysia
Prof. Saravana Prakash Thirumuruganandham, Technological University Indoamerica
Dr. Wan Maznah binti Wan Ishak, Universiti Malaysia Pahang Al-Sultan Abdullah
Assoc. Prof. Hon Cheong So, The Chinese University of Hong Kong
Prof. Shwu-Jen Chang, I-Shou University
Assoc. Prof. Yanni Sun, City University of Hong Kong
Assoc. Prof. Jin Liu, The Chinese University of Hong Kong (Shenzhen)
Prof. Sakda Daduang, Khon Kaen University
Assist. Prof. Jarunee Jungklang, Chiang Mai University
Prof. Shwu-Jen Chang, I-Shou University
Dr. Anooja Ali, REVA University
Assoc. Prof. Atit Silsirivanit, Khon Kaen University
Assoc. Prof. Ruslizam Daud, Universiti Malaysia Perlis
Assoc. Prof. Siriporn Proungvitaya, Khon Kaen University
Assist. Prof. Chih-Yang Wang, Taipei Medical University
Dr. Pornsuda Maraming, Khon Kaen University
Dr. Gamal Nasser Abdel-Hady, Hiroshima University
Prof. Adanela Musaraj, University of Pennsylvania
Assist. Prof. Myeong Gyu Kim, Ewha Womans University
Prof. M. Theradimani, Tamil Nadu Agricultural University
Dr. Vipendra Kumar Singh, The George Washington University
Asst. Prof. Dr. Viroj Boonyaratanakornkit, Chulalongkorn University
Asst. Prof. Dr. Attawut Chaibunruang, Khon Kaen University
Asst. Prof. Dr. Siriporn Jitkaew, Chulalongkorn University
Assoc. Prof. Dr. Panan Ratthawongjirakul, Chulalongkorn University
Assoc. Prof. Dr. Panan Ratthawongjirakul, Chulalongkorn University
Asst. Prof. Supaporn Phadungkit, Khon Kaen University
Asst. Prof. Dr. Pattarin Tangtanataku, Chulalongkorn University
Dr. AbhishekNarain Singh, E-Yuva Centre, Career College
Prof. Anastasia I. Lavrova, Saint-Petersburg State Research Institute of Phthisiopulmonology

Prof. Eugene B. Postnikov, Kursk State University

Dr. Sudarshana Deepa Vijaykumar, National Institute of Technology

Prof. Abdel Qader Al Bawab, Al-Zaytoonah University of Jordan

Asst. Prof. Nadia Tahiri, University of Sherbrooke

Dr. Priya Ramarao-Milne, Australian e-Health Research Centre, Commonwealth Scientific and Industrial Research Organisation

Assoc. Prof. Nguyen Quang Duc Tien, University of Sciences, Hue University

Dr. Le Thi Ha Thanh, University of Sciences, Hue University

Prof. Liang Wang, Southern Medical University affiliated Guangdong Provincial People's Hospital

Dr. Wen Chen, AO Foundation

Assoc. Prof. Zulhabri Othman, Manipal University College Malaysia

Assoc. Prof. Krishna Joshi, Atmiya University

Asst. Prof. Siew-Ying Mok, Universiti Tunku Abdul Rahman

Presentation Guidelines

Presentation Requirement

- At least one author should present for each abstract/full paper during the session.

Tips for Presentation

- English is the official language.
- Get your presentation PPT/Slides prepared.
- Keynote Speech: about 25 minutes of presentation and 5 minutes of Q&A.
- Invited Speech: about 15 minutes of presentation and 5 minutes of Q&A.
- Oral Presentation: about 12 minutes of presentation and 3 minutes of Q&A.
- One Best Oral Presentation will be selected from each session and announced at the end of the session.

Onsite Presentation Instructions

- Devices Provided by the Conference Organizer
- Laptop Computer (MS Windows Operating System with MS PowerPoint and Adobe Acrobat Reader). (b) Digital Projectors and Screen. (c) Laser Pointer. (d) Materials Provided by the Presenters: PowerPoint or PDF Files (Files should be copied to the Conference laptop at the beginning of each Session.)
- Instructions for Poster Presentation

Materials Provided by the Conference Organizer: The place to put posters. Materials Provided by the Presenters: (a) Home-Made Posters: Submit the poster to the staff when signing in. (b) Maximum poster size is A1. (c) Load Capacity: Holds up to 0.5 kg.

- Conference Material

All presented papers will be issued with hard/soft copy of conference materials: Receipt/Invoice, Participation and Presentation Certificate, Conference Program Book, etc.

Personal Insurance

- Along with your registration, you will receive your name badge, which must be worn when attending all conference sessions and activities. Participants without a badge will not be allowed to enter the conference venue.

- For your safety, please do not lend your name badge to the persons who are not involved in the conference and bring the unregistered persons into the conference venue.

- The conference organizers cannot accept liability for personal injuries, or for loss or damage of property spacing to conference participants, either during, or as a result of the conference. Please check the validity of your own insurance.

Online Presentation Instruction

- Equipment Needed:

  (a) Computer with an internet connection (wired connection recommended). (b) USB plug-in headset with a microphone (recommended for optimal audio quality). (c) Webcam (optional): built-in or USB plug-in. (d) Please set up your laptop time in advance.

- Download the ZOOM:

  https://zoom.us/download; https://www.zoom.com.cn/download .

- Learn the ZOOM skills:

  https://support.zoom.us/hc/en-us/articles/201362033-Getting-Started-on-Windows-and-Mac

- How to use ZOOM:

  (a) Set the language. (b) Test computer or device audio. (c) Join a meeting: Join the meeting with the "meeting ID" provided in the program, tap the name as "paper ID + name", e.g.: "BJ0001-XX", then click "Join". (d) Get familiar with the basic functions: Rename, Chat, Raise Hands, Start Video, Share Computer Sound and Share Screen, etc.

- Test Session:

  On Jan. 16, there are test session. On that day, all the above functions will be taught including how to use ZOOM. If you don't know how to use, please do not worry. However, please do download ZOOM and log in the meeting room in advance, then, you can join the conference.

- Voice Control Rules during the Presentation:

  (a) The host will mute all participants while entering the meeting. (b) The host will unmute the speakers' microphone when it is turn for his or her presentation. (c) Q&A goes after each speaker, the participant can raise hand for questions, the host will unmute the questioner. (d) After Q&A, the host will mute all participants and welcome next speaker.

- Conference Material:

  All presented papers will be issued with soft copy of conference materials: Receipt/Invoice, Participation and Presentation Certificate, etc.

- Note:

  (a) Log in the meeting room 15 minutes ahead of the session. (b) Learn the zoom skills. (c) Your punctual arrival and active involvement in each session will be highly appreciated. (d) Since the conference will be recorded, we will appreciate your proper behavior.

Contact Us

Contact us by email: icbbb@cbees.org for any inquiries.

Agenda Overview

Day 1, January 16, 2026, Friday (GMT+9)

Duration	Event	Venue
10:00-16:00	Arrival Registration & Conference Material Collection	Meeting Room (5F)
Note: the arrival registration can be done on Jan. 17, 2026.		

Duration	zoom **Meeting ID:** 893 3803 2428 **Link:** https://us02web.zoom.us/j/89338032428
14:30-14:40	**Online Test for** Dr. Siti Syairah Mohd Mutalip
14:40-16:00	**Online Test for** **Online Session- Bioactive Materials, Nanotechnology, and Data-Driven Biomedical Applications** KB0063, KB0137, KB0093, KB1017, KB0111, KB0138, KB0075, KB0104, KB2001-A, KB2024, KB0147, KB1019, KB0119-A

Note: This online testing session is only intended for authors who will attend the conference virtually. Onsite participants do not need to join this session.

Day 2, January 17, 2026, Saturday (GMT+9)-Morning

Duration	Event	Venue
09:00-09:10	**Opening Remarks** Prof. Tomohiro Araki, Tokai University	Convention Hall
09:10-09:40	**Keynote Speaker I** Asst. Prof. Tewin Tencomnao, Chulalongkorn University Speech Title: "Integrated Model Approaches for Identifying Natural Products Against Neurodegeneration and Ageing"	
09:40-10:10	**Keynote Speaker II** Prof. Sun Kim, Seoul National University Speech Title: "Decoding Complex Interactions in Biology and Medicine with Deep Learning Technologies"	
10:10-10:40	**Group Photo & Coffee Break**	
10:40-11:10	**Keynote Speaker III** Assoc. Prof. Ka-Chun Wong, City University of Hong Kong Speech Title: "AI in Omics: DNA Shape Motifs and Protein Peptides"	Convention Hall
11:10-11:30	**Invited Speaker I** Prof. Liang Wang, Guangdong Provincial People's Hospital/ Southern Medical University Speech Title: "Application of Artificial Intelligence in Medical Laboratories: Opportunities and Challenges"	
11:30-11:50	**Invited Speaker II** Prof. Chanchal Mitra, University of Hyderabad Speech Title: "Diabetes Mellitus and Personalization of Medical Care"	
11:50-13:20	**Lunch---Venue: Lounge**	

Day 2, January 17, 2026, Saturday (GMT+9)-Afternoon

Venue 1

Duration	Event	Venue
13:20-15:35	**Oral Session 1-Bioinformatics and Biomedical Data Science** KB0029-A, KB0039, KB0067-A, KB0082, KB0085, KB0118, KB2002-A, KB0058, KB0061	Lounge
15:35-15:50	**Coffee Break**	
15:50-18:05	**Oral Session 2- Computational Biochemistry and AI-Enabled Molecular Design** KB0020, KB0021, KB0028-A, KB0031, KB0040-A, KB0055-A, KB0070, KB2014-A, KB0145-A	Lounge

Venue 2

Duration	Event	Venue
13:20-15:35	**Oral Session 3- Microbiology, Virology, and Antimicrobial Biochemistry** KB0084-A, KB0016-A, KB0086, KB0109-A, KB0091, KB0110-A, KB0112, KB0114-A, KB1010-A	208 Seminar Room
15:35-15:50	**Coffee Break**	
15:50-18:05	**Oral Session 4- Bioscience of Immunity, Inflammation, and Disease Mechanisms** KB0034-A, KB0005, KB0094-A, KB0024-A, KB1012-A, KB0054-A, KB1018-A, KB2015-A, KB2021-A	208 Seminar Room

Venue 3

Duration	Event	Venue
13:20-15:05	**Oral Session 5- Biomaterials, Biotechnology, and Environmental Bioscience** KB0037, KB0071-A, KB0106-A, KB0130, KB0131, KB2029-A, KB0132	303 Seminar Room
15:05-15:30	**Coffee Break**	
15:30-17:30	**Oral Session 6-Bioactive Compounds, Biotechnologies and Biomedical Applications** KB0019-A, KB0108-A, KB0059-A, KB0103-A, KB0023-A, KB0041-A, KB0098-A, KB0136-A	303 Seminar Room

Venue 4

Duration	Event	Venue
14:00-15:40	**Poster Session 1-Biomedical Data Analysis and Computational Bioscience** KB0033-A, KB0035-A, KB0036-A, KB0076-A, KB0077-A, KB0080-A, KB1016-A, KB2027-A, KB0081-A, KB0121-A	Back of the Lounge
	Poster Session 2- Nanomaterials & Bioactive Platforms in Biomedicine KB0045-A, KB0049-A, KB0052-A, KB0122-A, KB0134-A, KB0144-A, KB2009-A, KB2025-A, KB0125-A, KB0065-A, KB0032-A, KB2019-A	
15:40-16:00	**Coffee Break**	
16:00-17:40	**Poster Session 3- Disease Mechanisms and Therapeutic Modulation** KB0007-A, KB0008-A, KB0050-A, KB0051-A, KB0057-A, KB0135-A, KB0139-A, KB0017-A, KB0126-A, KB0038-A, KB0083-A	Back of the Lounge
	Poster Session 4- Molecular Regulation and Functional Mechanisms KB0014-A, KB0025-A, KB0062-A, KB0064-A, KB0073-A, KB0102-A, KB0074-A, KB0105-A, KB0123-A, KB0069-A	
18:20-20:20	**Dinner**	

Day 3, January 18, 2026, Sunday (GMT+9)

Meeting ID: 893 3803 2428 Link: https://us02web.zoom.us/j/89338032428	
09:40-10:00	**Invited Speaker III** Dr. Siti Syairah Mohd Mutalip, Universiti Teknologi MARA (UiTM) Speech Title: "Revisiting the Essence of Vitamin E in Reproduction"
10: 00-13:15	**Online Session- Bioactive Materials, Nanotechnology, and Data-Driven Biomedical Applications** KB0063, KB0137, KB0093, KB1017, KB0111, KB0138, KB0075, KB0104, KB2001-A, KB2024, KB0147, KB1019, KB0119-A

Tips: Please arrive at the Conference Room 15 minutes ahead of the session. The duration for Keynote Speech: about 25 minutes of presentation and 5 minutes of Q&A. The duration for Invited Speech: about 15 minutes of presentation and 5 minutes of Q&A. The duration for Regular Presentation: about 12 minutes of presentation and 3 minutes of Q&A.

Opening Remarks

Duration	Venue
09: 00-09:10 January 17, 2026, Saturday (GMT+9)	Convention Hall

Prof. Tomohiro Araki
Tokai University

Keynote Speaker I

Duration	Venue
09: 10-09:40 January 17, 2026, Saturday (GMT+9)	Convention Hall

Asst. Prof. Tewin Tencomnao
Chulalongkorn University

Bio

Tewin Tencomnao has focused his research on Natural Products for Neurodegeneration and Anti-Ageing at Chulalongkorn University. With more than 10,664 citations and h-index 36, he has successfully upgraded the research quality in this field as evidenced by more than 200 publications. His research team employed a variety of experimental models such as cell culture, yeast and animal models to elucidate the mechanisms of natural products to fight against neurotoxicity, neuroinflammation, neurodegeneration and ageing.

Speech

Integrated Model Approaches for Identifying Natural Products Against Neurodegeneration and Ageing

Abstract: Public health problems in Thailand and worldwide include neurodegenerative diseases, infectious diseases, skin diseases, diabetes, etc., many of which are associated with inflammation, oxidative stress and endoplasmic reticulum stress. There is a collective evidence of the herbs' protective properties against stress and inflammation. Several models to identify natural products against neurodegenerative diseases and ageing were utilized for experimental phase prior to preclinical phase. To date, the experimental stage has included an integration of modern tools for application to discover various biological effects along with the molecular mechanisms of different medicinal plants, vegetable, and fruits as well as their phytochemicals. Using cell line, Caenorhabditis elegans (C. elegans) and yeast models, the aim of study is to discover and develop them to prevent and treat neurodegenerative and age-associated diseases. At the molecular level, the mechanisms of action via various signaling pathways by analyzing gene expression at the RNA, protein and metabolite levels were investigated to correlate with the functions and behaviors. Amazingly, C. elegans has been served as a promising model for study both healthspan and lifespan parameters. The study has provided insight into understanding how these herbal extracts and their constituents exhibit their activities against neurodegeneration and ageing. Altogether, these models are crucial for translational research.

Keynote Speaker II

Duration	Venue
09:40-10:10 January 17, 2026, Saturday (GMT+9)	Convention Hall

Prof. Sun Kim
Seoul National University

Bio

Sun Kim is Professor in the School of Computer Science and Engineering, Adjunct Professor of Biological Sciences, and Director of Bioinformatics Institute (2011-2021) at Seoul National University. He is a member of National Academy of Engineering, Korea and head of a brain and computing infrastructure division of Korea National Artificial Intelligence Committee (2024-2026). Until recently, he was President of Mogam Institute of Biomedical Research (2022-2024). Before joining SNU, he was Chair of Faculty Division C; Director of Center for Bioinformatics Research, an Associate Professor in School of Informatics and Computing at Indiana University (IU) Bloomington. Prior to joining IU in 2001, he worked at DuPont Central Research from 1998 to 2001, and at the University of Illinois at Urbana-Champaign from 1997 to 1998. Sun Kim received B.S and M.S and Ph.D in Computer Science from Seoul National University, KAIST and the University of Iowa, respectively. Sun Kim is a recipient of Outstanding Junior Faculty Award at Indiana University 2004, US NSF CAREER Award in 2003, and Outstanding Faculty Award in research 2021 in the College of Engineering at Seoul National University. He is actively contributing to the bioinformatics community, having serving on the editorial board for journals including editors for the METHODS journal (2013-2022) and, associate editor-in-chief for ACM/IEEE Transactions on Computational Biology and Bioinformatics (2019-2021), and also on the board of directors for ACM SIG Bioinformatics and for education for the IEEE Computer Society Technical Committee on Bioinformatics. Among many service activities in Korea, he served on Samsung Future Technology Committee (2016-2018), a member of The National Science and Technology Council of the Korean Government (2019-2020), President of Korea Artificial Intelligence Society (2016-2018) and Vice President of Korea Society of Bioinformatics and Systems Biology (2011-present).

Speech

Decoding Complex Interactions in Biology and Medicine with Deep Learning Technologies

Abstract: Decoding complex interactions is the fundamental problem in biology and medicine. Recent advances in deep learning and AI technologies help decode complex interactions in biology and medicine successfully. In this talk, I will share recent works from my research labs at Seoul National University and AIGENDRUG Co. Ltd. I will start with a big overview of AI-based drug discovery and focus on analyzing and modeling transcriptome data in the context of patient-level drug response. Translating drug response at the cell level to patient level is a critical task in medicine. Discrepancies among LINCS (gene-level), CCLE (cell-level), GDSC (cell-level) and TCGA (patient-level) are very large and connecting information in these databases is a challenging task for patient-level drug response prediction. Overcoming these discrepancies is critical for translating preclinical findings to clinical practice, ultimately advancing the field of precision medicine. Our group has been developing multiple approaches to address this challenge and, in this talk, I will share some of our recent approaches. For translation, we constructed a pre-trained model, Condition-Specific Gene-Gene Attention (CSG2A, Bioinformatics/ISMB 2024) is to improve drug response prediction in terms of cell lines in GDSC and patients in TCGA. Building upon CSG2A, we developed two deep learning models for patient-level prediction, THERAPI (in revision) and PREDIKTOR (in submission). Additionally, we will discuss how to combine traditional clinical features with transcriptome data for patient survival prediction (Briefings in Bioinformatics 2025). If time permits, I will share our work on learning histone codes for transcriptional control (Nature Communications 2022) and another work on relating drug and disease on knowledge graphs (Nature Communications 2023) with recent approaches utilizing large language models (unpublished).

Keynote Speaker III

Duration	Venue
10:40-11:10 January 17, 2026, Saturday (GMT+9)	Convention Hall

Assoc. Prof. Ka-Chun Wong
City University of Hong Kong

Bio

Ka-Chun Wong was born and raised in Hong Kong where he was lucky enough to be immersed in a multi-cultural environment. He received his B.Eng. in Computer Engineering from United College, The Chinese University of Hong Kong in 2008. He has also obtained his M.Phil. degree in the Department of Computer Science and Engineering at the same university in 2010. From 2011 to 2014, he has spent 3.5 years to finish his PhD degree in the Department of Computer Science at the University of Toronto. Right after his PhD study, Ka-Chun has started his research lab in the Department of Computer Science, City University of Hong Kong. His research group works have been published on Nature Biomedical Engineering, Nature Immunology, Nature Communications, Advanced Science, Nucleic Acids Research, iScience (Cell Press), Briefings in Bioinformatics, Bioinformatics, IEEE/ACM Transactions, NeurIPs, AAAI, IJCAI, ICONIP, and others. He is on the editorial boards and committees of international journals and conferences. Multiple keynote and invited speeches have been delivered worldwide. He was an ACM Distinguished Speaker from 2019 to 2022. He was ranked among the World Top 2% Most Highly Cited Scientists (versions 5,6,7,8) . Since 2025, he is also an Hong Kong Convention Ambassador, welcoming all of you to visit Hong Kong.

Speech

AI in Omics: DNA Shape Motifs and Protein Peptides

Abstract: This keynote explores the transformative role of artificial intelligence and statistical modeling in omics research, focusing on DNA shape motif discovery and peptide prediction. Recent advances have enabled the identification of DNA shape motifs using multiple structural features, moving beyond traditional sequence-based approaches. The presentation introduces a generalized, end-to-end framework for motif discovery, leveraging probabilistic models and novel algorithms (SMEM, SMEM-Gibbs, Gibbs sampling) to enhance accuracy and efficiency. Benchmarking demonstrates robust motif localization and stable enrichment patterns across diverse genomic datasets. In parallel, the development of TP-LMMSG—a graph neural network for peptide prediction—incorporates flexible amino acid property representation and advanced language model embeddings. This approach addresses key bottlenecks in therapeutic peptide modeling, such as data quality and combinatorial complexity, and achieves state-of-the-art performance on antimicrobial, antiviral, and anticancer peptide datasets. Together, these innovations highlight the synergy between AI and omics, offering new insights into biomolecular patterns, molecular interactions, and therapeutic design. The keynote will discuss methodological breakthroughs, practical applications, and future directions for integrating AI-driven analytics in biological research.

Invited Speaker I

Duration	Venue
11:10-11:30 January 17, 2026, Saturday (GMT+9)	Convention Hall

Prof. Liang Wang
Guangdong Provincial People's Hospital/ Southern Medical University

Bio

Prof. Liang Wang currently holds tenured full professor and distinguished medical researcher positions at Guangdong Provincial People's Hospital, a top-tier tertiary hospital at the national level, which is affiliated with the Southern Medical University and the South China University of Technology in China. He also serves as chief scientist and assistant director at the Laboratory Medicine Department of the hospital. Prof. Wang also holds adjunct research fellow positions at the University of Queensland and the University of Western Australia, and an adjunct professor position at Edith Cowan University. His research centers on advancing disease diagnosis via interdisciplinary methods such as intelligent medicine, digital health, and molecular biology. Prof. Wang has edited seven books and published over 130 peer-reviewed articles in esteemed journals such as The Lancet Microbe, npj Digital Medicine, and ISME J. Prof. Wang frequently presents at prestigious conferences like EuroCarb (Poland, 2025), ICID (South Africa, 2024), CHRO (Australia, 2024) and VAAM (Germany, 2023). He also serves as an editorial board member for multiple international journals, including Journal of Translational Medicine (Associate Editor, Computational Modelling and Epidemiology) and BMC Microbiology (Editor of Distinction Awards, 2025). He is the recipient of the American Chemical Society's Rising Star Award in measurement science and the Australia-China Helicobacter Research Fellowship.

Speech

Application of Artificial Intelligence in Medical Laboratories: Opportunities and Challenges

Abstract: Intelligent medicine driven by artificial intelligence (AI) is transforming medical laboratories by enhancing diagnostic accuracy, efficiency, and scalability. AI-driven tools enable rapid analysis of complex datasets, such as genomic profiles and pathology images, improving early disease detection and personalized treatment strategies. Automation of routine tasks reduces human error and frees laboratory personnel for higher-value work. Predictive analytics also optimizes resource allocation and laboratory workflows. However, challenges persist, including data privacy concerns, integration with existing systems, and the need for standardized protocols to ensure reliability. Ethical considerations, such as bias in AI algorithms and equitable access, remain critical. Additionally, regulatory hurdles and the high cost of implementation can limit adoption, particularly in resource-constrained settings. Addressing these challenges through interdisciplinary collaboration and robust policy frameworks will unlock the full potential of artificial intelligence and revolutionize laboratory medicine.

Invited Speaker II

Duration	Venue
11:30-11:50 January 17, 2026, Saturday (GMT+9)	Convention Hall

Prof. Chanchal Mitra
University of Hyderabad

Bio

Chanchal Mitra did his Bachelors and Masters from the University of Calcutta and Ph.D. from the Tata Institute of Fundamental Research (University of Bombay). He did his post doctoral work at the State University of New York at Albany (The University at Albany), USA and also at the University of Lund, Sweden. His research interests are Bioinformatics, Computational Biology and Biosensors (enzyme based). He joined University of Hyderabad in 1985 as a lecturer and retired in 2015 as Professor of Biochemistry. He has supervised several Ph.D. students, project students and research associates. He has over 100 publications in peer reviewed journals. According to google scholar, he has citations 1272, h-index of 20 and i10-index of 31. He lives in Hyderabad, India (2023).

Speech

Diabetes Mellitus and Personalization of Medical Care

Abstract: In diabetes, chronically elevated blood glucose induces oxidative stress and contributes to multiple complications, particularly affecting the eyes, kidneys, nervous system, and cardiovascular system. High glucose promotes non-enzymatic glycosylation of hemoglobin, forming HbA1c, which reflects average blood glucose over the preceding ~3–4 months due to the long lifespan of erythrocytes and is therefore the clinical gold standard for glycemic control. Although insulin is the primary hormone regulating postprandial glucose uptake, several tissues—including the brain, eyes, and kidneys—absorb glucose independently of insulin and are especially vulnerable to hyperglycemia-induced damage. In insulin deficiency or resistance, glucose uptake by muscle cells is impaired, leading to cellular energy deprivation and fatigue despite elevated blood glucose, while excess glucose is diverted toward glycogen and lipid synthesis. Conventional treatments that increase insulin levels may further enhance substrate storage rather than utilization, and when ATP production exceeds cellular demand, feedback inhibition of metabolic pathways can increase oxidative stress. These interconnected metabolic processes highlight the complexity of glycemic control and its role in diabetic complications.

Invited Speaker III

Duration	Venue
09:40-10:00 January 18, 2026, Sunday (GMT+9)	Meeting ID: 893 3803 2428 Link: https://us02web.zoom.us/j/89338032428

Dr. Siti Syairah Mohd Mutalip
Universiti Teknologi MARA (UiTM)

Bio

Dr. Siti Syairah Mohd Mutalip received her Doctor of Philosophy (PhD) degree from the Faculty of Medicine, Universiti Teknologi MARA (UiTM) Malaysia, and has over 10 years of experience in the field of reproductive health. Currently working as a Senior Lecturer at the Faculty of Pharmacy, UiTM Puncak Alam Campus, Selangor, Malaysia, she is actively involved in research in the related field. She is also active in scientific writing, having published numerous articles in indexed journals, conference proceedings, book chapters, and magazines, both at the national and international levels. She is an active reviewer for several journals in Biotechnology, Health Sciences, and Biology, and has been granted several research grants as both principal investigator and co-investigator.

Speech

Revisiting the Essence of Vitamin E in Reproduction

Abstract: Vitamin E, initially discovered in 1922 as a vitamin essential for reproduction, has been recognized for its antioxidant and health-promoting properties for a long time. However, its reproductive role remains underexplored despite over a century of discovery. This presentation revisits the reproductive significance of vitamin E, focusing on α-tocopherol (α-TOC) and its potential in ameliorating ovarian dysfunctions caused by nicotine exposure—a known endocrine disruptor. Using rodent models, the study examined morphological, histological, and ultrastructural changes in ovarian tissues and embryonic development following α-TOC intervention. Results demonstrated that α-TOC improved granulosa cell integrity, restored ovarian tissue structure, and supported normal embryogenesis. Additional studies involving annatto-derived δ-tocotrienol (δ-TCT) and Nigella sativa oil further revealed positive modulation of gene expression and hormonal balance. These findings suggest that vitamin E holds promising therapeutic potential in mitigating reproductive disorders and enhancing female fertility. Further investigation into its molecular mechanisms and broader reproductive outcomes is warranted.

Oral Session 1

January 17, 2026, Saturday (GMT+9)

Duration	Venue
13:20-15:35	Lounge

Topic:	Bioinformatics and Biomedical Data Science
Session Chair:	Asst. Prof. Dan Wang, Hong Kong Metropolitan University

Paper Detail

OS1-1	KB0029-A 13:20-13:35	Machine Learning-Based Treatment Efficacy Analysis of High-Flow Oxygen Therapy in Pneumonia and Obstructive Pneumonia **Ting-Yu Kuan**, Chun-Jung Chang, Ching-Hsia Hung, and Kuo-Sheng Cheng National Cheng Kung University Abstract: High-Flow Oxygen Therapy (HFOT) has become a critical intervention for managing acute respiratory failure, particularly in the context of the COVID-19 pandemic, significantly contributing to alleviating the global burden of respiratory diseases. Despite its clinical importance, the initiation and prediction of HFOT outcomes remain largely dependent on physician expertise and conventional assessments, which can introduce variability and limit objectivity. Furthermore, advanced diagnostic tools are not universally available in all clinical environments, especially during periods of high patient volume, as witnessed during the COVID-19 crisis. This highlights the need for predictive systems that can rely on easily obtainable physiological parameters. In this study, we collected clinical physiological data and applied preprocessing techniques, including normalization and data cleaning, to ensure feature robustness. Recursive Feature Elimination (RFE) is employed to identify the most informative parameters while reducing redundancy. Several machine learning algorithms—Support Vector Machine (SVM), Random Forest, and Logistic Regression—are applied and evaluated. The results demonstrated that models trained using basic physiological parameters alone achieves satisfactory predictive accuracy, suggesting that such data can effectively

		capture key indicators of HFOT outcomes. Our findings suggest that machine learning models based on simple physiological inputs can serve as reliable, objective decision-support tools for clinicians. This approach is particularly valuable in resource-limited settings and in the post-COVID clinical landscape, where rapid, consistent predictions are essential for optimizing patient management. Future research will focus on expanding the dataset with additional physiological signals, integrating electronic health record (EHR) data, and conducting prospective validation to further enhance the clinical applicability of this framework.
OS1-2	KB0039 13:35-13:50	More Data is Not Always Better: The Influence of RefSeq Database Grows on Metagenomic Taxonomic Classifica- tion **Matteo Comin,** Leonardo Lazzaro, and Enrico Rossignolo University of Padova Abstract: Current technologies allow for the sequencing of microbial communities directly from the environment without prior culturing. One of the major problems when analyzing a microbial sample is to taxonomically annotate its reads to identify the species it contains. In order to determine the role of the reference database in taxonomic sequence classification, we examine the influence of the database over time on the performance of Kraken 2 a widely used taxonomic classification and profiling method. We reported that changes in reference database over time influenced the accuracy of metagenomic taxonomic classification, and training the classifier with more data, e.g. new species, worsen the results.
OS1-3	KB0067-A 13:50-14:05	Unravelling the Genome of the Bacterial Endophyte Involved in Indole-3-acetic Acid Biosynthesis Via the Design of Experiment Strategy **Sohail Khan** and Ashwani Mathur Jaypee Institute of Information Technology Abstract: Sustainable agriculture increasingly requires eco-friendly alternatives to conventional chemical fertilizers and pesticides. In this regard, plant-associated endophytic bacteria have received increasing attention as a promising and environmentally responsible solution. However, their application in optimizing production remains unexplored by the limited characterization of genome-to-function relationships. Specifically, functional characteristics like indole-3-acetic acid (IAA) production are seldom validated using integrated genomic and experimental methodologies. This study investigated an endophytic

		bacterium from the medicinal plant Humulus lupulus. The isolated endophytic bacterium was analyzed using whole-genome sequencing, followed by genome annotation using COG classification and AntiSMASH to identify biosynthetic gene clusters, while KEGG analysis mapped the pathways responsible for IAA production. The genome of the isolate was approximately 5 Mb in size and harboured genes associated with IAA biosynthesis. Functional annotations were authenticated through quantification of IAA. Furthermore, a full factorial design of the experiment was employed to optimize intracellular and extracellular IAA production. The highest yield was achieved in extracellular IAA production from an endophytic bacterium. This study demonstrates an eco-friendly, scalable strategy for bacterial IAA production. Collectively, the findings underscore the considerable potential of endophytic bacteria as a platform for large-scale, sustainable IAA biosynthesis.
OS1-4	KB0082 14:05-14:20	Stability of Single-Cell Dimensionality Reduction Following Shuffling Test Yu-Ting Huang and **Jia-Ming Chang** National Chengchi University Abstract: Single-cell RNA sequencing (scRNA-seq) offers precise quantification of the transcriptome at an individual cell level, surpassing traditional bulk RNA-seq. Despite its advancements, the high-dimensional nature of scRNA-seq data complicates the extraction and visualization of underlying biological information. Various dimensionality reduction algorithms have been developed to aid biologists in uncovering cellular relationships, especially through clustering. However, the stability of single-cell dimension reduction has been largely overlooked, particularly the variation of neighbor relations or cluster quality in the reduced space. In this study, we generate alternative datasets by randomly shuffling rows or columns of the single-cell expression matrix. These alternative datasets are processed similarly to the original data. Stability is measured by comparing results from the original and alternative data using multiple metrics, including knn-preservation for neighbor relations, the Calinski-Harabasz, Davies-Bouldin, and Xie-Beni indexes for cluster internal evaluation, and the Jaccard Index for clustering consistency. Additionally, the RF-hierarchical metric evaluated the preservation of global meta-information. We employed Monocle 3, an R toolkit, to assess the stability of scRNA-seq visualizations using two popular methods: t-SNE and UMAP. Our evaluation

		involved six datasets, including two from the C. elegans Monocle 3 tutorial, two from the Single Cell Portal (PBMC ID 345 and islet ID 1526), and two comprising Mouse Retinal and Brain samples. Internal cluster scores varied after data shuffling, with the Jaccard Index of C. elegans-con dropping below 0.6, indicating instability, and the RF distance of SCP1526 reaching the maximum value. Our findings suggest that dimensionality reduction techniques vary in stability with shuffled inputs, indicating that claims of their robustness may be premature without considering input variations.
OS1-5	KB0085 14:20-14:35	A Zero-Shot Nlp-Based Pipeline for Automated Processing of Antimicrobial-Related Scientific Texts Oscar A. Bustos-Brinez, Fabio A González, and **Daniel Restrepo-Montoya** Universidad Nacional de Colombia Abstract: Information extraction from literature is a fundamental process in the construction of knowledge in the life sciences. However, it is also a process that often requires time and effort to obtain accurate results. This work proposes a fast and adaptable scheme for the automatic processing of article texts (abstracts) based on the use of NLP models, specifically designed to identify publications related to the evaluation of antimicrobial compounds. The proposed mechanism receives an abstract as input and determines whether the article meets a series of criteria, also generating a list of the chemical compounds present in the text. The NLP models applied to the texts are executed without additional training (zero-shot learning), and as many filtering criteria as necessary can be used. The quality of this proposal is determined by its use in 368 abstracts of articles, employing three acceptance criteria. The results indicate a high precision of the proposed mechanism for both classifying texts in the area of antimicrobial prospecting and recognizing chemical entities.
OS1-6	KB0118 14:35-14:50	StackFeat: A Convergent Algorithm for Optimal Predictor Selection in Genomic Data **Akbar Yermekov** PAfoS.AI Abstract: Background: Most methods of multivariate feature selection in high-dimensional gene expression analysis (hundreds or thousands of features vs. ~100 samples) produce inconsistent feature sets. This instability is a critical barrier to discovering reliable biomarkers. Thus, it is important to develop methods that produce reduced gene sets that are

		both consistent and predictive. We introduce StackFeat, a novel algorithm that achieves stability through iterative dual-criterion refinement. The algorithm performs repeated nested cross-validation across multiple data reshuffles, cumulatively aggregating both feature coefficients from an L1/L2-regularized ElasticNet selector and selection frequencies across bootstrap samples. At each iteration, features must satisfy both criteria through set intersection—ranking highly by both cumulative scores AND selection frequency. The process continues until performance-based convergence is reached (AUC stability < 0.02). Validating on a dataset of miRNA expression in COVID-19 vs healthy patients (GSE240888, Gao et al.), StackFeat achieved extreme dimensionality reduction, identifying a stable 5-feature set from 332 initial features (98.5% reduction). This minimal set achieved an AUC of 0.922, outperforming the benchmark study's 9-gene set (AUC 0.907). The 5-miRNA signature consisted of: hsa-miR-181b-5p, hsa-miR-4433b-5p, hsa-miR-1185-1-3p, hsa-miR-484, and hsa-miR-150-5p. StackFeat produces robust, minimal, and highly predictive gene sets by enforcing dual stability criteria—both predictive strength and selection consistency. This approach provides a practical solution to the feature instability problem in biomarker discovery, successfully identifying a biologically coherent 5-gene signature from high-dimensional data.
OS1-7	KB2002-A 14:50-15:05	FHIR-Based Secure Healthcare Data Collection Framework Pang Lun Lee, **Yu Ting Cheng**, Zi Chin Lo, Jiun Hung Lin, and Shih Tsang Tang Ming Chuan University Abstract: This study presents a mobile health monitoring framework integrating smartphone sensors with GPS positioning to capture step counts and location data in real time. The collected data is standardized and transmitted to a backend FHIR server for structured storage and analysis. To address security and integrity challenges in the Internet of Medical Things (IoMT), encryption mechanisms and authentication processes are implemented. An Android application was developed to demonstrate the system, and preliminary tests confirmed reliable recording of physiological and geographic data with seamless integration into medical databases. The results highlight the system’s feasibility and practicality for remote healthcare and mobile health monitoring.
OS1-8	KB0058	A Case Study of Severe Hemophilia B Due to Pathogenic C.676C>T

	15:05-15:20	Missense Mutation in the F9 Gene **Suprianto**, Niken Satuti Nur Handayani, Ni Gusti Ayu Galuh Candra Kirana, Indra Lesmana, and Usi Sukorini Chulalongkorn University Abstract: The variant and number of F9 gene mutations in Indonesia have not been reported. This study utilized the long-read sequencing method with PromethION24 from Oxford Nanopore Technologies plc (ONT). The subjects of this study is patient with severe hemophilia B. Amplification of the F9 gene was conducted using the forward primer F (5'-CGGAGCCAAATGTTCTTTTC-3') and reverse primer R (5'-CACCAACTGCTCATCTCTGG-3'). The three-dimensional structure of the mutant coagulation factor IX protein was predicted using SWISS-MODEL and visualized with Discovery Studio and UCSF Chimera. Long-read sequencing identified the missense mutation c.676C>T in the F9 gene, confirmed by Sanger sequencing. This pathogenic variant (p.Arg226Trp) alters the amino acid at position 226 in exon 6, affecting the activation peptide for the serine protease domain. 3D structural analysis shows changes in the coil region at residue 226, potentially disrupting atomic interactions and impairing factor IX activation, leading to Haemophilia B symptoms.
OS1-9	KB0061 15:20-15:35	PhyDBSCAN: Phylogenetic Tree Density-Based Spatial Clustering of Applications with Noise and Automatically Estimated Hyperparameters Lida Hooshyar, Ryan Godin, Anna Artiges, and **Nadia Tahiri** University of Sherbrooke Abstract: Phylogenetic analyses often generate numerous tree topologies, creating conflicts that require resolution through consensus strategies. Conventional single-tree consensus methods have inherent limitations, as they do not capture topological diversity and are sensitive to outliers. In this study, we present a novel approach, PhyDBSCAN, that applies the density-based spatial clustering of applications with noise (DBSCAN) algorithm to ensembles of phylogenetic trees. The refined DBSCAN method includes an optimized, data-driven procedure for estimating the hyperparameters $epsilon$ and $MinPts$, developed specifically for the Robinson-Foulds (RF) distance. This approach clusters trees, partitioning them into a single cluster for homogeneous data and multiple clusters for

		heterogeneous data, preserving topological diversity and enhancing consensus construction. PhyDBSCAN has a time complexity of $\mathcal{O}(nN^{2})$, where n is the number of leaves and N is the number of phylogenetic trees. The efficiency of the new method was assessed using real data comprising 35 genes from 43 methanogen species.

Oral Session 2

January 17, 2026, Saturday (GMT+9)

Duration	Venue
15:50-18:05	Lounge

Topic:	Computational Biochemistry and AI-Enabled Molecular Design
Session Chair:	Asst. Prof. Nadia Tahiri, University of Sherbrooke

Paper Detail

OS2-1	KB0020 15:50-16:05	Ai-Assisted Molecular Design of Quinolone Alkaloid Analogues as Pancreatic Lipase Inhibitor Candidates Hayato Suzuki, **Yoh Noguchi**, Kaito Watanabe, Chiawen Ying, Motokuni Nakajima, Ryota Morikawa, Yukiko Matsuo, and Masako Takasu Tokyo University of Pharmacy and Life Science Abstract: Pancreatic lipase (PL), a key enzyme in dietary fat absorption, remains a validated target for obesity prevention, yet existing inhibitors such as orlistat suffer from structural limitations and side effects. Here, we explored a molecular design workflow that integrates machine learning–based generation with iterative docking simulations, focusing on quinolone alkaloid–like scaffolds. Over 60 optimization cycles, the best candidate improved from an initial docking score of −8.0 to −13.5 kcal/mol. The top-scoring structure featured a polycyclic aromatic core linked by conjugated chains, with docking poses indicating π–π stacking with Phe77/Tyr114—consistent with a pocket-blocking mechanism that could impede substrate entry. In addition, we observed a polar approach near Ser152. Notably, despite starting from quinolone alkaloid scaffolds, the generator produced chemotypes resembling known inhibitors. Although the present study focuses on docking-based optimization, these findings suggest the potential of AI-assisted molecular design for identifying novel PL inhibitors. Nevertheless, further validation is clearly required, including systematic structure–activity analyses and experimental testing.
OS2-2	KB0021 16:05-16:20	Interaction Analysis of Quinolone Alkaloids Derived from Euonymus Rutaecarpa with Human Pancreatic Lipase by Docking Simulation

		Kaito Watanabe, Chiawen Ying, Hayato Suzuki, Motokuni Nakajima, Yoh Noguchi, Ryota Morikawa, Yukiko Matsuo, and Masako Takasu Tokyo University of Pharmacy and Life Science Abstract: Obesity is associated with various metabolic disorders, and pancreatic lipase inhibitors are important therapeutic agents that suppress fat absorption. Quinolone alkaloids isolated from Evodia rutaecarpa have been reported to exhibit inhibitory activity against pancreatic lipase. In this study, docking simulations were performed with 33 ligands, including 14 isolated quinolone alkaloids and 19 virtual stereoisomers, against human pancreatic lipase. The ligands were classified into three structural groups based on carbon chain saturation and the presence of hydroxyl groups, and their docking results were compared with experimental activity. Overall, the docking outcomes were consistent with experimental data, showing positive correlations for structural groups 1 and 3. Notably, Mol 10, interacting with His151, exhibited a high docking score despite low experimental activity, whereas Mol 14-1, interacting with His263, demonstrated strong inhibitory activity and a positive correlation with docking scores. These findings suggest that docking score may not always strongly correlate with experimental potency depending on the docking pose. This study highlights the potential of quinolone alkaloids as pancreatic lipase inhibitors and emphasizes the importance of analyzing ligand–residue interactions.
OS2-3	KB0028-A 16:20-16:35	Explore Dynamic Processes in the S100B – Aβ Complex Under Saturation With Copper Ions. Application of 19F Nmr and Hdx Mass Spectroscopy **Igor Zhukov**, Lesia Kolomiiets, Lilia Zhukova, Michal Dadlez, and Wojciech Bal Institute of Biochemistry and Biophysics, Polish Academy of Sciences Abstract: S100B protein plays an important role in the toxicity of Aβ-amyloid in Alzheimer's disease (AD). It protects neurons from degradation. Also, it controls the levels of Aβ peptide and the phosphorylation of Tau protein. In our project, we investigated the effect of copper ions on the formation of the S100B complex with Aβ (1-40) or Aβ (4-40) peptides, using HDX mass spectrometry to identify regions of S100B that become destabilized upon interaction with these Aβ peptides. We

		prepare the S100B (F43W) mutant, which includes a fluorinated 19F-Trp to reduce the paramagnetic effects of copper. Additionally, we synthesized the Aβ(1-40) and Aβ(4-40) peptides with 19F-Phe4 positioned within the copper-binding ATKUN motif. The differences in 19F chemical shifts between Phe and Trp residues enable us to apply 19F NMR spectroscopy to extract precise data about the interactions between S100B and Aβ in the presence of copper.
OS2-4	KB0031 16:35-16:50	Comparative Evaluation of Drug Response Metrics for Predicting Cancer Sensitivity Using Transcriptomic Profiles Yen Jung Chiu, **Pei-Qi Wu**, and Yen Hwa Huang National Yang Ming Chiao Tung University Abstract: Pharmacogenomic modeling aims to predict cancer drug sensitivity from molecular features such as gene expression. However, the choice of drug response metric can critically affect model performance. This study systematically evaluates three commonly used metrics—area under the dose–response curve (AUC), Z-score, and half-maximal inhibitory concentration (IC50)—to determine their relative suitability for machine learning-based prediction using transcriptomic data. Methods: We assembled an integrated dataset comprising 636 cancer cell lines and drug response profiles for 169 compounds, along with RNA-seq–based gene expression features. XGBoost regression models were trained separately using AUC, Z-score, and IC50 as response variables. Model performance was assessed using R^2, Pearson correlation, and mean absolute error. Additionally, gene-level correlation analyses were conducted to evaluate linear associations between gene expression and drug sensitivity. Results: AUC-based models consistently outperformed those based on Z-score and IC50 in terms of predictive accuracy and robustness. The highest-performing drugs under the AUC framework included Nelarabine (R^2 = 0.83), Sorafenib, and Venetoclax—all of which have established clinical relevance. In contrast, gene-wise Pearson correlation analysis revealed that most genes exhibited weak linear relationships with drug sensitivity across all metrics (|PCC| < 0.1), suggesting that response prediction depends on complex, multigenic interactions. Conclusion: AUC is a more reliable and informative drug response metric for transcriptome-based prediction of cancer sensitivity. The findings support the application of multivariate machine learning models and emphasize the importance of metric selection in pharmacogenomic modeling

		pipelines.
OS2-5	KB0040-A 16:50-17:05	Integrating Image Visibility Graph (IVG) and Radiomics Features for Predicting Immunotherapy Response in Hepatocellular Carcinoma **Xu-Teng Lin,** Chien-Yu Chen, Kuo-Sheng Cheng, and Hsin-Yu Kuo National Cheng Kung University Hospital Abstract: In clinical decision-making for liver tumor immunotherapy, developing a reliable tool to predict treatment outcomes is of critical importance. This study proposes a predictive model based on computed tomography (CT) liver images to distinguish treatment responders from non-responders. In this study, CT scans from approximately 200 patients were collected, and the liver, tumor, and vascular regions were segmented using both expert clinical annotations and an open-source segmentation model (TotalSegmentator). To enhance image quality, anisotropic diffusion filtering was applied as a preprocessing step, reducing noise while preserving edges, contours, and fine structural details. Conventional radiomics features—including shape, texture, and transform-based descriptors—were extracted to train baseline models. However, their predictive power was limited by insufficient discriminative capacity. To overcome this challenge, a novel feature extraction strategy is proposed: the three-dimensional Visibility Graph (3D-VG). In this approach, each voxel is represented as a node, and two voxels are considered “visible” and connected if no obstruction exists along a given direction. This transformation converts grayscale images into complex networks, from which topological features can be derived, thereby enriching the representation of tumor heterogeneity. Experimental results show that incorporating 3D-VG–derived features substantially improves the predictive accuracy of immunotherapy response compared to conventional radiomics alone. These findings highlight the potential of graph-based radiomics to enhance outcome prediction and support precision clinical decision-making in liver tumor immunotherapy.
OS2-6	KB0055-A 17:05-17:20	Anisotropic Gold Nanoparticles conjugated with AI-Designed CD8+ T-Cell Epitopes: Uptake in THP-1 Macrophages **Patricio Oyarzún,** Víctor Fica, Eduardo Zúñiga, Braulio Contreras, Jessica Lemus, Fabián Saez, Víctor Díaz-García, and Enrique Guzmán-Gutierrez Universidad San Sebastián Abstract: A novel immunoinformatic method to predict peptide-MHC class

		I presentation (peptide binging and proteasomal cleavage) was developed using protein language model embeddings and transfer learning. The architecture employed convolutional blocks to extract local features and a cross-attention module to extract peptide-MHC interaction features and integrates cleavage window features. Our model achieves state-of-the-art performance in predicting MHC Class I peptide presentation. On a matched hold-out set of 79,275 peptides, it yielded an AUC score of 0.9409, outperforming NetMHCpan-4.1 EL (AUC 0.8356) and similar to MHCflurry 2.0 (AUC 0.9611). Predicted T-cell epitopes (influenza virus) were conjugated on gold nanoparticles of different shapes and sizes. Spheres particles where synthetized via a microsynthesis method (23 nm 68 nm), rods where synthetized by seed mediated growth in CTAB (28x131 nm and 34x11 nm), stars where synthetized by a seed mediated growth from 23 nm spheres (46 nm and 110 nm) and prisms where synthetized through thiosulfate-mediated gold reduction (particle sizes 72 nm and 84 nm). Finally, cellular uptake in monocyte-derived THP-1 macrophages was characterized at several levels to monitor nanotoxicity and intracellular processing differences among the different nanoconjugates.
OS2-7	KB0070 17:20-17:35	Deep Learning on the Fusion of Chemical Sequences and Molecular Grids for Ligand-Based Virtual Screening Rongji Ke and **Debby D. Wang** Hong Kong Metropolitan University Abstract: Computational techniques have been widely applied in modern drug discovery to reduce cost and time. As a crucial component of computational drug discovery, predicting compound-protein interactions is becoming increasingly prevalent. Virtual screening serves as a cost-effective tool for predicting such interactions. However, current models often require input from both compounds and proteins, which is unfriendly for scenarios where the protein information is not valid. In this work, we propose a ligand-based prediction approach that leverages only the SMILES sequences and 3D grids of compounds in target-specific tasks. By learning these features through a cross-attention mechanism, our model can capture high-level structural features of the compounds in the prediction tasks. Experimental validation on the DUD-E dataset demonstrates that our model achieves competitive performance in both accuracy and efficiency. Particularly, it performs decently when large proteins are involved.

OS2-8	KB2014-A 17:35-17:50	Elucidating the Catalytic Mechanism of Prussian Blue Nanozymes with Self-Increasing Catalytic Activity **Kaizheng Feng** and Yu Zhang Southeast University Abstract: Although Prussian blue nanozymes (PBNZ) are widely applied in biomedical field, their catalytic mechanisms remain elusive. Here, we investigate the long-term catalytic performance of PBNZ as peroxidase (POD) and catalase (CAT) mimetics to elucidate their lifespan and underlying mechanisms. Unlike our previously reported Fe3O4 nanozymes, which exhibit depletable POD-like activity, the POD and CAT-like activities of PBNZ not only persist but slightly enhance over prolonged catalysis. We demonstrate that the irreversible oxidation of PBNZ significantly promotes catalysis, leading to self-increasing catalytic activities. The catalytic process of the pre-oxidized PBNZ can be initiated through either the conduction band pathway or the valence band pathway. In summary, we reveal that PBNZ follows a dual-path electron transfer mechanism during the POD and CAT-like catalysis, offering the advantage of a long service life.
OS2-9	KB0145-A 17:50-18:05	Deep Learning-Guided Discovery of Antimicrobial D-Peptides **Hui-Hsu Tsai**, Shao-Chi Wu, Ming-Yang Tsai, and Yu-Chen Chuang National Central University Abstract: The growing failure of conventional antibiotics has spurred interest in antimicrobial peptides (AMPs) as promising next-generation therapeutics. However, the design and optimization of AMPs remain challenging due to complex structure–function relationships, particularly in interactions with fluid membranes. Major limitations in their clinical application include short half-life and hemolytic toxicity. Incorporating non-natural D-amino acids into AMPs has emerged as a strategy to enhance protease resistance and stability, yet these D-amino acid-containing AMPs (D-AMPs) remain underexplored in current machine learning (ML) models. In this study, we address this gap by integrating three-dimensional structural information of D-AMPs into a deep learning framework using a Directed Message Passing Neural Network (D-MPNN). To facilitate high-throughput virtual screening of potent D-AMPs—generated via generative AI—we developed and combined multiple ML models, including: 1. D-AMP

		Predictor – for assessing antimicrobial activity, 2. D-Peptide Hemolysis – for predicting hemolytic potential, and 3. D-Peptide Half-life – for estimating peptide stability. Peptide structures were predicted using AlphaFold2 and their D-form structures are refined through molecular dynamics simulations to obtain accurate 3D conformations. The D-MPNN framework demonstrated superior performance in correlating D-AMP activity with structural features, achieving over 85% accuracy on an independent test set. Furthermore, Shapley value analysis provided interpretable insights into structure–activity relationships, enabling the rational optimization of low-potency D-AMPs. This integrated approach offers a powerful platform for accelerating the discovery and design of stable, selective, and potent antimicrobial peptides for clinical applications.

Oral Session 3

January 17, 2026, Saturday (GMT+9)

Duration	Venue
13:20-15:35	208 Seminar Room

Topic:	Microbiology, Virology, and Antimicrobial Biochemistry
Session Chair:	TBA

Paper Detail

OS3-1	KB0084-A 13:20-13:35	Efficacy of Medicinal Plant Extracts from Family Acanthaceae on Inhibition of Skin Pathogenic Bacteria, Antioxidant and Anti-Inflammation **Kullanun Mekawan** and Yingmanee Tragoolpua Chiang Mai University Abstract: The medicinal plants in Acanthaceae are widely used in Thai traditional medicine due to the increasing problem of bacterial drug resistance. Ethanolic extracts from four Acanthaceae species: Andrographis paniculata, Thunbergia laurifolia, Acanthus ebracteatus, and Rhinacanthus nasutus were investigated in this study. The phytochemicals in plants were analyzed by determination of total phenolic content (TPC) and total flavonoid content (TFC). Antioxidant activities were determined using DPPH and ABTS assays. Antibacterial potential of extract against skin pathogenic bacteria, including Pseudomonas aeruginosa, Cutibacterium acnes, Micrococcus luteus, Staphylococcus aureus, and methicillin resistant S. aureus, was assessed using agar well diffusion and broth dilution method. Moreover, cytotoxicity of the plant extracts on the RAW 264.7 cells was evaluated using the MTT assay. Anti-inflammatory activity of the extracts was examined on LPS-stimulated RAW 264.7 cells and inflammatory gene expressions were analyzed by RT-qPCR. The results showed that T. laurifolia extract exerted the highest levels of TPC and TFC, corresponding to the most potent antioxidant activities. All plant extracts demonstrated antibacterial activities against skin pathogenic bacteria, as indicated by the inhibition zones ranging from 7.11 to 21.19 mm. The minimum inhibitory concentration (MIC) and minimum bactericidal

		concentration (MBC) values of the extracts ranged from 1.95 to 125.00 mg/mL. In addition, all plant extracts, except A. ebracteatus, suppressed the expression of inflammatory genes. Therefore, this study revealed antioxidant, antimicrobial, and anti-inflammatory efficacy of Acanthaceae species that were traditionally used in folk medicine.
OS3-2	KB0016-A 13:35-13:50	DNA Extraction Kit Bias in Antimicrobial Resistance Gene Profiling of Seahorse Skin Microbiomes **Rose Chinly Mae Ortega-Kindica** University of the Philippines Cebu Abstract: Antimicrobial resistance genes (ARGs) are emerging environmental threats, particularly in marine ecosystems affected by anthropogenic activities. Seahorses (Hippocampus spp.), as benthic and ecologically sensitive organisms, are constantly exposed to biofilm-rich sediments and may act as bioindicators for environmental ARGs. This study investigates the skin microbiome of Hippocampus barbouri using shotgun metagenomics to assess the impact of two commercial DNA extraction kits, the HiMedia Water DNA Purification Kit (HMS) and Qiagen DNeasyPowerSoil Pro Kit (QKS) on ARG detection. DNA was extracted from the skin microbiome of Thirty (30) adult Hippocampus barbouri (Barbour's seahorse) collected from Cantiasay Island, Surigao del Norte, Philippines, followed by whole genome shotgun (WGS) sequencing. The resulting sequences were analyzed using the CARD database. Results revealed significant differences between kits and the QKS kit yielded higher DNA quality and a greater number of ARG families and genes, particularly multidrug, macrolide, β-lactam, and efflux pump-associated genes (e.g.mdtB, mexB, blaB). In contrast, the HMS kit underrepresented many ARG categories, potentially due to suboptimal lysis efficiency or inhibitor contamination. Heatmap and statistical analyses (P < 0.05) confirmed QKS's superior performance. These findings highlight that DNA extraction methods can significantly influence resistome profiling outcomes and emphasize the importance of protocol standardization in metagenomic studies. Moreover, the skin microbiome of H. barbouri harbors a diverse ARG repertoire, highlighting its potential as a sentinel species for environmental resistome surveillance. This first comparative analysis of DNA extraction kits for seahorse skin resistomes offers critical insights for marine microbial ecology and conservation biology, supporting efforts to monitor and mitigate antimicrobial resistance in aquatic environments.

OS3-3	KB0086 13:50-14:05	Inhibitory Efficacy of Black Tea Extracts on Herpes Simplex Virus Type 2 **Phuchong Robchangwat** and Yingmanee Tragoolpua Chiang Mai University Abstract: Herpes simplex viruses (HSV) are divided into two types: HSV-1 and HSV-2. HSV-1 typically causes infections in the oral and ocular regions, whereas HSV-2 is mainly transmitted sexually and predominantly affects the genital area. Current antiviral drugs, such as acyclovir, valacyclovir, and famciclovir, may cause undesirable side effects. Therefore, natural extracts should be used as an anti-viral agent for treatment of HSV infections. Camellia sinensis or tea is a globally consumed as a beverage that is rich in bioactive compounds including polyphenols, catechins, and theaflavins. These bioactive compounds exhibit strong antioxidant and anti-inflammatory properties. In this study, black tea was extracted using distilled water and 95% ethanol, yielding black tea aqueous extract and black tea ethanolic extract. Cytotoxicity on Vero cells was assessed by MTT assay. The CD_{50} values of black tea aqueous and ethanolic extracts were 70.5 and 237.97 µg/mL, respectively. Antioxidant activity of black tea aqueous and ethanolic extracts were 228.05 and 60.30 mg gallic acid equivalent/g extract when determined by DPPH assay. At non-toxic concentrations, black tea aqueous extract at 30 µg/mL and ethanolic extract at 120 µg/mL, inhibited HSV-2 when treatment after viral infection by 97.79% and 96.62%, respectively. These findings suggest that black tea extracts possess potent antioxidants and antiviral activities and could serve as promising natural alternatives for managing HSV infections.
OS3-4	KB0109-A 14:05-14:20	Iodinated Fmoc-Phenylalanine Disrupts Biofilm Integrity and Attenuates Virulence in Staphylococcus Aureus **Oluwatosin Oluwaseun Faleye** and Jintae Lee Yeungnam University Abstract: Staphylococcus aureus presents a major public health concern owing to its strong capacity for biofilm formation and virulence activities, which contribute to antibiotic resistance and treatment complications. To address this challenge, the antimicrobial potential of halogenated phenylalanine derivatives was evaluated, based on the hypothesis that halogenation enhances antimicrobial efficacy. Among 29 compounds tested, Fmoc-4-iodophenylalanine (Fmoc-Iodo-Phe) exhibited the highest antibiofilm activity, achieving 94.3% biofilm reduction at 50 µg/mL.

		Microscopic observations confirmed its ability to both prevent and disrupt mature S. aureus biofilms. At 10 μg/mL, Fmoc-Iodo-Phe significantly inhibited key virulence traits, such as cell surface hydrophobicity, hemolysin, and slime production. It demonstrated low resistance development potential and effectively inhibited biofilms formed by methicillin-resistant S. aureus (MRSA) and S. epidermidis, but showed no activity against Gram-negative bacteria. Gene expression, complemented by molecular docking, suggested that Fmoc-Iodo-Phe targets the AgrA quorum-sensing regulator through strong interactions with key residues at its DNA binding sites. Furthermore, it was non-cytotoxic in Caenorhabditis elegans and satisfied ADMET prediction. These findings highlight Fmoc-Iodo-Phe as a promising antimicrobial candidate for controlling S. aureus infections.
OS3-5	KB0091 14:20-14:35	Biological Properties of Honey from APIs Mellifera and Efficacy on Inhibition of Herpes Simplex Virus Infection and Antioxidant Activity **Kajornpan Wichaiprom** and Yingmanee Tragoolpua Chiang Mai university Abstract: Herpes simplex virus (HSV) is a common cause of oral and genital lesions and remaining latent in nerve ganglia. Current antiviral treatments often use antiviral drugs like acyclovir, valacyclovir, and famciclovir. However, these drugs have side effects and drug resistant strains may emerge. Thus, natural products such as honey are being explored as an alternative agent for viral inhibition. This study aimed to investigate the antioxidant activity of longan, lychee, and polyfloral honeys, and evaluate efficacy of honey against HSV-1 infection via plaque reduction assays. The HSV-1 was treated with three different types of honey before, during, and after viral attachment to human epidermal keratinocyte (HaCaT) cells. The highest total phenolic content of 1.375 ± 0.02 mg GAE/g and the highest antioxidant activity of 0.850 ± 0.06 mg GAE/g were observed from longan honey. All three different types of honey exhibited less than 50% inhibition when treated before and after viral attachment. However, during viral attachment, all types of honey inhibited HSV-1 infection by more than 50% at a concentration of 3.125% W/V. The highest HSV-1 inhibition of 70.87±3.72% was observed when treatment with polyfloral honey. These results suggest that the antiviral mechanism of honey involves disrupting the virus during attachment and penetration into the cell. Therefore, the finding supports the potential of Thai honey, particularly polyfloral honey

		demonstrated anti-viral activity.
OS3-6	KB0110-A 14:35-14:50	Antimicrobial Activities and Low Toxicity Potential of Polyhalogenated Phenols against Staphylococcus Aureus **Rauf Olalekan Olanrewaju** and Jintae Lee Yeungnam University Abstract: Staphylococcus aureus is a common pathogen that readily acquires antibiotic resistance and forms biofilms, reducing its susceptibility to conventional therapies. This study identified the multi-halogenated phenol, pentabromophenol (PBP), as a potent antimicrobial agent against S. aureus. PBP exhibited a minimum inhibitory concentration (MIC) of 0.5 μg/mL, outperforming ciprofloxacin (1 μg/mL) and tetracycline (2 μg/mL). It dose-dependently inhibited biofilm formation and hemolytic activity, decreased metabolic activity, and increased N-phenyl-1-naphthylamine (NPN) uptake, indicating enhanced membrane permeability. PBP showed minimal resistance development, with only a 4-fold MIC shift after 30 passages, compared with over 1000-fold for ciprofloxacin. It exhibited significant synergy with vancomycin, lowering effective dose by 16-fold. qRT-PCR revealed downregulation of virulence and regulatory genes (hla, psm-α, sarA, sigB, and arlR/S). Toxicity evaluations demonstrated safety up to 20 μg/mL (40× MIC) in HepG2 cells, 10 μg/mL (20× MIC) in Caenorhabditis elegans, and an LD_{50} of 270–290 mg/kg in Sprague–Dawley rats. QSAR and ADMET analysis show improved pharmacokinetics performance, and unlike conventional antibiotics, PBPs' high potency at low doses may reduce environmental accumulation and selective pressure that drives antimicrobial resistance. Overall, these results highlight PBP as a promising low-toxicity antimicrobial candidate, suggesting that targeted multi-halogenation enhances phenolic bioactivity while mitigating toxicity.
OS3-7	KB0112 14:50-15:05	Inhibitory Effects of Green Tea Leaf Stalk Extracts on Colibactin-Producing Escherichia Coli and Colorectal Cancer Cells **Wipawadee Teppabut**, Yingmanee Tragoolpua, and Thida Kaewkod Chiang Mai University Abstract: Colorectal cancer (CRC) is the third most commonly diagnosed cancer and the second leading cause of cancer-related deaths worldwide. colibactin-producing Escherichia coli strains, particularly those carrying the pks gene cluster, have been increasingly detected in CRC patients, complicating treatment and highlighting the need for alternative

		therapeutic strategies. Tea (Camellia sinensis var. assamica) leaf stalks, a byproduct of tea processing, are often discarded during production, even though they are rich in bioactive compounds and have been less studied for their biological activities. This study evaluated young and mature green tea leaf stalk extracts for their chemical compositions, antioxidant activity, antibacterial activity, and cytotoxicity against HT-29 and Caco-2 colorectal cancer cells. The result revealed that tea leaf stalk extracts contained the phenolics and flavonoids compounds that related to antioxidant activity. In addition, young and mature green tea leaf stalks contained the bioactive compounds including epigallocatechin gallate (EGCG) and catechin by HPLC detection. For antibacterial activity, the young and mature green tea leaf stalk extracts exhibited the lowest MIC and MBC values at 62.5-250 mg/ml against all isolates of colibactin-producing E. coli (BA1, BA2, CA5, HA2, and VA2). Furthermore, cytotoxicity assay was showed that mature tea leaf stalk extract effectively inhibited HT-29 and Caco-2 cells, with lower IC50 values of 0.402 ± 0.029 mg/ml and 0.195 ± 0.028 mg/ml, respectively comparing to young tea leaf stalks (0.627 ± 0.044 mg/ml and 0.218 ± 0.035 mg/ml). These new findings suggested that young and mature green tea leaf stalks are a promising natural source of bioactive compounds with potential antioxidant, antibacterial and anticancer effects, providing a safer alternative or complementary approach to conventional CRC therapy while mitigating associated side effects.
OS3-8	KB0114-A 15:05-15:20	Role of 2'-5' Oligoadenylate Synthetase-Like 1- (OASL1-) in a Mouse Model of Pseudorabies Virus Infection **Tien Huyen Ton Nu Bao,** Mwense Leya, Thach Phan Van, Gaeul Ham, ByungKwan Oh, Sang-Ik Oh, Won-Il Kim, Seok-Chan Park, and Bumseok Kim Jeonbuk National University Abstract: Pseudorabies virus (PRV), a neurotropic alphaherpesvirus, infects a wide range of mammals and causes Aujeszky's disease, which poses a major threat to the swine industry. However, the mechanisms underlying the interaction between PRV and the host innate immune response remain poorly understood. It has been reported that 2'–5' oligoadenylate synthetase-like 1 (OASL1) negatively regulates type I interferon (IFN) production by inhibiting the translation of the IFN regulatory factor 7 (IRF7). Here, we investigated the role of OASL1 in the host response to PRV infection using OASL1-deficient (Oasl1−/−) mice. The results showed that the expression level of OASL1 significantly upregulated during PRV

		infection both in myeloid-derived dendritic cells, macrophages, and in the spleens, lungs, and brains of wild type (WT) mice. Oasl1−/− mice did not develop any clinical symptoms and all survived after infection with PRV, while WT mice exhibited severe neurological symptoms and showed 100% mortality. Furthermore, Oasl1−/− mice showed significantly lower mRNA expression of PRV in the spleens, brains and lungs compared to WT mice. In response to the virus challenge, WT mice displayed elevated levels of inflammatory cytokines including interleukin 1β (IL-1β), IL-6 and tumor necrosis factor α (TNF-α) in the spleen and brain. Histopathological examination revealed moderate inflammatory cell infiltration in the brain of Oasl1−/− mice. Moreover, Oasl1−/− mice had much higher concentrations of interferons α (IFN-α) in the serum relative to results obtained with WT mice. Collectively, these data reveal that Oasl1−/− mice are more resistant to PRV infection than WT animals by enhancing type I interferon responses and limiting inflammatory pathology. Our findings suggest that OASL1 has a potential role in PRV infection and could be evaluated as a target for antiviral therapy.
OS3-9	KB1010-A 15:15-15:35	Liposome-Based Delivery of DNA Aptamers to Inhibit Antibiotic Resistance **Swagata Patra,** Damini Sahu, Leena L. Badgujar, P. I. Pradeepkumar, and Ruchi Anand Indian Institute of Technology Bombay Abstract: The misuse of antibiotics has accelerated the rise of multidrug-resistant (MDR) bacterial strains, posing a serious global health threat. A major resistance mechanism involves sitespecific methylation of ribosomal RNA (rRNA), which impairs antibiotic binding. Erythromycin-resistant methyltransferases (Erms), methylate the A2058 residue in the nascent peptide exit tunnel (NPET) of rRNA, blocking macrolide, lincosamide, and streptogramin B (MLSB) antibiotics [1,2]. To counter this, we previously employed SELEX to identify DNA aptamers that selectively bind and inhibit Erm. To enhance aptamer stability and intracellular delivery, we encapsulated them in liposomes composed of DOTAP, DOPE, and DSPE-PEG lipids, using the thin-film hydration method. These liposomes protect aptamers from enzymatic degradation and facilitate cellular uptake. The formulations were characterized via dynamic light scattering (DLS), UV–vis spectroscopy, fluorescence spectroscopy, and transmission electron microscopy (TEM). The inclusion of DOPE, a fusogenic lipid, promotes membrane fusion and enhances intracellular

		delivery. We demonstrate successful delivery of aptamerloaded liposomes into Staphylococcus aureus, a Gram-positive pathogen. Flow cytometry and confocal laser scanning microscopy (CLSM) confirmed efficient uptake and localization. The aptamers effectively reached the intracellular target, inhibited Erm activity, and restored erythromycin sensitivity. This liposomal platform not only improves aptamer bioavailability and stability but also provides a non-toxic, controlled-release system with strong therapeutic potential against S. aureus.

Oral Session 4

January 17, 2026, Saturday (GMT+9)

Duration	Venue
15:50-18:05	208 Seminar Room

Topic:	Bioscience of Immunity, Inflammation, and Disease Mechanisms
Session Chair:	Assoc. Prof. Rose Chinly Mae Ortega-Kindica, University of the Philippines Cebu

Paper Detail

OS4-1	KB0034-A 15:50-16:05	Enhancing the Antitumor Activity of CD19/Bcma Car-T Cells in Vitro with a pd1il7r Chimeric Switch Receptor **Kai Yan** and Zhongdang Xiao Southeast University Abstract: Chimeric antigen receptor (CAR)-T cell therapy has revolutionized the treatment of hematologic malignancies, but its long-term efficacy is hindered by antigen escape, T-cell exhaustion, and the immunosuppressive tumor microenvironment (TME). Programmed death ligand 1 (PD-L1) expression in the TME inhibits CAR-T cell function, limiting persistence and cytotoxic capacity. To address this, we engineered CD19/BCMA-targeted CAR-T cells co-expressing a PD1IL7R chimeric switch receptor (CSR). This novel receptor converts PD-L1-mediated inhibitory signals into IL7R-driven pro-survival and proliferative pathways, enhancing CAR-T cell expansion, persistence, and cytotoxicity in a PD-L1–dependent but antigen-specific manner. In vitro, CD19/BCMA-PD1IL7R CAR-T cells exhibit improved central memory T-cell formation, increased cytokine secretion, and superior antitumor activity compared to conventional CAR-T cells. Notably, these functional enhancements were evident even at low levels of PD-L1 expression on target cells, and no off-target effects were observed. Our findings suggest that incorporating the PD1-IL7R switch receptor into CAR-T cells effectively overcomes PD-L1–mediated immunosuppression, enhancing both their persistence and antitumor efficacy. This approach offers a versatile strategy for improving CAR-T therapy in the treatment of both hematologic and solid tumors.

OS4-2	KB0005 16:05-16:20	Review of Liver Fibrosis and Inflammation **Qingrui Zeng** Beijing Forestry University Abstract: Liver fibrosis is a common pathological process triggered by chronic liver diseases (such as viral hepatitis, non-alcoholic fatty liver disease, and alcoholic liver disease), posing a serious threat to global public health. This article provides a systematic review of the epidemiology, pathogenesis, major cell types, key signaling pathways, and treatment advances in liver fibrosis. The core of fibrosis lies in the activation of hepatic stellate cells (HSCs) and their sustained synthesis of extracellular matrix (ECM). Macrophages, as important immune regulatory cells, play a bidirectional regulatory role in inflammatory responses and fibrosis reversal. The paper focuses on elucidating the regulatory mechanisms of immune activation mediated by DAMPs/PAMPs, TGF-β/Smad, and PDGF signaling pathways on HSC activation, as well as the polarization dynamics of M1/M2 macrophages. Research has shown that liver fibrosis has a certain degree of reversibility, and early intervention can promote the inactivation or apoptosis of activated HSCs, restoring tissue structure. Based on these mechanisms, drugs targeting key factors such as CCL2/CCR2 and TGF-β, as well as emerging therapeutic approaches like stem cells, gene editing, and gut microbiota modulation, have become key directions for future treatment. Although no specific anti-fibrotic drugs have been approved yet, mechanistic research provides a solid foundation for personalized precision therapy.
OS4-3	KB0094-A 16:20-16:35	Propofol Exerts Rapid Antidepressant Effects via Modulation of Excitatory Neuronal Activity in the Ventromedial Hypothalamus **Dan Wang** and Yonggui Yuan Southeast University Abstract: Major depressive disorder (MDD) is the leading cause of disability globally, and standard antidepressants necessarily require weeks to gain efficacy. Rapid-acting agents with the ingredient ketamine point to the promise that anesthetics themselves can serve as antidepressants, but the mechanisms are not yet clear. Propofol, a GABA_A receptor–potentiating anesthetic, is itself proposed to modulate affective state, yet how it plays a role in depressive-like behavior and corresponding neural substrates is not understood. Utilizing the chronic social defeat stress (CSDS) mouse model,

		we investigated the antidepressant-like properties of intravenous propofol. Behavioral end points (tail suspension test, forced swim test, sucrose preference) were evaluated at several time points following injection. c-Fos immunofluorescence to determine neural activity changes with cell-type specificity defined through VGAT or VGLUT2 colabeling. Calcium dynamics of ventromedial hypothalamus (VMH) excitatory neurons were captured through fiber photometry. Chemogenetic inhibition or activation of VMH excitatory neurons explored causality, and viral tracing delineated downstream projections. Propofol generated quick, transient antidepressant-like effects at 1 h after injection in the CSDS mice. Immunohistochemistry indicated upregulated VMH neuronal activity for the CSDS mice, and substantially reduced it with propofol. The suppressed c-Fos signal localized to excitatory neurons, but not inhibitory neurons. Fiber photometry verified the reduction of calcium activity amongst VMH excitatory neurons with propofol. Chemogenetic inhibition recapitulated the behavioral effects of propofol, but activation induced depression-like phenotypes. Projection mapping revealed primary VMH excitatory neurons outputs to the BNST, PAG, and LH, suggesting a circuit mechanism for the observed behavioral changes.
OS4-4	KB0024-A 16:35-16:50	Differential Gene Expression Analyses on a Unique Behavioral Phenotype of Hyperbilirubinemic Gunn Rat Models **Julia Theresa Aujero Regalado**, Claudio Tiribelli, and Silvia Gazzin Fondazione Italiana Fegato Abstract: Gunn rats are commonly utilized to study the neurotoxic effects of elevated unconjugated bilirubin (hyperbilirubinemia), a condition caused by homozygous mutations in the UGT1A1 gene (jj). When established in 2007, our colony displayed no apparent phenotype. However, beginning in 2016, a subset of rats exhibited visible motor deficits, including wobbly gait, tremors, and inability to maintain the rear end position. This distinct behavior was designated as the severe phenotype (SP) and has since been inherited until the F9 generation. To investigate the potential genetic basis of SP, we performed reference-based transcriptomic assembly comparing jj and SP animals. Followed by variant calling which revealed 126,911 variations unique to SP. Principal component analysis (PCA) demonstrated marked dissimilarity between SP samples, while jj samples clustered more closely together. Differential gene expression (DGE) further highlighted robust differences

		between phenotypes, identifying 183 upregulated genes and 41 downregulated genes in SP. Downstream transcriptomic analyses confirmed pronounced genetic differences corresponding to the phenotypic behavior observed in our colony. This study provides the first evidence that the emergence of SP in Gunn rats is associated with specific genetic determinants which serves as a foundation for further investigations into the molecular mechanisms underlying this phenotype.
OS4-5	KB1012-A 16:50-17:05	Single-Cell Transcriptome Sequencing Reveal the Effect and Underlying Mechanisms of Gzmk+CD8+CD27+CCR7+ T Cells in Patients with Acute Ischemic Stroke **Hui Ren** Southeast University Abstract: Splenic sympathetic activity critically modulates peripheral immunity after ischemic stroke, thus intervention in spleen sympathetic activity represents a promising therapeutic strategy for stroke. However, the mechanisms underlying spleen-brain-immune axis communication remain poorly understood. Here, we utilized a surgical denervation protocol to perform splenic sympathetic denervation (SDN), which significantly attenuated brain injury following stroke. Through single-cell RNA sequencing, we identified a novel GZMK+CD8+CD27+CCR7+ T-cell subset in patients with acute ischemic stroke (AIS), which we designated stroke-associated T (Tsa) cells. The expansion of Tsa cells was positively correlated with the severity of clinical symptoms and was driven by the splenic sympathetic nervous system. Stroke-induced sympathetic activation triggers the release of splenic norepinephrine (NE), which preferentially signals through ADRB2 on Tsa cells to promote their mobilization. Additionally, ischemic injury induces endothelial cell-specific expression of CCL19, which chemoattracts Tsa cells into the brain parenchyma via their cognate CCR7 receptor, exacerbating neuroinflammatory injury and neurological deficits in a transient middle cerebral artery occlusion (tMCAO) mouse model. We developed a CCR7-targeting peptide to disrupt this chemotactic axis and reduce T-cell infiltration, thereby mitigating brain injury. Our findings highlight SDN as a promising therapeutic strategy to attenuate ischemia–reperfusion injury and suggest its potential as an adjunctive therapy for reperfusion treatment in AIS patients.
OS4-6	KB0054-A	Perilla Frutescens Seed Residue Extract Prevent Prostate Enlargement and

	17:05-17:20	Modulate Gut Microbiota in a Rat Model of Benign Prostatic Hyperplasia **Chatsiri Siriwathanakul** and Teera Chewonarin Chiang Mai University Abstract: Benign prostatic hyperplasia (BPH), a common condition in aging men characterized by prostate enlargement, impairs urinary function and is associated with inflammation, hormonal imbalance, and metabolic dysregulation. This study investigated the therapeutic potential of bioactive compounds from Perilla frutescens seed residue crude extract (PCE), enriched with rosmarinic acid, luteolin, and apigenin, in a testosterone-induced rat model of BPH, compared to finasteride (a standard drug). BPH was induced by subcutaneous implantation of testosterone propionate, followed by 30 days of oral PCE administration. Results showed that BPH rats exhibited significantly increased serum testosterone at day 15. PCE treatment normalized the prostate weight/body weight ratio (PCE 1 mg/kg: 9.4 ± 0.8 mg/g; BPH control: 12.1 ± 1.2 mg/g; sham: 6.1 ± 0.9 mg/g), comparable to finasteride. Notably, PCE modulated gut microbiota, enriching Akkermansia muciniphila and Tuzzerella spp., both associated with anti-inflammatory and metabolic benefits. These findings suggest that PCE may prevent testosterone-induced prostate enlargement. Ongoing histopathological, molecular, and serum metabolomic analyses will further elucidate the mechanisms underlying these effects.
OS4-7	KB1018-A 17:20-17:35	Glp-1R-Independent, Microbiota-Dependent Antidepressant Actions of Semaglutide Though Elevating 2-Arachidonoylglycerol Levels **Liang Bian** Southeast University Abstract: While GLP-1R agonists like semaglutide are widely used for metabolic disorders, their neuropsychiatric impacts remain unclear, with clinical studies reporting both increased depression risk and reduced suicidal ideation. Animal models similarly show paradoxical outcomes. Our study demonstrates that semaglutide attenuates depressive-like behaviors in Glp1r−/− mice, indicating that its antidepressant effects are independent of GLP-1R. However, gut microbiota depletion abolishes semaglutide's antidepressant efficacy. Mechanistically, semaglutide induces gut microbial remodeling with specific enrichment of Lactobacillus delbrueckii strains, which are typically depleted in depressive states,

		subsequently elevating the endocannabinoid 2-arachidonoylglycerol (2-AG) levels. This endogenous cannabinoid metabolite suppresses neuronal hyperactivation in the basolateral amygdala and dorsomedial hypothalamus, key nodes in emotional and stress circuits. Notably, fecal transplantation from semaglutide-treated mice or direct L. delbrueckii colonization recapitulated the efficacy of semaglutide, confirming the GLP-1R-independent and gut microbiota-dependent antidepressant effects of semaglutide. In conclusion, our findings resolve the prior contradictions by proposing a microbiota-dependent mechanism for GLP-1 analogs' neuropsychiatric effects. This work advances the translational potential of targeting the microbiota-endocannabinoid-brain axis, offering a framework for repurposing metabolic drugs in psychiatry.
OS4-8	KB2015-A 17:35-17:50	E5 Peptide-Functionalized Platinum Nanozymes Mediate Immune Microenvironment Reprogramming in B-cell Lymphoma **Mengjun Wang**, Rong Guo, Yitong Zhao, Ying Wang, Wenxin Fu, Guancheng Wang, Mingze Lu, Haoan Wu, Ming Ma, Yunfei Bai, and Yu Zhang Southeast University Abstract: To address the complexity of structural design and synergistic optimization of biological effects of nanozymes in the field of oncology therapy, this study constructed a nanozymes platform (Pt@E5) with a facile and highly efficient preparation process for precision targeting of lymphoma. Pt@E5 nanozymes assemblies were directly prepared by a one-step reduction method, and the modification of E5 peptide ensured the dimensional homogeneity and stability of the platinum nanoparticles. This nano enzymatic platform combines dual enzyme activity with chemokine receptor 4 (CXCR4) targeting. It can inhibit tumor metastasis by targeting CXCR4 and thus specifically blocking the CXCR4/CXCL12 (stromal cell derived factor 1α) signaling pathway. In addition, it induces mitochondria mediated apoptosis and immunogenic cell death (ICD) in tumor cells by catalyzing the production of reactive oxygen species (ROS) using dual enzyme activity. In a mouse lymphoma model, the therapeutic results showed that Pt@E5 treatment effectively remodeled the tumor immunosuppressive microenvironment by promoting cytotoxic T cell infiltration (CTLs) and reducing regulatory T cell (Treg) levels. It also eliminated A20 cells from the bone marrow and peripheral blood, leading to significant tumor

		regression compared to the control group. In conclusion, this study offers a promising translational strategy for the multifaceted collaborative treatment of diffuse large B-cell lymphoma (DLBCL) based on a simple nanozyme-peptide assembly.
OS4-9	KB2021-A 17:50-18:05	Targeting Proinflammatory Myeloid Cells with anti-TNF Antibody-Conjugated Prussian Blue Nanoparticles alleviates inflammation in Inflammatory Bowel Disease **Ying Wang**, Jingxian He, Wenxiang Lu, Yitong Zhao, Kaizheng Feng, Haoan Wu, Yu Zhang, and Yunfei Bai Southeast University Abstract: Inflammatory bowel disease (IBD) is characterized by immune dysregulation and oxidative stress. The persistence activated proinflammatory myeloid cells are associated with the nonresponse to anti-TNF therapy in IBD patients. Reactive oxygen species (ROS) act as a pivotal pathogenic hub, bridging TNF-driven NF-κB activation to NLRP3-inflammasome signaling and fueling a chronic inflammatory microenvironment (IME). Thus, we developed a dual-functional infliximab antibody-Prussian blue nanoparticle conjugate (PB@IFX) that concurrently scavenges ROS and neutralizes TNF. Using a TNBS-induced chronic colitis model integrated with single-cell transcriptomics, we demonstrate that PB@IFX effect reduces inflammatory myeloid cells ($Spp1^+$ macrophages, $Ly6c^+$ monocytes, neutrophils, and pDCs) and activated fibroblasts, while restoring epithelial integrity and expanding regulatory T cells. Consequently, PB@IFX suppresses the expression of genes encoding proinflammatory mediators (e.g., Tnf, Il1b, Il6, Osm, Cxcl1, Cxcl2, Ccl2), and nicotinamide adenine dinucleotide phosphate (NADPH) oxidase genes (Cybb, Ncf1) and the formation of neutrophil extracellular traps (NETs). Furthermore, PB@IFX reprograms macrophage polarization toward a pro-resolving phenotype. The reshaped IME of the intestine supports recovery of microbiome balance, increasing beneficial bacteria and reducing pathogenic bacteria. Our findings illustrate a synergistic nanotherapeutic strategy that simultaneously resolves immune dysregulation and oxidative damage while providing mechanistic insights into successful IBD therapy and identifying potential targets for enhanced treatment efficacy.

Oral Session 5

January 17, 2026, Saturday (GMT+9)

Duration	Venue
13:20-15:05	303 Seminar Room

Topic:	Biomaterials, Biotechnology, and Environmental Bioscience
Session Chair:	Asst. Prof. Thida Kaewkod, Chiang Mai University

Paper Detail

OS5-1	KB0037 13:20-13:35	Comparing the Role of Dopamine D1 and D3 Receptors in Mediating Aversive Learning in Zebrafish **Siew-Ying Mok,** Pek-Yee Tang, Zhai-Yong Wong, and Hong-Yao Lai Universiti Tunku Abdul Rahman Abstract: Dopamine is a key neuromodulator in the vertebrate brain. Despite accumulating evidence of dopamine's involvement in learning and memory regulation, the roles of individual receptor subtypes remain unclear. This study investigates the effects of SCH-23390 and SB-27011-A, selective antagonists of the D1 and D3 dopamine receptors on learning and memory in zebrafish. Using an associative learning task in a T-maze with electric shocks as stimuli, we assessed the impact of these drugs on zebrafish performance. Our results show that SCH-23390 at both 1 mg/L and 5 mg/L and SB-27011-A at 5 mg/L altered behaviors. However, the effects observed at 5 mg/L were confounded by impaired locomotion, suggesting that reliable cognitive assessments should focus on lower doses. Although no significant differences were observed in percentage of correct arm entries, the SCH-23390 group at 1 mg/L showed a significantly lower proportion of fish with correct first arm entries and significantly more time spent in the wrong arm, whereas no such effects were seen in the SB-27011-A group. These findings suggest that D1 receptors, but not D3 receptors, play a crucial role in associative learning involving aversive stimuli. Further research is necessary to clarify how dopamine receptor subtypes contribute to different learning paradigms.
OS5-2	KB0071-A 13:35-13:50	Biosequestration of Carbon Dioxide Using Novel Β- And γ-Carbonic Anhydrase From Bacterium Lysinibacillus SP. Wh

		Zerlinda Mara Ditta, Prinya Chindaprasirt, and Jindarat Ekprasert Khon Kaen University Abstract: The challenge of global climate change requires the development of effective carbon dioxide (CO2) mitigation strategies. Biocatalytic carbon sequestration, which uses the enzyme carbonic anhydrase (CAs) is a reliable and clean process for transforming CO2 into stable carbonate minerals (CaCO3). This study reports the identification and functional characterization of the novel β-CAs and γ-CAs variants derived from the bacterium Lysinibacillus sp. WH. Enzymatic activity was quantified in crude extract using two distinct methods, Willbur-Anderson unit (WAU) assay and secondary esterase assay. The β-CAs and γ-CAs variants exhibited hydratase activities of 14.58 WAU/mL and 28.27 WAU/mL, respectively. Correspondingly, esterase activity was recorded at 16.23 mg/mL and 16.52 mg/mL, respectively. Furthermore, the crude enzyme extract was evaluated for its capacity to catalyze mineral carbonation, the precipitation of CO2 into CaCO3. The results indicated a rapid rise in turbidity within the enzyme samples, demonstrating successful mineral precipitation when compared to non-enzymatic control. These findings confirm the high catalytic potential of Lysinibacillus sp. WH CAs, establishing them as a promising biocatalyst for scalable CO2 sequestration.
OS5-3	KB0106-A 13:50-14:05	Whole Genome Signals of Ergosterol Pathway Amplification in Low Earth Orbit Aspergillus Niger **Siphiwengesihle Kuhle Silindile Mbamali,** Nikwando Mohlomi, Magrieta van der Nest, Nokuthula Peace Mchunu, and Kugen Permaul Durban University of Technology Abstract: Filamentous fungus like Aspergillus niger are opportunistic pathogens that, while less virulent than A. fumigatus, remain clinically relevant in aspergillosis. Extreme environments such as the International Space Station (ISS) present unique stressors (microgravity, radiation) known to alter fungal physiology. This work thus aimed to compare genomic DNA profiles of A. niger isolates from Earth and low Earth orbit to identify adaptive genetic signatures. Whole-genome sequences of A. niger from ISS and diverse Earth cohorts (Africa, Europe, Americas, Asia) were compared. A reference-guided analysis quantified per-gene DNA read counts, and differential abundance testing with pathway enrichment was used to pinpoint cohort-specific gene copy number variations in

		stress-response and antifungal-resistance pathways. Spaceflight isolates showed elevated genomic representation of key ergosterol biosynthesis genes (squalene epoxidase SQLE and 14α-demethylase CYP51) relative to terrestrial strains, suggesting an up-tuned sterol production capacity in microgravity. ISS genomes also exhibited cohort-biased shifts in proteostasis machinery: notably a "leaner" 26S proteasome regulator gene profile (fewer high-abundance regulatory subunit genes) compared to some Earth groups. Concurrent enrichment of mitochondrial, autophagy/mitophagy, and protein-folding pathway genes was also observed in ISS isolates. No gross genomic defects were evident, and ribosomal gene differences appeared to reflect static copy-number variation rather than true expression changes. Genomic differences between ISS and Earth A. niger suggest that the space environment selects for enhanced membrane sterol synthesis and tightened protein homeostasis control. These DNA-level adaptations likely help fungi withstand microgravity-induced membrane and proteotoxic stress. The findings raise the prospect of altered antifungal susceptibility in space-adapted strains and underscore the need for functional studi
OS5-4	KB0130 14:05-14:20	Improving Mangrove Restoration Efficacy Through Husk-Assisted Stability and Arbuscular Mycorrhizal Fungi in Nutrient Facilitation Maikel Schoenmakers, Xavier Kardjono, Kuncoro Kohar, **Willyanto Anggono,** and Edwin Setiawan SMA Cita Hati West Campus Abstract: Mangrove ecosystems are vital for coastal resilience, serving as natural barriers against erosion, nurseries for marine life, carbon sinks, and biodiversity hotspots. However, they are rapidly declining due to natural and human-induced pressures. Two major threats are tidal erosion, which dislodges young propagules before roots can anchor, and crab predation. To address these challenges, this study explores the combined use of Cocos nucifera (husk waste) and Arbuscular mycorrhizal (AM) fungi as a low-cost, sustainable restoration method. Coconut husks were chosen for their lignin and cellulose content, offering physical stability, moisture retention, and gradual nutrient release. AM fungi were used to enhance nutrient uptake and plant resilience. Four environmental treatments were tested over four months, and results showed that the combination of coconut husk with fungi achieved the highest growth performance, increasing root amount by 103.6% compared to the control and increasing leaf length by 30.1-38.1%

		compared to the other treatments in the first month. Additionally, it showed a 27.6-50.5% increase in root amount compared to the other environmental groups and a 19.1-40.5% increase in leaf length in the fourth month. This indicates that combining agricultural waste and symbiotic fungi can significantly improve mangrove propagule survival.
OS5-5	KB0131 14:20-14:35	Effect of Theobromine from Theobroma Cacao L. on Cervical Cancer Treatment Budi Santoso, Josephine Eugenia Wirianata, Maria Louise Ulina Dimu, Rhiana Abigail Katu, **Willyanto Anggono,** and Edwin Setiawan Petra Christian University Abstract: Theobroma cacao L. (Forastero variety) is a tropical plant widely cultivated in the Sumba region, Indonesia. The cacao beans contain theobromine, which has a notable therapeutic potential. This study investigates the possibility of cacao beans as a treatment for cervical cancer. Using a quantitative method, cacao beans were processed into three different formulations (F1, F2, F3) and evaluated through an organoleptic test to determine the most preferred formulation. F3 was the most approved formulation in aroma, colour, texture, and taste. The 20 respondents did not experience any adverse side effects within 24 hours of consumption. A clinical trial was done on F3 involving early-stage cervical cancer patients. For over 14 days, patients showed improvements, including reduced vaginal discharge, bleeding, and pelvic pain. Laboratory results indicated an increase in haemoglobin from an average of 11.0 to 12.0 g/dL. Haematocrit also increased from 35.67% to 36.10%, and erythrocyte counts improved from 4.27 to 4.73 µL. Meanwhile, neutrophils decreased from an average of 67.5% to 63.25%, and basophils declined from 0.95% to 0.65%. The anthocyanin reaction time increased from an average of 4.6 to 10.3 seconds, indicating reduced oxidative activity. These findings suggest that cacao beans contribute to anticancer effects.
OS5-6	KB2029-A 14:35-14:50	Anionic liposome assisted membrane fusion enabling rapid multiplexed detection of EV miRNAs **Jing-Yuan Ma** and Yu Zhang Southeast University Abstract: Extracellular vesicle (EV) microRNAs (miRNAs) are promising liquid biopsy biomarkers for non-invasive diagnosis, monitoring, and therapeutic evaluation of cancer. However, sensitive EV miRNA

		detection is hindered by complex pre-analytical processing. Here, we present an anionic liposome (AL) assisted membrane fusion strategy enabling one-step multiplexed quantification of EV miRNAs directly from plasma without EV isolation or RNA extraction. Liposomes encapsulating probes were prepared using a microfluidic chip, achieving catalytic signal amplification after target recognition. Systematic lipid screening identified ALs as optimal carriers, showing minimal background and superior sensitivity over cationic and neutral liposomes. The AL-based assay delivered accuracy comparable to qPCR with a streamlined workflow. Applied to 106 clinical samples from lymphoma patients and healthy controls, integration with artificial intelligence achieved high accuracy (AUC > 0.99). In summary, this study demonstrates a platform enabling direct and sensitive plasma EV miRNA detection, offering strong potential for clinical translation in cancer liquid biopsy.
OS5-7	KB0132 14:50-15:05	Apigenin Extracts from Myrmecodia Pendans and Their Potential Role in Coronary Heart Disease Mitigation Budi Santoso, Nirel Andisfyl Sarungallo, Beatrix Melany Wattimena, **Willyanto Anggono,** and Edwin Setiawan Petra Christian University Abstract: Myrmecodia pendans is an epiphytic plant native to Papua that contains apigenin, a compound with antioxidant, anti-inflammatory, and vasodilator effects. Apigenin is associated with the prevention of coronary heart disease (CHD) and offers an environmentally friendly alternative to synthetic drugs. This study investigates the possibility of apigenin from M. pendans as a treatment for coronary heart disease. Using a quantitative method to test three types of treatments with a constant amount of Coffea arabica L. (12 g) and water (200 ml), but varying dosages of M. pendans: Treatment A (6 g), Treatment B (9 g), and Treatment C (12 g). The physiological parameters, including blood pressure, heart rate, oxygen saturation, total cholesterol, low-density lipoprotein (LDL), and high-density lipoprotein (HDL), were measured before and after consumption. Treatment B demonstrated the greatest improvement, with blood pressure decreased (from 155/101 mmHg to 119/80 mmHg). According to the laboratory results, HDL levels increased from 39 mg/dL to 45 mg/dL while LDL levels decreased from 140 mg/dL to 83 mg/dL. These results indicate that apigenin has potential as a promising herbal therapy

		candidate in preventing coronary heart disease.

Oral Session 6

January 17, 2026, Saturday (GMT+9)

Duration	Venue
15:30-17:30	303 Seminar Room

Topic:	Bioactive Compounds, Biotechnologies and Biomedical Applications
Session Chair:	Asst. Prof. Siew-Ying Mok, Universiti Tunku Abdul Rahman

Paper Detail

OS6-1	KB0019-A 15:30-15:45	The Inflammatory Biomarker of Adhesion Molecules VCAM-1 and ICAM-1 in the Progression of Premature Atherosclerosis **Zulhabri Othman**, Jamunarani Murugan, Norwahidah Abdul Karim, Lilik Herawati, and Norshafarina Shari Manipal University College Malaysia Abstract: Endothelial cell adhesion molecules have been reported to play an important role in developing inflammation and atherosclerosis. This study aims to investigate the gene expression of adhesion molecules as inflammatory biomarkers in the development of premature atherosclerosis. Gene expression of intercellular adhesion molecule-1 (ICAM-1) and vascular cell adhesion molecule-1 VCAM-1 gene was performed by Real-Time PCR using SYBR Green, between two the groups of Sprague-Dawley rats, high-fat diet (HFD) and normal diet (ND) groups at week 8 and week 16. The ICAM-1 gene expression analysis has shown a significant difference in the gene expression at week 8 ($p=0.031$; $F=7.830$) between HFD group (Ct value=33.55±0.86) and ND group (Ct value=12.50±15.02). The VCAM-1 gene expression analysis has shown a significant difference in gene expression at week 8 ($p=0.023$; $F=9.213$) between HFD group (Ct value=35.88±0.57) and ND group (Ct value=8.89±17.78). There was a significant difference in VCAM-1 gene expression at week 8 ($p=0.996$; $F=0.001$), with the Ct values at 29.28±12.26 and 29.24±13.25 for the HFD and ND groups, respectively. The study has suggested that adhesion molecules VCAM-1 and ICAM-1 might play an

		important role as inflammatory biomarkers in the development of premature atherosclerosis.
OS6-2	KB0108-A 15:45-16:00	Imaging of Intracellular Oxygen Partial Pressure in Cultured Cells Using a Cell-Permeable Phosphorescent Probe **Hidenari Emoto,** Mitsuru Yuba, Yuma Taniguchi, and Kosuke Tsukada Keio University Abstract: Molecular oxygen is utilized for energy production in cellular mitochondria, and acts as a mediator that regulates metabolism and the tumor microenvironment, depending on the oxygen concentration. However, due to technical limitations, no universal method has yet been established for visualizing intracellular oxygen partial pressure (pO2). This study aimed to visualize intracellular oxygen distribution using a cell-permeable phosphorescent probe. HeLa and HepG2 cells were cultured on 35-mm dishes and incubated with 2 μM of the oxygen-sensitive probe LOX-1 for 12 hours. The cells were irradiated with a 405-nm laser at a modulation frequency of 50 kHz, and oxygen-dependent phosphorescence was detected using a photomultiplier tube. The phosphorescence lifetime was analyzed by the phasor plot method and converted to pO2 using the Stern–Volmer equation. Two-dimensional scanning provided pO2 images of the cells. The pO2 image of the tumor cell colony revealed hypoxic conditions at the center, suggesting that the pO2 gradient depends on the balance between oxygen supply and consumption by the cells. This laser microscopy system is also expected to be applicable to the quantitative imaging of oxygen metabolism in cell spheroids and organoids.
OS6-3	KB0059-A 16:00-16:15	MAPK Targeting in Diffuse Intrinsic Pontine Glioma **Stefana Duca,** Felicity de Cogan, Weng Chan, and Andrew Lewis University of Nottingham Abstract: Diffuse intrinsic pontine glioma (DIPG) is a highly aggressive paediatric brain tumour lacking effective therapies. Aberrant MAPK pathway activation, arising from canonical mutations or epigenetic dysregulation, represents a promising therapeutic target. To investigate this, we performed a focused drug screen to rank MAPK inhibitors by efficacy in DIPG in vitro models and assessed their selectivity relative to other tumour types and non-malignant cell lines. Complementary RNA-sequencing of treated DIPG cells revealed transcriptional adaptations

		associated with survival and relapse, providing candidate biomarkers and potential targets for rational combination therapies. Together, these findings highlight the MAPK pathway as a potential therapeutic target for DIPG and underscore the value of integrating biochemical and molecular profiling to optimise treatment strategies.
OS6-4	KB0103-A 16:15-16:30	Molecular and In Silico Insights into the Cytoprotection of Aqueous Methanolic Bark Extracts of Alstonia scholaris (L.) R. Br. against RSL3-induced Ferroptosis **Katrina Lorraine Ching Chua,** Anne Nicole Sabuco Tensuan, Mica Xiena Yungca, Charisse Tugahan, Virgilio Linis, and Rafael Atillo Espiritu De La Salle University Manila Abstract: Ferroptosis is a damaging iron-mediated process implicated in various human pathophysiological conditions. Regulating this cell death mechanism using plant-derived bioactive compounds known to target various diseases could be a promising therapeutic strategy. The role of Alstonia scholaris (L.) R. Br. in ferroptosis regulation remains unexplored despite reported bioactivities. In this study, aqueous methanolic Alstonia scholaris bark extracts have exhibited significant radical scavenging activity (IC50 = 0.24 mg/mL) as demonstrated by 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay, which may be due to modest total phenolic (26.83 ± 3.51 mg gallic acid equivalent/g crude extract) and flavonoid (7.59 ± 1.59 mg quercetin equivalent/g crude extract) content. Extracts at 0.1875 mg/mL rescued HT-29 cells against RAS-selective lethal 3 (RSL3)-induced ferroptosis, comparable with the standard inhibitor ferrostatin-1. Observed antioxidant activity could be due to the potential presence of quinic acid and magnolol, as suggested by gas and liquid chromatography-mass spectrometry (GC-MS and LC-MS) analyses. Molecular docking of both compounds with heme oxygenase 1 (HO-1) demonstrated preferable interactions comparable with a co-crystalized inhibitor (binding free energy, BFE = −7.64 kcal/mol), particularly magnolol (BFE = −7.22 kcal/mol). Overall, novel ferroptosis regulators may be present in the extract, and future studies conclusively confirming their presence and activities are recommended.
OS6-5	KB0023-A 16:30-16:45	Production and Evaluation of Immunoglobulin Y Against Malayan Pit Viper Venom **Vichununt Kerdput**, Vararut Yodkamol, Mattika Sookprasong, and Charin Thawornkuno

		Mahidol University Abstract: The World Health Organization (WHO) recognizes snakebite envenoming as a neglected tropical disease and a major cause of morbidity and mortality worldwide. In Thailand, antivenom production depends exclusively on horses, but the 2020 outbreak of African Horse Sickness (AHS), which caused widespread horse deaths, highlighted the vulnerability of this approach and the need for alternative platforms. This study explored the feasibility of producing snake antivenom in egg-laying hens. Five hens were immunized three times at 2-week intervals with crude Malayan pit viper (Calloselasma rhodostoma, CR) venom. Venom-specific immunoglobulin Y (IgY) was transferred into egg yolks and extracted by ammonium sulfate precipitation, yielding ~45 mg per egg at 85% purity. ELISA confirmed IgY binding activity, with the strongest response observed one week after the third immunization. In vivo efficacy was evaluated in mice: pre-incubation of 1.66 mg IgY with 159 µg CR venom (3 × LD50) followed by intraperitoneal injection reduced lethality by 75%. These results demonstrate that hens can serve as a scalable, non-invasive, and sustainable source of antivenom, offering a promising alternative or complement to equine-derived antibodies.
OS6-6	KB0041-A 16:45-17:00	Maternal and Fetal Dyslipidaemia and Differential Expressions of Proteins of Lipid Metabolism Are Associated with Fetal Overgrowth in Diabetes-In-Pregnancy. **Kamila Thalapalliyil,** Zachariah Bobby, Gowri Dorairajan, and Pampa Ch Toi Jawaharlal Institute of Post graduate and Medical Research (JIPMER) Abstract: Background: Diabetes-in-Pregnancy (DIP) is associated with poor maternal and fetal outcomes, particularly fetal overgrowth (macrosomia). Altered systemic and placental lipid metabolism could be one of the reasons of the complications of DIP. Objectives: Assessment of maternal & cord blood lipid profile and biochemical parameters related to placental lipid metabolism in DIP. Methods: Maternal blood, cord blood, and placental samples were collected from women with DIP and healthy controls. Lipid profiles were measured using a clinical chemistry analyser. Placental gene expressions (PPARα, PPARγ, SCD1, FAS, LPL) were analysed, while protein expressions (LXRα, SREBP1, FAS, PPARα, PPARγ) were assessed by western blotting and IHC. Lipid droplet accumulation was visualized using Oil-Red-O staining. Observed significant dyslipidaemia in

		maternal and fetal circulation in DIP comparison to controls. Maternal and fetal triglyceride levels were significantly higher in DIP compared to controls. Placental proteins LXRα, FAS, and SREBP1 were upregulated, whereas PPARα and PPARγ were reduced. Maternal lipid profile correlated with fetal lipid profile and adverse perinatal outcomes. Conclusion: Altered placental protein expressions in DIP may promote triglyceride accumulation, contributing to fetal overgrowth and associated complications.
OS6-7	KB0098-A 17:00-17:15	Prebiotic Activity of Medicinal Plant Extracts for Enhancing Probiotic Growth and Preventing Obesity in Drosophila Model **Thida Kaewkod** Chiang Mai University Abstract: Medicinal plants are rich sources of prebiotic and anti-obesity compounds that help maintain gut microflora balance and regulate lipid metabolism. This study investigated four plant extracts including Terminalia catappa (leaves), Psidium guajava (leaves), Sandoricum koetjape (fruit), and Aegle marmelos (fruit) that prepared by hot-water extraction. High-performance liquid chromatography (HPLC) was used to quantify prebiotic sugars, including fructooligosaccharides (FOS) and inulin. Inulin was detected in P. guajava, S. koetjape, and A. marmelos, with the highest content found in S. koetjape (3.452 ± 0.143 mg/g extract), followed by A. marmelos (0.800 ± 0.009 mg/g) and P. guajava (0.446 ± 0.012 mg/g). T. catappa and S. koetjape extracts showed strong resistance to α-amylase and artificial gastric juice hydrolysis. The effects of the extracts on probiotic strains such as Lactiplantibacillus plantarum TISTR 2070, Lacticaseibacillus casei TISTR 1340, and Bifidobacterium bifidum TBRC 7153 were evaluated by total plate count. S. koetjape and A. marmelos extracts significantly promoted probiotic growth, especially S. koetjape, which increased L. plantarum by 1.28 log CFU/ml ($p \leq 0.001$) at 24 h. At 15.63 mg/ml, both extracts enhanced B. bifidum growth by 1.45 and 2.20 log CFU/ml ($p \leq 0.002$), respectively. Moreover, the extracts reduced lipid content in transgenic Drosophila through upregulation of Bmm expression, indicating triacylglycerol (TAG) lipolysis activation. These findings suggest that S. koetjape and A. marmelos extracts possess promising prebiotic and anti-obesity potential as functional food ingredients.
OS6-8	KB0136-A 17:15-17:30	Discovery of New Secondary Metabolites from Umbilicaria antarctica and Their Apoptosis-Inducing Activity

Jinkyu Lee
Korea University

Abstract: Triple-negative breast cancer (TNBC) is a clinically aggressive tumor type that lacks well-defined molecular targets, prompting continuous efforts to identify new bioactive molecules and alternative therapeutic approaches. Extremophilic organisms that inhabit harsh environments, particularly Antarctic lichens, have been recognized as valuable sources of structurally unusual and biologically meaningful natural metabolites. In this study, a detailed chemical analysis of the Antarctic lichen Umbilicaria antarctica resulted in the isolation of fifteen previously unreported secondary metabolites. Among these, two compounds-carboxygyrophoric acid (1) and umbiliquinone (2)-were identified and structurally characterized as new natural products. Their biological activities were assessed across three human cancer cell lines, SK-OV-3, A549, and MDA-MB-231, with compound (2) exhibiting a notably strong and selective growth-inhibitory effect in TNBC cells. Mechanistic investigations further revealed that (2) induces apoptotic signaling, accompanied by activation of p38 MAPK, modulation of the Bax/Bcl-2 ratio, and cleavage of caspase-3. In addition, molecular docking and molecular dynamics simulations supported a strong interaction between (2) and the anti-apoptotic protein Bcl-2, suggesting a plausible binding-driven mechanism. Collectively, these findings highlight Antarctic lichens as a promising reservoir of unique anticancer agents and establish umbiliquinone as a potential lead compound for TNBC-focused drug development.

Poster Session 1

January 17, 2026, Saturday (GMT+9)

Duration	Venue
14:00-15:40	Back of the Lounge

Topic:	Biomedical Data Analysis and Computational Bioscience

Paper Detail

P1-1	KB0033-A	Machine Learning Based Approach for the Reconstructed Muscle Image Correction in Electrical Impedance Tomography **Hui-Chien Hsieh** and Kuo-Sheng Cheng National Cheng Kung University Abstract: Sarcopenia is characterized by muscle mass loss and functional decline, which impairs mobility and increases the risk of falls and fractures. Conventional tools such as MRI, CT, DXA, and BIA provide quantitative muscle assessment but remain limited in dynamic monitoring, portability, and accessibility. Electrical Impedance Tomography (EIT) is a noninvasive imaging technique capable of reconstructing conductivity distributions from current injections and voltage measurements, thus offering the potential for continuous monitoring of muscle changes. However, EIT image reconstruction often suffers from poor spatial resolution, making it difficult to accurately identify muscle regions. Firstly in this study, a performance comparison of several reconstruction algorithms in EIDORS is evaluated, and the absolute Gauss–Newton method with NOSER regularization is the best one selected as the baseline approach. Based on these findings, a novel correction framework that extracts statistical, gradient, and boundary features from reconstructed images and applies machine learning regression is proposed to predict muscle region size and conductivity. Experimental results demonstrate that the proposed correction method significantly reduces estimation errors compared with the original reconstruction, yielding clearer boundaries and more accurate conductivity values. This approach can improve the accuracy of muscle localization and compensate for the limited resolution of EIT reconstructions, thereby enhancing its reliability for sarcopenia

		assessment and real-time physiological monitoring.
P1-2	KB0035-A	Leveraging Diverse Sequence Descriptors for Improved Hemolytic Peptide Prediction **Ching-Tai Chen,** Sih-Han Chen, and Jen-Chieh Yu National Chung Hsing University Abstract: Peptides have emerged as promising therapeutic agents for treating cancer, immune disorders, hypertension, and microbial infections due to their high selectivity, low production cost, and fewer side effects compared to traditional small molecule drugs. However, a major challenge is that some peptides exhibit hemolytic activity, disrupting erythrocyte membranes and reducing red blood cell lifespan, which necessitates computational tools for hemolytic peptide identification in drug discovery. We present HEPAD, a machine learning predictor that identifies hemolytic peptides using adaptive feature engineering and diverse sequence descriptors. The method generates feature vectors of nearly 4000 numeric values for each peptide through sequence descriptors, followed by an adaptive feature engineering approach that produces customized feature subsets for different datasets, resulting in 250, 350, 90, and 130 selected features across four datasets. Five machine learning methods were employed for cross-validation and independent testing, with HEPAD achieving Matthew's correlation coefficients of 0.973, 0.643, and 0.609 on three independent datasets, representing improvements of 1.9% to 13.3% over existing approaches. Data visualization confirms that customized feature subsets effectively separate hemolytic from non-hemolytic peptides, demonstrating HEPAD's efficiency in identifying potential hemolytic peptides and expediting experimental procedures in drug discovery.
P1-3	KB0036-A	A MCI Early Screening System Using Three Input Measurements with Conditional Diffusion Model-based Data Augmentation **Ping Hung Lee** and Kuo Sheng Cheng National Cheng Kung University Abstract: With the rapid aging of the global population, the early detection of Mild Cognitive Impairment (MCI) has become increasingly important. The Montreal Cognitive Assessment (MoCA) is one of the most widely adopted screening tools; however, its drawing-based tasks are subject to evaluator bias and human error. Moreover, conventional AI models applied

		to MoCA analysis often face barriers to clinical acceptance due to their "black-box" characteristics. To address the challenge of limited and imbalanced clinical datasets, this study applies a Conditional Diffusion Model for data augmentation. This generative approach, known for stable training and high-fidelity image synthesis, produces diverse and realistic MoCA images conditioned on clinical labels (e.g., MCI scores). By selectively supplementing underrepresented cases, the method enhances data balance and strengthens model generalization. For classification, Self-Attention–based architecture instead of traditional Convolutional Neural Networks (CNNs) is adopted. Unlike CNNs, which are constrained by local receptive fields, the Self-Attention mechanism captures long-range dependencies and global structural relationships within drawings. This enables dynamic weighting of salient visual features, leading to more precise discrimination between normal and impaired cognitive patterns. From the experimental results, the performances with and without diffusion-based augmentation for MCI screening system are compared and analyzed. The proposed system is demonstrated to be feasible for clinical applications. In addition, by integrating Grad-CAM visualizations, the system outcomes may be interpretable for clinical understanding.
P1-4	KB0076-A	Pharmacodynamic Modeling of Temperature-Dependent Susceptibility and Serial Resistance Development in Aquaculture Pathogens Using Berkeley Madonna Simulation Si-Heon Song, Hyeon-Ju Lee, Eun-Seop Lee, and **Eon-Bee Lee** Pukyong National University Abstract: We evaluated how temperature and dosing interval influence antibiotic efficacy and resistance risk in three aquaculture pathogens: Listonella anguillarum, Edwardsiella tarda, and Aeromonas hydrophila. Minimum inhibitory concentration (MIC), time-kill kinetics in colony-forming units (CFU), growth by optical density at 600 nm (OD600), and β-lactamase activity with Nitrocefin at 490 nm (OD490) were measured. Amoxicillin, gentamicin, lincomycin, and oxytetracycline were tested against Listonella anguillarum and Edwardsiella tarda; florfenicol, gentamicin, oxytetracycline, and enrofloxacin against Aeromonas hydrophila. Representative MICs (μg/mL) were 0.5–512 for Edwardsiella tarda, 0.125–32 for Listonella anguillarum, and 0.03125–16 for Aeromonas hydrophila. Time-kill assays revealed survival at 1×MIC across species and persistence at 2×MIC in selected pairs. In Edwardsiella tarda at 37 °C,

		repeated ½×MIC treatments elevated MIC up to 8×MIC, accompanied by increased β-lactamase activity. Pharmacodynamic simulations using Berkeley Madonna in olive flounder (Paralichthys olivaceus) indicated prolonged residence within the mutant selection window (MIC–MPC) under 24-h dosing, suggesting enhanced resistance risk. Shorter dosing intervals (16–20 h) may improve therapeutic efficacy while minimizing selection pressure in aquaculture environments.
P1-5	KB0077-A	Interplay Between Genetic Risk and Lifestyle in the Development of Chronic Kidney Disease **Yang-Gyun Kim,** Manu Shivakumar, Su Woong Jung, Ju-Young Moon, Sang-Ho Lee, Sang-Hyuk Jung, Jakob Woerner, and Dokyoon Kim Kyung Hee University Abstract: To quantify the interplay between genetic predisposition and lifestyle modification, we evaluated the association of adherence of a favorable lifestyle with incident CKD(chronic kidney disease) risk across polygenic risk score(PRS) strata. The impact of five different lifestyle factors- BMI, eating habit, physical activity, smoking, and salt adding- along with a composite lifestyle classification (favorable, intermediate, unfavorable), was evaluated for their association with CKD development in 254,610 European individuals from the UK biobank (UKB) and validated in 6,940 Korea Association Resource Study (KARE) cohort. In UKB, the individuals with high PRS and unfavorable lifestyle had a 28% increased risk of incident CKD (HR=1.28, 95% CI:1.12–1.46, P<0.001) compared to the reference group. However, adopting a favorable lifestyle in those with high PRS conferred substantial protection (HR=1.09, 95% CI:0.97–1.22, P=0.132), representing a 15% relative risk reduction. A similar gradient was observed in KARE (HR=2.57, 95% CI:1.71–3.86, P< 0.001), while those with a favorable lifestyle had a lower but still elevated (HR=1.72, 95% CI:1.13–2.62, P=0.012), corresponding to a 33% reduction. Across both cohorts, lifestyle-related risk reduction was more pronounced in individuals with higher CKD-PRS percentiles. This study emphasizes the actionable potential of combining genetic risk profiling with lifestyle interventions in precision health strategies for CKD prevention.
P1-6	KB0080-A	Real-Time Quantification and Comparative Analysis of Lipid Droplets in Oleaginous Yeasts via Deep Learning-Based Microscopy Segmentation Yu Mi Kang, Jeong-Joo Oh, Hyeokhyeon Kwon, Eun ho Choe, Hyeok Ju Yang, Kyeong Jae Yang, Changmin Lee, and **Young Jin Ko**

		Jeju National University Abstract: Lipid droplets (LDs) are dynamic intracellular organelles that act as carbon reservoirs in oleaginous yeasts, directly influencing biofuel and nutritional lipid biosynthesis. Efficient real-time visualization and quantification of LDs in living cells are essential for improving strain performance and optimizing lipid yield. In this study, we established a deep learning–driven segmentation framework to automatically identify and measure LDs in Lipomyces starkeyi from light microscopy images. The optimized model demonstrated high recognition accuracies for yeast cells (98%) and LDs (92%), allowing reliable estimation of intracellular lipid levels based on pixel-based analysis. The predicted lipid quantities showed a strong correlation with results obtained through gas chromatography–mass spectrometry (GC–MS), validating the model as a rapid and cost-effective alternative for lipid quantification during fermentation. Furthermore, morphological comparisons across different oleaginous yeast strains revealed that both average LD diameter and LD-to-cell area ratio increased proportionally with total lipid accumulation. These results highlight the potential of this segmentation model as a practical computational tool for monitoring lipid biosynthesis in real time and for supporting comparative evaluation of strain productivity.
P1-7	KB1016-A	Personalized Diabetes Treatment: Moving Toward Individualized Care **Vishnu Eesam** and Chanchal K Mitra University of Hyderabad Abstract: Diabetes mellitus is a significant worldwide health issue that demands new and effective approaches to improve patient outcomes. Recently, personalized medicine has emerged as an innovative approach that tailors treatment to an individual's unique genetic makeup, lifestyle, and health characteristics. This paper looks forward to a future where personalized medicine plays a crucial role in diabetes care, helping to improve patient outcomes and support more effective, targeted treatment worldwide. Personalized management of diabetes relies on individual characteristics that influence the response to medication. It is challenging to apply findings from diabetes genetics studies, often conducted in young, healthy participants, to the broader population of people with diabetes. Personalized treatment plans, tailored to each patient's unique genetic and environmental factors, can help them adhere to their treatments and

		achieve better health outcomes. CYP2D6 gene variants are now well understood; however, using single-nucleotide polymorphisms (SNPs) to guide drug treatment remains challenging. Developing this approach will be an essential step toward personalized medicine.
P1-8	KB2027-A	An Integrated Gut Microbiota–APOE Genotype Model for Predicting Dementia Risk and Cognitive Impairment Severity **Sang Hyuk Lee**, Sehee Lee, Yong Hyuk Cho, Sang Jun Son, Chang Hyung Hong, and Sun Hwa Hong Ajou University Abstract: Dementia is a multifactorial disorder influenced by complex interactions among genetic, biological, and environmental factors. In particular, the APOE ε4 allele is a well-established genetic risk factor for dementia, and recent studies have suggested that alterations in gut microbiota composition are strongly associated with cognitive decline and cerebrovascular pathology. However, predictive research that integrates genetic information, gut microbiome profiles, and diverse clinical variables remains limited. This study aimed to develop and evaluate an integrative model that predicts dementia risk and cognitive impairment severity by combining genetic and microbiome data from 292 patients. Clinical information, APOE genotypes, and gut microbial metagenomic data were analyzed across three cognitive stages: subjective memory impairment (SMI), mild cognitive impairment (MCI), and dementia. Additionally, correlations among genetic risk, Alzheimer's disease pathology, and brain structural changes were assessed, and statistical analyses were performed to evaluate the predictive contribution of genotype–microbiome interactions. Results showed that APOE ε4 carriers were not observed in the SMI group but were most frequently identified in the dementia group. Gut microbial composition differed significantly according to the level of genetic dementia risk (low vs. moderate-to-high), and the integrated model combining genetic and microbiome information demonstrated higher predictive accuracy than models based on individual domains. Notably, patients with moderate-to-high genetic risk exhibited distinct increases in Escherichia/Shigella, Ruminococcus gnavus group, and Eggerthella species. This study proposes a novel dementia prediction framework that integrates genetic and gut microbiome data, highlighting its potential utility in identifying high-risk individuals and informing

		personalized dementia risk-prediction programs.
P1-9	KB0081-A	Enterotype-Dependent Effects of Red Beetroot on Gut Microbiota, Metabolites, and Immunity **Gwang-Pyo Ko,** Hyejun Jo, Kyung-Hwan Boo, and Chang Sook Kim Jeju National University Abstract: The gut microbiota mediates diverse metabolic and immunological effects of dietary components, which vary according to the dominant enterotype. Red beet (Beta vulgaris L.), rich in fermentable fibers, was investigated for its enterotype-specific effects using fecal samples from thirty healthy adults. Two enterotypes were identified: type 1, dominated by Bacteroides and Bifidobacterium, and type 2, dominated by Prevotella. Fecal samples from three donors per enterotype underwent in vitro gastrointestinal digestion–fecal fermentation with red beet powder (RBP) for 24 hours. RBP treatment markedly altered the microbial community in type 1, enriching beneficial genera including Bifidobacterium and Lactobacillus, whereas type 2 showed minimal microbial shifts. Metabolomic profiling revealed distinct enterotype-dependent pathways: type 1 exhibited enhanced glycine, serine and threonine metabolism, cysteine and methionine metabolism, and butanoate metabolism, while type 2 uniquely displayed nicotinate and nicotinamide metabolism. Application of fermentation-derived metabolites to RAW 264.7 macrophages showed that only type 1 supernatant significantly enhanced immune responses. These findings demonstrate that red beet induces distinct microbial and metabolic responses depending on enterotype and modulates immunity in an enterotype-specific manner.
P1-10	KB0121-A	Integrative Analysis of Differentially Expressed Genes and Hub Networks Reveals Potential Biomarkers in Triple-Negative Breast Cancer (TNBC) **Baiq Mira Nurfatihah** and Irshad Ahmad King Fahd University of Petroleum and Minerals Abstract: Triple-negative breast cancer (TNBC) is the most dangerous subtype of breast cancer due to its rapid growth and spread, high risk of recurrence, limited treatment options, and relatively poor prognosis compared to other subtypes. In this study, we performed an integrative transcriptomic analysis using publicly available GSE65216 and GSE96860 datasets to identify differentially expressed genes (DEGs) in TNBC compared to HER2, Luminal A, Luminal B subtypes, and normal breast

		tissue. The DEG is visualized using volcanic plots and Venn diagrams to assess distributions and overlaps across comparisons. The top 100 upregulated and downregulated genes comparison were selected, and duplicates were analyzed using STRINGdb to investigate protein-protein interaction networks (PPIs) and functional enrichment analysis. In addition, the top 600 genes from each dataset in the Venn analysis were duplicated, and the resulting dataset was further analyzed using STRINGdb. Consistently identified key hub genes were observed across both analysis workflows (volcano plot and Venn diagram) including SLC2A10 and ERBB4 (upregulated) and IRX1, PSAT1, and KRT5 (downregulated). Biological relevance assessments indicated that KRT5 is consistent with basal-like TNBC literature, ERBB4 is upregulated in specific TNBC subtypes, and SLC2A10, IRX1, and PSAT1 represented novel biomarker candidates that require further validation through qPCR, survival analysis, and literature mining. Functional enrichment analysis highlights the critical molecular processes and pathways involved in TNBC. This integrative approach identifies potential diagnostic biomarkers and therapeutic targets, providing a basis for future experimental validation and clinical translation in TNBC management.

Poster Session 2

January 17, 2026, Saturday (GMT+9)

Duration	Venue
14:00-15:40	Back of the Lounge

Topic:	Nanomaterials & Bioactive Platforms in Biomedicine

Paper Detail

P2-1	KB0045-A	Bacterial Nanocellulose – Zno/Cao@Curcumin Membranes Fabricated via in Situ Fermentation for Biomedical Applications **Dariela Núñez,** Rodrigo Cáceres, Camila Rodríguez, Kelly Torres, Matías Hepp, Estrella Armijo, Matías Araneda, Patricio Oyarzún, and Varaprasad Kokkarachedu Universidad Católica de la Santísima Concepción Abstract: The development of advanced biomaterials has greatly contributed to progress in tissue regeneration and infection control, particularly through the use of metallic nanoparticles as antibacterial agents. Despite their high effectiveness, their clinical application remains limited due to cytotoxicity toward normal cells, underscoring the need for safer and more biocompatible alternatives. In this study, zinc oxide and calcium oxide nanoparticles coated with curcumin (ZnO/CaO@Curcumin) were synthesized via microwave-assisted precipitation and incorporated into bacterial nanocellulose (BNC) matrices using in situ fermentation. The nanoparticles were characterized by SEM, FTIR, UV-Vis spectroscopy, DLS, and zeta potential measurements, showing an average size of 56 nm, polydispersity, and good stability. Cytotoxicity was evaluated on human keratinocytes (HaCaT) using Crystal Violet and XTT assays, revealing dose-dependent effects. Concentrations up to 50 µg/mL did not significantly affect cell viability, whereas 200 µg/mL induced a marked reduction. Curcumin coating effectively reduced cytotoxicity, ensuring safer integration into the BNC membranes. These findings confirm the biocompatibility of ZnO/CaO@Curcumin nanoparticles at optimal concentrations and support their potential as candidates for wound dressings and other biomedical applications in tissue engineering.

P2-2	KB0049-A	Retinal Delivery of the Protein Kinase C-β Inhibitor Ruboxistaurin Using Non-Invasive Nanoparticles of Polyamidoamine Dendrimers **Fadilah Sfouq Aleanizy** King Saud University Abstract: Ruboxistaurin (RBX) is an anti-vascular endothelial growth factor (anti-VEGF) agent that is used in the treatment of diabetic retinopathy and is mainly given intravitreally. To provide a safe and effective method for RBX administration, this study was designed to develop RBX nanoparticles using polyamidoamine (PAMAM) dendrimer generation 5 for the treatment of diabetic retinopathy. Drug loading efficiency, and in vitro release of proposed complexes of RBX: PAMAM dendrimers were determined and the complexation ratio that showed the highest possible loading efficiency was selected. The drug loading efficiency (%) of 1:1, 2.5:1, and 5:1 complexes was 89.2%, 96.4%, and 97.6%, respectively. Loading capacities of 1:1, 2.5:1, and 5:1 complexes were 1.6%, 4.0%, and 7.2% respectively. In comparison, the 5:1 complex showed the best results in the aforementioned measurements. The in vitro release studies showed that in 8 h, the RBX release from 1:1, 2.5:1, and 5:1 complexes was 37.5%, 35.9%, and 77.0%, respectively. In particular, 5:1 complex showed the highest drug release. In addition, particle size measurements showed that the diameter of empty PAMAM dendrimers was 214.9 ± 8.5 nm, whereas the diameters of loaded PAMAM dendrimers in 1:1, 2.5:1, 5:1 complexes were found to be 461.0 ± 6.4, 482.4 ± 12.5, and 420.0 ± 7.1 nm, respectively. Polydispersity index (PDI) showed that there were no significant changes in the PDI between the free and loaded PAMAM dendrimers. The zeta potential measurements showed that the free and loaded nanoparticles possessed neutral charges due to the presence of anionic and cationic terminal structures. Furthermore, the safety of this formulation was apparent on the viability of the MIO-M1 cell lines. This nanoformulation will improve the therapeutic outcomes of anti-VEGF therapy and the bioavailability of RBX to prevent vision loss in patients with diabetic retinopathy.
P2-3	KB0052-A	Oral Daclatasvir Dihydrochloride as Biodegradable Nanoparticles **Bushra T. Al Quadeib** and Iman M. Alfagih King Saud University Abstract: Every year, a significant percentage of mortality worldwide is

		attributed to viral and microbial diseases. Hepatitis C is a serious chronic viral condition that, if untreated, can lead to severe liver inflammation. Internationally, more than 70 million people's diagnosed with chronic hepatitis C virus 1-3. Treatment of Hepatitis C is done by administration of direct-acting antiviral, Dactalasvir (DAC), the safest and most effective, act by blocking the action of proteins. It belongs to class II drugs in accordance with the Bio-pharmaceutics Classification System as the drug is insoluble in water and has good lipid permeability; it has only 67% extent of absorption 4. This study aims to develop oral DAC-loaded mucoadhesive microparticles using alginate and chitosan polymers (ALG-CS) at different ratios utilizing the ionic gelation method. These polymers are expected to have a long residence time in the gastrointestinal tract due to their bioadhesive property. The tested formulation of DAC-ALG-CS will be subjected to in vitro characterization will be performed to evaluate the proposed microparticles 5-8. This will be included, particle size, polydispersity index, encapsulation efficiency, and in vitro drug release. The proposed microparticles will be visualized using scanning electron microscopy (SEM) and Fourier transform infrared spectroscopy (FTIR). Suitable high performance liquid chromatography technique will be modified, to measure the drug content, drug loaded as well as in vitro release, in vivo, ex vivo measurement. Furthermore, in vivo studies will then be performed on the promising formulation using Wistar rats as an animal model. DAC microparticles are expected to enhance the absorption and bioavailability of DAC after oral delivery and will provide better therapeutic outcomes.
P2-4	KB0122-A	Adapter-assisted Catalytic Hairpin Assembly for Sensitive Molecular Detection **Tung-Chien Hsu** Center for Disease Control Abstract: Toehold-mediated strand displacement (TMSD) reaction is a target-specific, entropy driven, enzyme-free reaction that employs a short single-stranded DNA overhang domain (toehold) to hybridize with matched target and initiates sequence specific hybridization reaction by displacing complementary sequence like opening a zip-zap. TMSD make detection of rare nucleic acid targets possible by designing two (or more) oligonucleotide hairpin probes, one for target sequence hybridization and other(s) for hybridizing with displaced sequence of target hybridized

		probe. Thus, repetitive hairpin hybridization occurs in a manner like stacking folded sheets and therefore results in linear signal amplification as was demonstrated in the traditional hybridization chain reaction (HCR). However, detection of rare target by linear amplification is time consuming and limits traditional HCR for clinical application. Recycling target template by repetitive displacing target-hybridized probe, a mechanism termed catalytic hairpin assembly (CHA), became a method of choice to facilitate detection of limited target. We present here an alternative way of CHA reaction that allows not only recycling of model template but artificially generating a cross-stranded template-like sequence for another round of CHA. This is based on the finding that loop region of hairpin probe (termed loop-toehold probe, LPT probe) can be used as toehold for TMSD reaction. When target-complementary loop sequence of LPT recognizes its target, TSMD occurs, relieving the stem-region of the LPT, leaving both 5' and 3'-end available for CHA. A second hairpin probe designed for CHA with linear toehold at 3'-end (OpenCHA probe) could then recognize part of the 5'-end of LPT, displace the LPT, recycle the target template for another round of LPT mediated hybridization. A third oligodeoxynucleotide adapter with molecular beacon structure was added to generate 5' portion of sense region of target sequence, along with the disp
P2-5	KB0134-A	Efficient Non-Viral Gene Delivery in Immune Cells via Cytidine Triphosphate–Incorporated Polyplexes **Jieun Han,** Hana Cho, and Hanchang Kang Soonchunhyang University Abstract: Efficient gene delivery into hard-to-transfect immune cells, including T-, B-, and NK-cells, remains a major challenge due to limited cellular uptake, rapid endo/lysosomal sequestration, and inefficient nuclear trafficking. To address these intracellular barriers, we developed multifunctional polyplexes composed of branched polyethylenimine (bPEI), cytidine triphosphate (CTP), and plasmid DNA (pDNA) via electrostatic interactions. The effects of CTP on gene delivery were systematically evaluated by examining cellular internalization, endosomal escape, nuclear localization, decomplexation kinetics, mRNA synthesis, and protein expression in immune cells. The resulting bPEI/CTP/pDNA polyplexes formed nano-sized particles with an average size of approximately 550 nm, and their zeta potential decreased proportionally with increasing CTP content, indicating enhanced complex stabilization and biocompatibility. In

		Jurkat cells, the bPEI/CTP4nmol/pDNA polyplex showed approximately 40-fold higher transfection efficiency compared to the CTP-free controls, with 4–6-fold increased nuclear uptake and 25–50-fold higher mRNA expression. These results indicate that CTP facilitates multiple intracellular steps of gene delivery, including cellular uptake, endosomal escape, nuclear trafficking, and transcriptional activation, thereby enhancing overall transgene expression. In conclusion, CTP acts as a multifunctional gene delivery enhancer, providing a promising strategy to develop efficient, safe, and non-viral gene delivery systems for functionalizing difficult-to-transfect immune cells in both research and therapeutic applications.
P2-6	KB0144-A	High-Throughput Sars-Cov-2 Colorimetric Detection on a Paper-Based Elisa Using a Simple Pneumatic Valve-Based Centrifugal Microfluidic Platform **Vu Minh Phan,** Thi Thuy Huong Nguyen, and Tae Seok Seo Kyung Hee University Abstract: A pneumatic valve-based centrifugal microfluidic chip is presented for high-throughput paper-based ELISA (p-ELISA), enabling simultaneous analysis of up to 30 samples in a single run. By finely balancing pneumatic back pressure against centrifugal force, ELISA reagents are aliquoted into 30 reaction chambers in one rotation. A minimalistic two-step fluidic sequence: low-speed aliquoting followed by high-speed liquid discharge, supports fully automated sandwich ELISA without complex directional flow control or external actuators. Paper substrates integrated into each chamber provide an enlarged surface area for antibody immobilization, accelerate antibody-antigen interaction kinetics, yielding locally intensified signals with reduced diffusion loss. Optimized assay conditions reduce the total sample-to-answer time to 20 min, evidently shorter than conventional ELISA protocols. Colorimetric signals are captured using a custom 3D-printed imaging module with warm white LEDs and processed via a custom smartphone application that extracts HSB intensity values for quantitative analysis. The resulting color shift on the paper serves as both visual indicator and a robust metric for viral antigen quantification. The platform achieves a detection limit of 10ng/mL for SARS-CoV-2, demonstrating high analytical sensitivity. With its rapid turnaround, high-throughput, and smartphone-based analytical capabilities, the developed microsystem for p-ELISA offers significant potential as a versatile tool for clinical diagnostics.

P2-7	KB2009-A	Development of A Pulsed Laser Detector for Deep Depth Indocyanine Green Signal Detection Kyoung Won Jang, In Kook Chun, Ki-Taek Han, and **Hyung-Sik Kim** Konkuk University Abstract: Indocyanine green (ICG) is a cyanin-based fluorescent dye used in medical diagnostics. It is utilized in various tumor detection, blood flow measurement, radiotherapy, and angiography. Its applications are gradually expanding due to its minimal toxicity and side effects. Therefore, research is needed to improve the sensitivity and spatial resolution of redshift signals generated from ICG, as well as acquire signals from deep within the body. In this study, we developed a robust redshift signal detection system for indocyanine green (ICG). The system consists of a pulsed laser generator, an optical probe, and an optical signal acquisition unit. The laser generator uses a 785 nm Fabry-Perot laser diode to excite ICG. The pulse drive of the laser diode uses a high-speed switching SiC-MOSFET NVH4L030N120M3S, and a wide band voltage-controlled current source circuit is configured for easy control. The optical probe uses a coupled fiber capable of simultaneously transmitting laser light and detecting its reflection and backscattering. The optical detector uses a silicon PIN photodiode connected to a negative voltage via a transimpedance amplifier. This diode has a maximum sensitivity of 825 nm. To verify the developed system, 0.2 mL droplets ICG were injected into a slide glass using a syringe at concentrations of 10 nM (0.00775 μg/mL) and 0.1 nM (0.0000775 μg/mL), which are the detection concentrations of sentinel lymph nodes (SLNs) inside the body. The laser pulse width was 200 ns, the output was 300 mW, and the repetition rate was 1 Hz, and the distance between the ICG solution and the probe was fixed at 40 mm. As a result of the experiment, redshifted signals were obtained from all laser pulses. The signal-to-noise ratio (SNR) of the obtained signals was 276±11 for 10 nM and 193±8 for 0.1 nM. The SNR of the continuous laser experiment using the same output power was 176±21 for 10 nM and 43±14 for 0.1 nM. These results are believed to be because the energy per unit tim
P2-8	KB2025-A	DSN-Enhanced Split Aptamer Colorimetric Detection of Estradiol **Chia-Chen Chang**, Tzu-Ling Wang, Shen-Hsing Hsu, Yi-Shan Wang, Pin-Yu Lin, and Chih-Wei Yang

		Chang Gung University Abstract: Estradiol (E2) plays essential physiological roles, yet its trace-level detection remains challenging with conventional analytical techniques. We present a simplified colorimetric approach that couples duplex-specific nuclease (DSN) amplification with split aptamer recognition on gold nanoparticles (AuNPs). Binding of E2 promotes aptamer assembly on AuNP surfaces, enabling DSN-mediated cleavage that modulates DNA passivation and drives distinct AuNP growth during gold(III) reduction. The resulting color changes allow visual and spectroscopic quantification. The method enables low-level detection of E2 while retaining reasonable discrimination from structurally related hormones. Thus, this DSN-assisted split aptamer–AuNP platform offers a simple and sensitive analytical strategy suitable for small-molecule detection.
P2-9	KB0125-A	Camellia Sinensis (L.) Attenuates Cuonps-Induced Lung Inflammation and Mucus Hypersecretion via Suppression of Mapk Signaling and muc5ac Expression **Ba-Reun Jin,** Sin-Hyang Park, and In-Sik Shin Chonnam National University Abstract: Copper oxide nanoparticles (CuONPs) are widely applied in industrial and commercial fields. However, inhalation exposure can lead to severe respiratory tissue injury. Camellia sinensis L. has been reported to possess significant anti-inflammatory and antioxidant properties, which are largely mediated by its bioactive compounds. This study aimed to evaluate the therapeutic potential of Camellia sinensis L. ethanolic extract (CSE) against CuONPs-induced pulmonary inflammation, with a specific focus on the mitogen-activated protein kinase (MAPK) signaling pathway. The administration of CSE decreased neutrophil and macrophage counts and downregulated IL-1β, IL-6, and TNF-α levels in CuONPs-exposed mice. These effects were accompanied by decreased inflammatory cell infiltration within lung tissue and suppressed mucus production by goblet cells. Additionally, CSE effectively inhibited the CuONPs-driven activation of MAPK pathway components such as p-p38, p-JNK, p-ERK, and MUC5AC. Overall, the anti-inflammatory effect of CSE on CuONPs-exposed lungs appears to be mediated through MAPK pathway inhibition. These findings indicate that CSE may serve as a promising herbal agent for managing

		CuONPs-driven lung inflammation.
P2-10	KB0065-A	Cisplatin-Induced Oxidative Stress and Ionocyte Apoptosis in Zebrafish Embryos **Li-Yih Lin** National Taiwan Normal University Abstract: Cisplatin (CDDP) is a widely used platinum-based chemotherapeutic drug, yet its environmental release raises concerns about aquatic toxicity. In this study, zebrafish embryos were used as an in vivo model to investigate the impact of cisplatin on mitochondria-rich ionocytes. Embryos were exposed to different concentrations of CDDP for up to 96 hours, and mitochondrial function, oxidative stress, and apoptosis were assessed using fluorescent probes (Rhodamine123, CellROX, MitoSOX, and Acridine orange). Cisplatin exposure significantly reduced the number of ionocytes, induced mitochondrial oxidative stress, and triggered concentration-dependent apoptosis. Gene expression analysis revealed upregulation of antioxidant genes (sod1, sod2, gpx1a, cat) and apoptosis-related casp3a. Furthermore, acute exposure (1 mM, 0.5–2 h) confirmed rapid increases in ROS generation and apoptotic signals. These findings demonstrate that zebrafish ionocytes are highly sensitive to cisplatin-induced oxidative stress and apoptosis, highlighting their utility as a model for evaluating drug-induced mitochondrial dysfunction and aquatic toxicology.
P2-11	KB0032-A	Calcium-Modified Magnesium Alloys with Improved Biocompatibility and Osteogenic Performance for Implant Applications Tzu-Hung Ma, **Yu-Chih Tzeng,** Bo-Yu Wang, Ching-Yun Chen, and I-Hsuan Wu National Central University Abstract: Biodegradable magnesium alloys are promising candidates for temporary implants due to their mechanical compatibility and biological safety. In this study, Mg-4.6Sn-2.4Zn-0.07Na alloys with trace calcium additions (0, 0.1, 0.3 wt%) were fabricated by stir casting, and their structural, electrochemical, and biological responses were systematically evaluated. Calcium addition refined the α-Mg matrix and promoted the formation of Mg_2Sn and CaMgSn phases, leading to improved hardness and tensile strength. Notably, the 0.1 wt% Ca alloy (TZS420-0.1Ca) exhibited the best balance of properties, with enhanced yield strength (88

		MPa), ultimate tensile strength (131 MPa), and superior cell viability (~90%). Electrochemical tests revealed that calcium altered the corrosion mode from severe localized attack to pitting, while in vivo implantation demonstrated partial alloy integrity and significant collagen deposition after 13 weeks, suggesting enhanced osteogenic potential. These results highlight the role of calcium ions in improving cellular response and bone regeneration, identifying TZS420-0.1Ca as a promising biodegradable alloy for biomedical applications.
P2-12	KB2019-A	Intraoperatively Implantable Passive Wireless Sensor Based on IDC and Loop Antenna for Postoperative Blood Flow Monitoring in Free Flap Surgery **Yih-Chein Chen**, Chu-Chun Hsu, Chun-Chieh Tseng , Kuei-Ling Yeh, Cheng-Yuan Chou, Shu-Hung Huang, Ping-Ruey Chou, Ling-Zhen Kao, and Yu-Sheng Lin Lunghwa University of Science and Technology Abstract: This paper presents the design and simulation of a wireless biomedical sensing system for postoperative venous blood flow monitoring, with the aim of future extension to venous pressure applications following free flap surgery. The system is composed of three key components: (1) an external planar reader antenna fabricated on an FR4 substrate, (2) a pressure-sensitive Interdigital Capacitor (IDC) sensor, and (3) a miniaturized loop antenna that transmits sensing data wirelessly from within the body. The reader antenna serves as the primary interface, providing electromagnetic excitation and receiving the resonant signal from the implanted sensor. It is realized as a large planar loop (106 mm × 106 mm) with a 0.035 mm copper layer on an FR4 substrate. Its simulated 3D radiation pattern exhibits a bi-lobed, omnidirectional profile with a peak gain of 0.23 dBi, ensuring robust near-field coupling with the implantable unit regardless of slight positional misalignment.

Poster Session 3

January 17, 2026, Saturday (GMT+9)

Duration	Venue
16:00-17:40	Back of the Lounge

Topic:	Disease Mechanisms and Therapeutic Modulation

Paper Detail

P3-1	KB0007-A	The Chemo-Sensitizing Effects and Dual Modulatory Mechanisms of Raddeanin a in the Drug Efflux Transporter Overexpressed Hepatocellular Carcinoma Cell Line **Yu-Ning Teng** China Medical University Abstract: Multidrug resistance (MDR) is an ever-changing challenge in cancer treatment, and the overexpression of drug efflux transporters (ATP-binding cassette transporters, such as P-gp, MRP1, and BCRP, encoded by ABCB1, ABCC1, and ABCG2 genes, respectively) plays a significant role. The development of inhibitors for ABC transporters from natural resources attracts much attention in this field. This study investigates the cancer MDR reversing effects of a triterpenoid isolated from Anemone raddeana Regel, Raddeanin A. Using hepatocellular carcinoma parallel cell lines (drug-sensitive and drug-resistant), and ABC transporter over-expressed cell lines, the chemo-sensitizing effects and the underlying mechanisms are explored. The results show that Raddeanin A exhibits synergistic ability on MDR cancer reversion in the HepG2/VIN cell line, and the fluidity of the cell membrane is significantly improved. Furthermore, Raddeanin A downregulates the ABCB1 and ABCG2 gene expression and shows prominent inhibitory effects on P-gp-mediated drug efflux. Besides, the ATPase activity of MRP1 and BCRP is inhibited by Raddeanin A at higher concentrations. These promising results imply that Raddeanin A might be a potential natural compound for MDR cancer reversion, not only influencing the ABC efflux transporters but also the cell membrane fluidity, exhibiting dual modulatory mechanisms.
P3-2	KB0008-A	Isx – TWIST1 Reprograms CD47 – Inflammasome Signaling to Reshape the

		Immune Microenvironment in Liver Cancer **Li-Ting Wang** and Shih-Hsien Hsu National Taiwan Normal University Abstract: The efficacy of immunotherapy is often compromised by the complex and immunosuppressive tumor microenvironment. In this study, we uncover a pivotal ISX–CD47–inflammasome signaling axis that orchestrates immune evasion and drives liver cancer progression. Elevated ISX expression promotes CD47 and inflammasome cytokine production, facilitating M2-like macrophage polarization and tissue-resident memory (TRM) T cell accumulation in the hepatic niche—features strongly associated with tumor burden, disease stage, and lymphovascular invasion. Using liver-specific ISX mutant mice and xenograft models, we demonstrate that depletion of these immune subsets significantly impedes tumor progression. Mechanistically, ISX forms a complex with TWIST1 and directly binds a degenerate promoter motif (“-GGDWYR-”) to transcriptionally activate CD47–SIRPα and inflammasome-related genes. Transcriptomic analyses further support ISX as a master regulator linking inflammation, immune suppression, and tumorigenesis. These findings highlight ISX as a context-specific immune modulator and a promising therapeutic target, offering new insights into the treatment of liver cancer and other inflammation-driven malignancies.
P3-3	KB0050-A	Microrna-219 Loaded Chitosan Nanoparticles for Treatment of Glioblastoma **Fulwah Yahya Alqahtani** King Saud University Abstract: Recent evidence has implicated microRNA-219 (miR-219) in regulation of gene contributed in glioblastoma (GBM) pathogenesis. This study aimed to prepare miR-219 in chitosan (CS) nanoparticles (NPs), characterize and investigate their efficacy on human GBM cell line (U87 MG). NPs were prepared using ionic gelation method. The influence of process parameters on physicochemical characteristics of NPs was investigated. Apoptotic effect of miR-219 was examined on U87 MG cells. Formulated NPs showed particle size of 109 ± 2.18 nm, with poly dispersity index equal to 0.2 ± 0.05, and zeta potential of +20.5 ± 0.7 mV. Entrapment efficiency of miR-219 in loaded NP has reached 95%. The in vitro release study demonstrated sustained release pattern of miR-219 from CS-NPs. Gel

		retardation assay has confirmed the integrity of miR-219 after production process. The fabricated NPs reduced the survival of U87 MG cells to 78% after 24 h of post-transfection, and into 67.5% after 48 h. However, fibroblasts were not affected by the NPs, revealing their specificity for GBM cells. Given the tumour suppressing function of miR-219, and advantage of CS-NPs for gene delivery to the central nervous system, the presented NPs have a great potential for treatment of GBM.
P3-4	KB0051-A	Kmt2c Mutation as a Positive Predictor of Immune Checkpoint Inhibitor Response in Urothelial Carcinoma **Han-Ni Chuang,** Sheng-Chun Hung, and Han-Yu Ye Taichung Veterans General Hospital Abstract: Urothelial carcinoma (UC) remains a major global health burden, with immune checkpoint inhibitors (ICIs) offering therapeutic benefit in advanced settings. However, clinical outcomes vary considerably, highlighting the need for reliable molecular predictors. We retrospectively analyzed 57 patients with advanced UC treated with ICIs between 2015 and 2021. Formalin-fixed tumor specimens underwent next-generation sequencing (NGS) to characterize somatic mutations and tumor mutational burden (TMB). Survival outcomes were evaluated using Kaplan–Meier analysis and Cox proportional hazards models. The study cohort included 39 males (68.4%) and 18 females (31.6%), with a mean age of 68.6 ± 10.6 years. Most patients presented with advanced disease (Stage IV, 80.7%; Stage III, 19.3%). Patients harboring KMT2C mutations demonstrated improved overall survival following ICI therapy compared with wild-type counterparts. TP53 alterations and co-mutation patterns were also assessed for potential impact on clinical outcomes. Our findings suggest that the KMT2C mutation serves as a positive predictor of ICI efficacy in UC, consistent with pan-cancer evidence. These results highlight the potential utility of integrating genomic profiling into patient stratification for immunotherapy. Further validation in larger, independent cohorts is warranted.
P3-5	KB0135-A	CHIP-Mediated K63/K27 Ubiquitination of STX17 Enhances Autophagosome-Lysosome Fusion and Protects Against NAFLD Progression **Uijin Kim,** Hyunjin Rho, and Jaewhan Song Yonsei University Abstract: Nonalcoholic fatty liver disease (NAFLD) is closely associated with

		impaired autophagosome–lysosome fusion, yet the molecular mechanisms governing this step remain incompletely understood. Here, we identify the E3 ligase CHIP as a key regulator of hepatic lipophagy through non-degradative ubiquitination of STX17. Hepatocyte-specific CHIP knockout mice exhibited marked NAFLD-related phenotypes when challenged with high-fat or high-fructose diets, accompanied by P62 and LC3 accumulation indicative of defective autophagy. Mechanistically, CHIP catalyzed K63- and K27-linked polyubiquitination of STX17 at lysine 198, which was essential for promoting STX17–SNAP29–VAMP8 SNARE complex formation. The STX17 K198R mutant failed to undergo ubiquitination, showed impaired interaction with VAMP8, thus failed to prevent steatosis in mice. Conversely, AAV8-mediated hepatic overexpression of CHIP enhanced autophagic flux, improved SNARE complex assembly, and significantly attenuated NAFLD/NASH phenotypes. Human NASH samples also displayed reduced CHIP and STX17 expression. These findings reveal that CHIP-dependent ubiquitination of STX17 is essential for maintaining autophagosome-lysosome fusion.
P3-6	KB0057-A	Bioinformatics-Driven Identification of Paeoniflorin and Cinnamic Acid as Potential Therapeutics for Colorectal Cancer **Ji-Hun Jang,** Khalish Arsy Al Khairy Siregar, and Seung-Hyun Jeong Chonnam National University Abstract: Colorectal cancer (CRC) ranks among the most common malignancies globally and is projected to become the third leading cause of cancer-related mortality in Korea by 2024, following lung and liver cancer. While its incidence is particularly high in men aged 35–64, the prevalence in women steadily increases with age. The development of novel, effective, and safe therapeutic strategies for CRC is therefore a pressing clinical need. This study investigated the potential of paeoniflorin (PF), cinnamic acid (CA), and their combination as CRC therapeutics using an integrated bioinformatics approach. Candidate targets of PF and CA were identified from multiple bioinformatics databases and cross-referenced with colorectal cancer gene expression profiles from the Gene Expression Omnibus (GEO). Overlapping genes were further analyzed through protein–protein interaction (PPI) network construction, Gene Ontology (GO) and KEGG pathway enrichment, and expression profiling. Molecular docking was subsequently conducted to assess the binding affinity of PF and CA against the identified hub genes compared to known inhibitors.

		Five critical targets were highlighted: IL1B, IL6, PTGS2, BCL2, and ESR1. Docking simulations revealed that PF exhibited strong or comparable binding affinities relative to reference inhibitors, whereas CA demonstrated lower affinity but retained significant potential. The combination of PF and CA suggests a complementary therapeutic effect. These findings support PF and CA, both individually and synergistically, as promising candidates for CRC therapy. Nonetheless, further experimental validation through in vitro studies, animal models, and clinical evaluation is required to confirm these computational insights.
P3-7	KB0139-A	Ebastine-Mediated Destabilization of E3 Ligase MKRN1 Attenuates Metabolic Dysfunction-Associated Steatohepatitis **Subin Kang,** Seungyeon Kim, and Jaewhan Song Yonsei University Abstract: Metabolic dysfunction-associated steatotic liver disease (MASLD) encompasses metabolic dysfunction-associated steatotic liver (MASL) and metabolic dysfunction-associated steatohepatitis (MASH), conditions that can progress to fibrosis, cirrhosis, or hepatocellular carcinoma. The heterogeneous and complex nature of MASLD complicates optimal drug development. This study examined whether destabilizing the E3 ubiquitin ligase MKRN1 could attenuate MASH development and whether ebastine, an antihistamine, can pharmacologically target this pathway. We used high-fat, high-fructose diet–induced MASH mouse models with liver-specific knockdown or genetic deletion of MKRN1 to assess both the impact of MKRN1 loss and the therapeutic potential of ebastine. MKRN1 deficiency attenuated key features of MASH, highlighting its functional relevance in disease development. Consistently, ebastine treatment reduced MKRN1 protein stability, enhanced AMP-activated protein kinase (AMPK) activation and alleviated MASH symptoms. Ebastine directly interacted with MKRN1 and promoted its autoubiquitination, leading to proteasomal degradation. These results indicate that MKRN1 plays an important role in MASH pathogenesis and that ebastine-mediated MKRN1 destabilization could be a promising therapeutic agent for MASH treatment.
P3-8	KB0017-A	A Glucagon-Like Peptide-1 (Glp-1) Receptor Agonist Exhibits Anti-Zika Virus Activity via Suppression of Ampk/TORC2-Mediated Gluconeogenesis **Jin-Ching Lee**, Wei-Chun Chen, and Yu-Wen Wu National Sun Yat-sen University

		Abstract: Zika virus (ZIKV) is a global health threat linked to severe neurological disorders, including microcephaly and Guillain–Barré syndrome, with no approved antivirals or vaccines available. Here, we evaluated the antiviral potential of liraglutide, a clinically approved glucagon-like peptide-1 receptor (GLP-1R) agonist for diabetes, using cell-based assays and ZIKV-infected AG129 mice. Liraglutide suppressed viral RNA replication in a dose-dependent manner (IC_{50} = 5.5 ± 0.6 μM) without significant cytotoxicity at effective concentrations, and reduced viremia ~15-fold while prolonging survival in infected mice. Mechanistically, liraglutide activated AMP-activated protein kinase (AMPK) phosphorylation, leading to phosphorylation of the CREB coactivator TORC2 and downregulation of key gluconeogenic enzymes—phosphoenolpyruvate carboxykinase (PEPCK) and glucose-6-phosphatase (G6Pase). Inhibition or knockdown of AMPK abrogated these effects, confirming AMPK/TORC2-mediated gluconeogenesis as a critical pathway for liraglutide's antiviral action. Due to the well-established clinical use and safety profile, liraglutide emerges as a promising candidate for rapid repurposing against ZIKV infection.
P3-9	KB0126-A	Matrix Metalloproteinase-9-mediated Anti-inflammatory Effects of Loranthus Tanakae Franch. & Sav. in OVA-induced Asthma **Sin-Hyang Park,** Ba-Reun Jin, and In-Sik Shin Chonnam National University Abstract: Allergic asthma is a type 2 immune-mediated chronic respiratory disease characterized by clinical symptoms such as coughing, dyspnea, wheezing, and sputum production. Matrix Metalloproteinase-9 (MMP-9) plays a crucial role in airway remodeling, a key pathological feature of asthma, by exacerbating airway inflammation and mucus production. Loranthus tanakae Franch. & Sav. is a traditional medicinal plant known for its potent anti-inflammatory and antioxidant properties. In this study, we investigated the protective effects of L. tanakae ethanol extract (LTE) against OVA-induced allergic airway inflammation. Mice were sensitized and challenged with OVA, and LTE was administered via oral gavage. LTE treatment markedly attenuated airway hyperresponsiveness (AHR) and downregulated serum immunoglobulin E (IgE) and proinflammatory cytokine levels. Histological analysis confirmed that LTE effectively alleviated inflammatory cell infiltration and mucus

		hypersecretion within lung tissues. Mechanistically, LTE notably suppressed MMP-9 expression and the activation of mitogen-activated protein kinase (MAPK) signaling pathways. Consequently, these findings suggest that LTE ameliorates allergic asthma via the regulation of MMP-9 and MAPK pathways, indicating its potential as a therapeutic candidate for asthma.
P3-10	KB0038-A	Mechanistic Investigation of the Anti-Colorectal Cancer Potential of Linagliptin, an Anti-Diabetic Medication: Critical Role of the FOXM1/SKP2/P27 Axis **Wen-Chyi Dai,** Fan-Chieh Cheng, Wei-Ju Huang, and Chia-Che Chang National Chung Hsing University Abstract: Colorectal cancer (CRC) ranks among the top three most common cancers globally, with rapidly increasing incidence and mortality rates. Due to the lack of noticeable early symptoms, most cases are diagnosed at advanced stages, where clinical treatments are often associated with severe side effects and poor prognosis. Thus, identifying effective therapeutic options for CRC remains a critical need. This study investigates the potential of repurposing Linagliptin, an anti-diabetic drug, as an anti-CRC agent along with the underlying mechanism. Our findings reveal that Linagliptin induces G1 phase cell cycle arrest in CRC cells by downregulating SKP2, a protein promoting S-phase progression. This inhibition prevents the ubiquitination of p27KIP1, effectively halting the cell cycle. Overexpression of SKP2 or knockdown of p27KIP1 counteracts the drug's effects, confirming that Linagliptin inhibits CRC cell proliferation primarily through the SKP2/p27KIP1 axis. Furthermore, Linagliptin downregulates FoxM1, a well-known transcription factor for SKP2. Importantly, overexpression of FOXM1 rescues SKP2 expression along with downregulation of p27KIP1. Collectively, these results suggest that Linagliptin, by targeting the SKP2/p21/p27KIP1 signaling pathway, demonstrates significant anti-tumor potential against CRC. This study highlights the therapeutic promise of Linagliptin for CRC treatment.
P3-11	KB0083-A	Biochemical and Hematological Predictors of Mortality in Thai Patients with COVID-19 **Monpat Chamnanphon**, Rutchaporn Taweerutchana, Kitsarawut Khuancharee, Pornparn Rojanasang, Pongwut Suwannarat, Prapaporn Panichchob, Pornsuk Romputtan, Nopparut Teravaninthorn, Nichapat Wiriyakunakorn, and Supaporn Wiwattanakul Srinakharinwirot University

Abstract: Background Coronavirus disease (COVID-19), caused by SARS-CoV-2 infection, presents a broad spectrum of clinical manifestations, ranging from asymptomatic cases to severe and fatal outcomes. Studies have shown that laboratory parameters fluctuate in patients with COVID-19, and these parameters serve as valuable biomarkers for monitoring disease progression. This study examines the relationship between changes in biochemical and hematological markers and patient survival among early COVID-19 cases. Material and methods In this retrospective cohort study, data from adult (⩾18 years) hospitalized COVID-19 patients with positive PCR results at HRH Princess Maha Chakri Sirindhorn Medical Center, Srinakharinwirot University, Nakhon Nayok, Thailand, between March and December 2021, were analyzed. Univariate and multivariate logistic regression analyses were conducted on mortality-related laboratory parameters. Results The cohort included 397 patients with pneumonia (median age: 52.2 years (IQR: 40.5-64.6); 61.96% female). Among them, 42 patients (10.58%) succumbed during hospitalization, with a median hospital stay of 12.92 days (IQR: 10.03-15.94). Independent mortality predictors were identified as follows: age (aOR = 1.11; 95% CI: 1.04-1.19; p = 0.002), potassium (aOR = 6.27; 95% CI: 1.31-29.93; p = 0.021), creatinine (aOR = 1.62; 95% CI: 1.05-2.50; p = 0.028), hemoglobin A1c (aOR = 1.96; 95% CI: 1.30-2.97; p = 0.001), red cell distribution width (aOR = 1.45; 95% CI: 1.05-2.02; p = 0.026), respectively. Furthermore, Patients with lower platelet counts had a notably higher risk of mortality (aOR = 0.98; 95% CI: 0.97-0.99; p = 0.001). Conclusion Our findings suggest that age, potassium, creatinine, hemoglobin A1c, red cell distribution width, and platelet count are significant predictors of mortality risk in patients with COVID-19. Clinicians should consider these biochemical and hematological markers critically before initiating treatment for COVID-19 patients.

Poster Session 4

January 17, 2026, Saturday (GMT+9)

Duration	Venue
16:00-17:40	Back of the Lounge

Topic:	Molecular Regulation and Functional Mechanisms

Paper Detail

P4-1	KB0014-A	Single-Cell Transcriptomics Reveals SENP1–PP4C Axis as a Protective Regulator in Idiopathic Pulmonary Fibrosis **Yu-Chih Wu** Taipei Medical University Abstract: Idiopathic pulmonary fibrosis (IPF) is characterized by fibroblast-to-myofibroblast transition (FMT) and excessive extracellular matrix deposition, yet the role of sumoylation in this process remains poorly defined. To investigate this, we performed single-cell RNA sequencing (scRNA-seq) on lung tissues from IPF patients and healthy donors, identifying significantly reduced expression of SUMO-specific peptidase 1 (SENP1) in IPF fibroblasts. Gene set enrichment analysis (GSEA) enabled the selection of disease-relevant cell populations for downstream molecular studies. In vitro experiments revealed that TGF-β1–induced miR-145 suppresses SENP1, leading to increased sumoylation, PP4C destabilization, and impaired HDAC3 dephosphorylation, thereby promoting FMT and collagen I accumulation. Co-treatment with sumoylation inhibitors and antifibrotic agents reduced the required drug dosage. These findings highlight SENP1 and PP4C as protective regulators in IPF and potential therapeutic targets.
P4-2	KB0062-A	Investigating Estrogen Receptor Dimerization under Endocrine Disruption via BRET Analysis **Yum Soomin** Pusan National University Abstract: Endocrine-disrupting chemicals (EDCs) are exogenous compounds that interfere with endogenous estrogen signaling by binding

		to estrogen receptors (ERs), thereby perturbing hormone-regulated physiological processes. In our previous investigation, we established a bioluminescence resonance energy transfer (BRET)-based platform to quantify ER dimerization as a means to detect EDC activity. To assess the feasibility of BRET as a stand-alone bioassay for EDC identification, we characterized ER–ligand interactions in both pre- and post-dimerization states. Biophysical analyses using isothermal titration calorimetry (ITC) and dynamic light scattering (DLS) confirmed that certain EDCs facilitate ER dimerization in a ligand-dependent manner. Accordingly, the BRET assay demonstrated high sensitivity and specificity in detecting ER dimerization and revealed its functional association with EDC-induced disruption of downstream signaling pathways. To further delineate the transcriptional consequences of EDC exposure, we performed chromatin immunoprecipitation sequencing (ChIP-seq), followed by gene ontology (GO) enrichment analysis. Functional annotation revealed that EDCs modulate a range of biological processes, including antibody-dependent cell-mediated cytotoxicity, bone morphogenetic protein (BMP)-driven cardiac induction, and hepatocyte growth factor (HGF) receptor signaling. Collectively, our findings provide mechanistic insight into how EDCs alter ER dimerization and disrupt hormone-dependent signaling cascades. This study underscores the utility of the BRET-based ER dimerization assay as a robust tool for EDC detection and advances our understanding of the molecular basis underlying endocrine disruption.
P4-3	KB0025-A	Single-Cell Multi-Omics Characterization of Candidate T Cell Repertoire Features in Antithyroid Drug-Induced Agranulocytosis of Graves' Disease **Yu-Ting Weng**, Sheng-Kai Lai, Yi-Hui Huang, Yu-Hsuan Yang, Pei-Lung Chen, and Chien-Yu Chen National Taiwan University Abstract: Single-cell multi-omics provides a high-resolution framework for investigating immune repertoire dynamics in autoimmune disorders. We analyzed peripheral blood mononuclear cells (PBMCs) from 29 individuals, including Graves' disease (GD; n = 9), antithyroid drug-induced agranulocytosis (TiA; n = 6), and healthy controls (n = 14), using single-cell RNA sequencing with paired T cell receptor (TCR) profiling. High-resolution HLA genotyping and germline adaptive immune receptor repertoire (gAIRR) profiling were incorporated to explore genetic influences on repertoire composition. To systematically capture disease-relevant

		features, our workflow integrated machine learning-driven feature selection. TiA and GD were compared to identify repertoire patterns enriched in TiA but absent in GD, while excluding those present in controls to highlight TiA-specific signatures. Incorporation of gAIRR data further enabled assessment of whether these repertoire differences between TiA and GD might be germline-driven. In this exploratory analysis, TiA samples exhibited candidate VDJ combinations and CDR3 sequence motifs within T cells, co-occurring with repertoire patterns potentially associated with specific HLA alleles. In contrast, certain V-gene usage trends were observed across all cohorts, suggesting shared germline-related repertoire features. These findings underscore the value of integrating single-cell transcriptomic and immune receptor repertoire analyses to generate hypotheses for autoimmune disease mechanisms and biomarker discovery.
P4-4	KB0064-A	Organ-Specific Transcriptomic Profiling of Low-Dose Environmental Toxicants Reveals Divergent Molecular Responses in Human Cell Lines **Woo Seok Kang** Pusan National University Abstract: Environmental toxicants pose risks to human health, yet their molecular effects across organ-specific cell types remain unclear. Here, we examined the responses of four human organ–derived cell lines intestinal epithelial cells (HIEC6), hepatocytes (HL7702), bronchial epithelial cells (BEAS-2B), and keratinocytes (HaCaT) to ten representative chemicals, including phthalates (DBP, DINCH, DEHP), bisphenols (BPA, BPS), perfluorinated compounds (PFOA, PFTeDA), and metals ($NiCl_2$, $AlCl_3$). For each line, the inhibitory concentration reducing cell viability by 1% (IC_1) was determined, followed by RNA sequencing and gene set enrichment analysis (GSEA). Distinct organ-specific transcriptional responses were observed. In intestinal epithelial cells, bisphenol exposure downregulated gene sets related to chromosome segregation and cell cycle progression, suggesting impaired division and genomic stability. In keratinocytes, phthalates upregulated ribosome biogenesis and rRNA metabolism, indicating activation of protein synthesis. These findings demonstrate that low-dose toxicant exposure elicits divergent molecular responses across human cell types and provide a foundation for evaluating organ-specific vulnerability in toxicological and health risk assessments. [This research was supported by a grant (25192MFDS004) from Ministry of Food and Drug Safety in 2025.]

P4-5	KB0073-A	Insights from the Chloroplast Genome: Comparative Genomics of Endemic Adenophora taquetii and Its Relatives **Song-I Han,** Sheikh Mansoor, Jiwon Kim, Jae-Hoon Kim, and Kyung-Hwan Boo Jeju National University Abstract: Adenophora taquetii is an endemic wild species native to Jeju Island, South Korea, traditionally used in oriental medicine and as an ornamental plant. This study presents the complete chloroplast genome of A. taquetii and its comparison with other Adenophora species. The chloroplast genomes of A. verticillata, A. stricta, and A. taquetii were analyzed, with genome sizes of 218,670 bp, 157,851 bp, and 161,722 bp, respectively. The large single-copy (LSC), small single-copy (SSC), and inverted repeat (IR) regions measured 113,770 bp, 27,738 bp, and 10,132 bp. A total of 129–141 genes were annotated, including 88 protein-coding and 96 RNA genes. Twenty-five simple sequence repeats (SSRs) were identified, with T-repeats being the most common. A. taquetii contained 1,161 single-nucleotide polymorphisms (SNPs), of which 636 were in genic regions and 534 in coding sequences. Phylogenetic analysis revealed a close relationship between A. taquetii and A. triphylla, indicating a recent common ancestry. These results provide valuable insights into the chloroplast genome evolution and genetic diversity within the genus Adenophora.
P4-6	KB0102-A	Iodoacetic Acid Induces Metabolic and Oxidative Damage in Porcine Uterine Epithelial Cells and Oviduct Epithelial Cells **Qin-Yue Lu** and Xiang-Shun Cui Chungbuk National University Abstract: Iodoacetic acid (IAA), a highly cytotoxic disinfection byproduct commonly detected in drinking water, poses a potential risk to female reproductive health. The direct molecular mechanisms underlying its effects on the reproductive system epithelium remain unclear. This study demonstrates that IAA induces glycational stress in primary porcine uterine (UECs) and oviduct epithelial cells (OECs), acting as an upstream driver of extensive cellular toxicity. IAA exposure inhibited GAPDH enzymatic activity and promoted accumulation of the advanced glycation end product Nε-(carboxymethyl)lysine (CML), triggering mitochondrial dysfunction, redox imbalance, calcium dyshomeostasis, and endoplasmic reticulum

		stress. These disturbances activated a dysregulated signaling network involving p38 MAPK, AKT, and NF-κB pathways, ultimately causing G1/S cell cycle arrest and apoptosis. Notably, pretreatment with the AGEs inhibitor pyridoxamine reduced CML accumulation, restored mitochondrial function, and alleviated apoptotic cell death. These findings reveal glycational stress as a key initiating mechanism for IAA-induced reproductive epithelial toxicity, providing mechanistic insight into the potential health risks of environmental disinfection byproducts.
P4-7	KB0074-A	Advanced Optimization of a Trv-Based Virus-Induced Gene Silencing (Vigs) System for Functional Genomics in Spinach **Jiwon Kim,** Surim Lee, Eunsu Ko, and Kyung-Hwan Boo Jeju National University Abstract: Virus-induced gene silencing (VIGS) provides a rapid and efficient approach for functional genomics in plants. We optimized a tobacco rattle virus (TRV)-based VIGS system for Spinacia oleracea to enhance its applicability in functional genomics. Using the SoPDS (phytoene desaturase) gene as a visual reporter, we systematically examined various factors influencing silencing efficiency. The most effective silencing was achieved with Agrobacterium tumefaciens strain GV2260 at an optical density (OD_{600}) of 1.0, combined with sandpaper-assisted wound infiltration on true leaves. Under these optimized conditions, SoPDS transcript levels were reduced by more than 80%, accompanied by a 69% decrease in total chlorophyll content. Cotyledon infiltration also induced substantial silencing, reducing SoPDS expression by over 60% with a comparable decline in chlorophyll content. Importantly, this optimized system enabled simultaneous silencing of multiple genes, such as SoPDS and SoTCM, suppressing both transcripts by more than 65%. Taken together, these results establish a robust and reproducible TRV-VIGS platform, significantly advancing functional genomics in spinach and other leafy vegetables.
P4-8	KB0105-A	Stage-Specific Inhibition of Aberrantly Upregulated Genes Improves Blastocyst Development in Porcine IVF Embryos **Cheng-Lin Zhan** and Xiang-Shun Cui Chungbuk National University Abstract: Porcine embryos derived from in vitro fertilization (IVF) consistently show reduced blastocyst formation rates and inferior

		developmental quality relative to in vivo embryos. To uncover the molecular basis of these impairments, we conducted transcriptome profiling during the developmental progression from the 4-cell stage to the blastocyst stage in both in vivo– and IVF-derived embryos. Genes exhibiting divergent expression trajectories—those that remain stable or are downregulated in in vivo embryos yet are upregulated in IVF embryos—were pinpointed as candidate drivers of developmental compromise. Stage-specific functional inhibition of selected aberrantly upregulated genes, including PPARG, CREBBP, and FOXO1, was performed to evaluate their impact on blastocyst formation and quality. Targeted suppression of these genes at precise developmental windows markedly enhanced blastocyst formation rates, increased total cell numbers, normalized the expression of lineage specification markers (OCT4, NANOG, GATA6, SOX17), and attenuated DNA damage and apoptotic signals. These results indicate that aberrant activation of specific transcriptional networks during early embryogenesis underlies the diminished developmental competence of IVF embryos, and that temporally precise inhibition of these pathways can rescue normative developmental progression.
P4-9	KB0123-A	Two Magnesium Ion Binding Sites of class Ⅱ Pyruvate Aldolases Han-Gyeol Woo and **Jeong-Sun Kim** Chonnam National University Abstract: Metal ions are essential cofactors in metalloenzymes, and recent structural studies have revealed that they can undergo small but distinct positional shifts within active sites during catalysis. However, the structural basis and catalytic significance of this metal movement remain poorly understood. To address these questions, we characterized two class II pyruvate aldolases from Achromobacter xylosoxidans (AxADL) and Pseudomonas aeruginosa (PaADL) and determined high-resolution crystal structures of both enzymes in their apo, Mg^{2+}-bound, and Mg^{2+}/pyruvate-bound states. AxADL and PaADL adopt a canonical TIM-barrel fold and assemble into hexamers via C-terminal α-helix exchange, and their active sites harbor conserved residues that coordinate the catalytic Mg^{2+} ion and promote enolate formation. Comparative analysis of these states shows that, upon substrate binding, the catalytic Mg^{2+} shifts by approximately 2–3 Å toward the active center, reorganizing the active site into a geometry for direct substrate coordination in both enzymes. A methionine residue positioned adjacent to the metal-binding

		site exerts a steric effect that helps drive this displacement, and replacement with leucine enhances catalytic activity. Together, these findings provide structural evidence that class II pyruvate aldolases employ controlled metal repositioning as a key element of their catalytic strategy and show that this displacement is governed not only by coordination geometry but also by steric contributions from nearby residues.
P4-10	KB0069-A	Developmental Impacts of Bongkrekic Acid Exposure in a Zebrafish Model **Jiun-Lin Horng,** Giun-Yi Hung, and Li-Yih Lin Taipei Medical University Abstract: Bongkrekic acid (BA), a mitochondrial toxin produced by Burkholderia gladioli, has been associated with foodborne poisoning leading to fatal organ failure. However, its developmental and organ-level toxic profiles during vertebrate embryogenesis remain incompletely characterized. In this study, we employed zebrafish embryos to explore the dose-dependent effects of BA on growth, morphology, and organ function. Embryos were exposed to BA concentrations ranging from 0.01 to 1 mg/L for 96 hours post-fertilization. A clear concentration–response relationship was observed, with notable increases in lethality and developmental malformations at doses ≥0.05 mg/L. BA exposure disrupted body patterning, eye and otic development, and yolk absorption, indicating metabolic and morphogenetic dysregulation. Functional assessments revealed pronounced cardiac suppression, reduced locomotor responsiveness, and diminished neuromast integrity, implying cardiotoxic and neurobehavioral consequences. Hepatic and ion-regulatory alterations were also evident, suggesting broader impacts on metabolic and electrolyte homeostasis. Collectively, our findings demonstrate that BA exerts multi-organ developmental toxicity in zebrafish embryos, providing mechanistic insights into its pathogenic potential in early vertebrate development.

Online Session 1

zoom

January 18, 2026, Sunday (GMT+9)

Duration	Venue
10: 00-13:15	Meeting ID: 893 3803 2428 Link: https://us02web.zoom.us/j/89338032428

Topic:	Bioactive Materials, Nanotechnology, and Data-Driven Biomedical Applications
Session Chair:	TBA

Paper Detail

Online1-1	KB0063 10:00-10:15	Study of Lavender Essential Oil Encapsulated Chitosan-Derivative Nanoparticles on Shampoo Applications **Wanyue Zeng** and Jumao Yuan Suyan Innovation Lab Abstract: Since lavender essential oil (LEO) contains antibacterial, anti-inflammatory, and calming qualities, it is commonly utilized in hair care products. However, adding LEO conventionally results in quick evaporation and a shorter product shelf life due to its high volatility. In this study, chitosan-derivative nanoparticles (CSNPs) were initially prepared by degradation, modification, and purification. LEO was then encapsulated to create LEO-CSNPs, and FTIR, DLS, TEM, and ^{1}H-NMR were used to evaluate both CSNPs and LEO-CSNPs. The effectiveness of the shampoos was next assessed by clinical trials and in vitro tests, such as malassezia inhibition, sebocyte lipid secretion, DPPH radical scavenging as well as qPCR for inflammatory markers with varying concentrations of LEO-CSNPs. The findings confirmed successful encapsulation since LEO-CSNPs (352.27 nm) had a higher particle size than CSNPs (218 nm). With a 15.5 mm Malassezia inhibition zone, 87.71% sebocyte lipid inhibition, 79.03% DPPH scavenging rate, and a notable downregulation of IL-6 and IL-8 expression. Meanwhile, the 0.5% LEO-CSNPs group demonstrated concentration-dependent efficacy. In terms of clinical results, fragrance longevity was increased to 7.2 hours, scalp flaking was decreased by 77.73%, and itching was also decreased by 69.05%. In conclusion, encapsulating LEO in chitosan-derived nanoparticles resolved its volatility

		problem and improved the antifungal, sebum-regulating, antioxidant, and anti-inflammatory properties in shampoo. Finally, the ideal concentration of LEO-CSNPs is between 0.3% and 0.5%, laying the groundwork for multipurpose shampoo.
Online1-2	KB0137 10:15-10:30	A Comprehensive Preprocessing Pipeline for TCGA-BRCA Multi-Omics Data Integration **Varad Pai,** Yash Gawhale, Vinay E Palled, Nagathejas M S, and Bhaskarjyoti Das PES University Abstract: The largest multi-omics resource for breast cancer research is the Cancer Genome Atlas (TCGA) Breast Invasive Carcinoma cohort, but fragmented data distribution, inconsistent identifier systems, and platform-specific preprocessing requirements continue to limit its usefulness for machine learning applications. We offer a thorough, repeatable preprocessing pipeline that unifies clinical data, copy number variation, RNA-seq, and DNA methylation into a single, analysis ready matrix. Through cross-platform gene-level alignment, systematic UUID-to-barcode mapping, and modality-specific normalization techniques (log2(TPM+1) for RNA-seq, beta values for methylation, and GISTIC2 scores for CNV), our method tackles important technical issues. Crucially, we use ComBat with empirical Bayes shrinkage to implement explicit batch effect correction, which preserves biological signals while lowering technical variance from 80.2% to 24.9% in RNA-seq and 72.8% to 23.0% in methylation data. A high-fidelity dataset of 710 high quality patients across 17,014 genes with thorough biological validation is produced by multi-tier quality control and KNN imputation: expression-methylation anti-correlation (ρ=−0.74, p < 10−121), expression-CNV dosage correlation (ρ= 0.48, p < 10−121), and 89% PAM50 subtype classification accuracy. Our pipeline achieves quantified quality improvements (13% noise reduction), 20% larger sample size, and 70% greater gene coverage when compared to current resources. The validated and well documented framework with its generalizable methodologies that can be used across different cancer types and multi-omics platforms forms a solid ground for machine learning applications in survival prediction, molecular sub-typing, and biomarker discovery.
Online1-3	KB0093 10:30-10:45	Development of Mao Tea Polyphenol-Loaded Sophorolipid Nanomicelles for Shampoo

		Yiqiu Shen and Jumao Yuan Suyan Innovation Lab Abstract: Increasing consumer demand for eco-friendly and safe cosmetic products has highlighted the need to replace environmentally toxic antifungal agents commonly used in anti-dandruff shampoos. There is a critical demand for developing effective, natural alternatives that provide antifungal benefits without compromising environmental safety and scalp health. This study utilized microbial-fermented sophorolipids and catechin-rich Mao tea polyphenols to formulate nanomicellar co-delivery systems encapsulated within shampoo bases. The nanomicelles enhance the stability and bioavailability of polyphenols which are otherwise heat, light, and pH sensitive. Four different ratios of sophorolipid to Mao tea extract were tested. Antifungal efficacy against malassezia furfur was evaluated alongside antioxidant capacity, foam stability, skin compatibility, and clinical scalp assessments. The nanomicellar formulations demonstrated potent antifungal inhibition of malassezia growth in vitro. The shampoo showed improved antioxidant activity and foam stability compared to controls. Safety evaluation confirmed the gentleness of the formulation on skin and scalp. Clinical testing revealed significant reduction in dandruff severity, scalp erythema, itch, and sebum levels after regular use, indicating both therapeutic and cosmetic benefits. Sophorolipid-loaded Mao tea polyphenol nanomicelles present a promising sustainable alternative to traditional chemical agents for effective dandruff control. Stabilizing natural actives via nanotechnology enables enhanced performance and safety, aligning with the rising trends in environmentally conscious cosmetic formulations.
Online1-4	KB1017 10:45-11:00	Tertadesmus Obliquus-Mediated Silver Nanoparticles: A Green Route to Potent Antibacterials **Mahmoud R. Ali,** Marwa Elkady, Jelan Mofeed, Ahmed Sayed Saad, and Amr A. Nassrallah Biotechnology Department, Faculty of Basic and Applied Sciences, Egypt-Japan University of Science and Technology(E-JUST) Abstract: Using algae for nanoparticle biosynthesis offers a green, cost-effective alternative to other chemical and physical methods. This study uses the cell-free supernatant of Tetradesmus obliquus. to produce silver nanoparticles (AgNPs) sustainably, achieving notable stability and

		antimicrobial activity. An initial experimental design was used to optimize the production process to maximize nanoparticle yield. The study examined the effects of key variables, including the ratio of extract to silver nitrate solution, the type of capping agent, and the medium pH. The custom design included 12 experiments with varying values for each variable, and we measured absorbance at 420 nm during both short- and long-term assessments to evaluate yield and stability. The results showed that SDS was the most effective stabilizer, resulting in an eightfold increase in nanoparticle production compared to sodium citrate after 2 weeks. At pH 9, with SDS, a rapid synthesis with maximum production was achieved even at lower $AgNO_3$ concentrations. AgNPs (3.90-10.83 nm average diameter, charge= -23.3 mV) were characterized using Zeta potential, FT-IR, XRD, and TEM.
Online1-5	KB0111 11:00-11:15	Research on the Improvement Effect of Essential Oil-based Mouthwash on Oral Ulcers **Du Wang** and Jumao Yuan Suyan Innovation Lab Abstract: This study aimed to identify the optimal concentration ratio of tea tree oil (TTO) and eucalyptus essential oil (EEO) in an antimicrobial mouthwash through evaluating the safety, efficacy and sensory profile of four experimental formulations. Safety was assessed using the chick embryo chorioallantoic membrane (CAM) assay, while antibacterial effects were tested against oral pathogens. Anti-inflammatory properties were measured with qPCR in human gingival fibroblasts, and a randomized controlled clinical trial design was outlined for evaluation. In the results, low concentrations of essential oils caused little or no irritation in the CAM assay, while higher concentrations increased irritation. Additionally, the formulations demonstrated strong antibacterial activity (>99.9% inhibition for E. coli, S. aureus, and S. mutans, and ~93% against P. gingivalis). Meanwhile, qPCR revealed significant suppression of pro-inflammatory cytokines, with higher oil ratios showing stronger effects but lower taste acceptance. In summary, essential oil-based mouthwashes indicated promising antibacterial and anti-inflammatory effects for oral ulcer management. In summary, the 0.2% TTO + 0.2% EEO formulation offers the best balance of efficacy, safety, and consumer acceptability.
Online1-6	KB0138 11:15-11:30	Parkinson’s Disease Detection Through Static Handwriting Analysis Using CNNs and SVM Ensemble

		Myk Erolf Durano Roble and Heart Alvern Santarita Sumicad University of San Carlos Abstract: Parkinson's Disease is a progressive neurological disorder marked by motor impairments, often reflected in handwriting anomalies such as tremors, micrographia, and stroke irregularities. Conventional diagnostic tools, though effective, can be invasive, or reliant on subjective evaluation. This thesis explores a non-invasive framework for PD detection using static handwriting samples, specifically spiral and wave drawings. The method applies an ensemble learning strategy that fuses deep features from two pre-trained Convolutional Neural Network (CNN) architectures: ResNet50 and DenseNet121. These complementary feature representations are integrated and classified using a single Linear Support Vector Machine (SVM). This approach leverages static images and dual-CNN fusion to improve classification potential on limited medical datasets. The model was initially trained and evaluated using a publicly available handwriting dataset, achieving an accuracy of 97.28%, demonstrating high reliability under controlled conditions. When independently verified using a local dataset, the system maintained strong generalization with an accuracy of 95.19%, 97.04% recall for PD cases, and 93.33% for healthy controls, indicating consistency across populations. The results confirm that dual-CNN feature fusion significantly improves detection stability and adaptability between datasets. This framework offers an objective screening tool that can complement neurological assessments and clinical environments.
Online1-7	KB0075 11:30-11:45	Formulation of Green PGD Polymeric Nanoparticles of Curcumin: Physicochemical Characterization, Stability testing and Docking Study Targeting BTK **Rania Hassan Hussein Ahmed,** Mahmoud E. Soliman, Sherif F. Hammad, Hesham S. M. Soliman, and Ahmed Abdel-Mawgood Egypt-Japan University of Science and Technology Abstract: Polymers structured as nanoparticles for encapsulating the hydrophobic drugs is a strategy considered as a useful way to improve drug absorption and lower off-target activity. Curcumin is well-known for its anti-inflammatory properties, but it is not clinically used much because it does not dissolve well in water (600 ng/mL), this hampers its targeted delivery and bioavailability. Formulating a green, non-toxic and

		biocompatible nanoparticle system to retain curcumin utilizing poly(glyceryl succinate-adipate) polymer via a polycondensation process, tackled these challenges and made curcumin a powerful anti-inflammatory agent against many inflammatory diseases as arthritis. The formulation revealed a remarkable increment in solubility and stability in deionized water intended for intra-articular injection. Also, the particle size was refined to fit as a therapeutical nanoparticle that can reach the intra articular cells easily. This technology gives drugs the chance to stay in the body longer, release more efficiently, and spread out more evenly than the free drug. As curcumin reaches deep tissues, it gains the ability to interact with new more targets as Bruton's Tyrosine Kinase, this may give curcumin a new therapeutic potential as BTK inhibitor. This study viewed a full physicochemical characterization for the produced formulation, tested its short-term stability by different concentrations of sodium sulphate, and did a molecular docking analysis to see how well it binds and how useful it is as a treatment.
Online1-8	KB0104 11:45-12:00	The Composition Analysis of Endophytic Bacteria Community and Genetic Investigation of Major Strains in Jimai 44 Seeds **Fengning Yang** and Jinpeng Wang Shandong Agricultural University Abstract: In this research, the community composition and specific strains of endophytic bacteria in the seeds of Triticum aestivum L. cv. Jimai 44 were cultured in vitro and initially identified. The taxonomic status of four target strains was analyzed in detail, and their functions in promoting wheat growth or resisting wheat diseases and pests were evaluated and inferred. Additionally, in vitro culture experiments were conducted to verify the capabilities of the endophytic bacterial samples to metabolize major nutrient elements.
Online1-9	KB2001-A 12:00-12:15	Non-Invasive Prediction of Hepatic Venous Pressure Gradient Using a Fully Connected Neural Network Model **Jiyang Zhang**, Taoping Bai, and Wentao Jiang Sichuan University Abstract: The hepatic venous pressure gradient (HVPG) is the gold standard for assessing portal hypertension and guiding treatment decisions, particularly for transjugular intrahepatic portosystemic shunt (TIPS) procedures. However, its measurement requires invasive

		catheter-based techniques, which brings posing risks, high costs, and operational complexity. Thereby limiting widespread clinical application. This study proposes a non-invasive approach for predicting HVPG using a fully connected neural network (FCNN) model that integrates 14 routinely available clinical indicators, including biochemical markers, routine blood tests, and hemodynamic parameters. Data from 75 patients who underwent invasive HVPG measurements were collected and randomly divided into training (n=60) and testing (n=15) sets. A five-layer FCNN model with decreasing neuron counts was designed to establish a nonlinear mapping between input features and HVPG. The model achieved a mean squared error (MSE) of 152.85 $mmHg^2$, mean absolute error (MAE) of 7.42 mmHg, and R-squared (R^2) of 0.652 on the test set. Furthermore, in the classification task distinguishing compensated from decompensated patients (threshold HVPG = 12 mmHg), the model achieved an area under the ROC curve (AUC) of 0.84. These findings demonstrate the feasibility of FCNN-based pre-HVPG prediction model and lay the groundwork for future multimodal prediction models incorporating imaging and other data sources.
Online1-10	KB2024 12:15-12:30	A Novel Depression Detection Method based on Nonlinear Feature Fusion of EEG Signals Yongchun Ma, **Jing Kan**, Wei Tong, Bicheng Wu, and Kewei Chen Peking University Abstract: To explore an efficient and convenient screening solution, this study proposes a depression detection method based on portable dry-electrode EEG. Although the nonlinear characteristics of EEG signals have been confirmed as important biomarkers for diagnosing depression, traditional methods mostly rely on multi-channel EEG systems (e.g., 20 or 32 channels), where excessive channel numbers hinder clinical convenience. To address this issue, we propose a depression detection framework based on nonlinear features extracted from 8-channel EEG. This framework employs fuzzy entropy, permutation entropy, and differential entropy as nonlinear representations of EEG, and has been validated on the public MODMA dataset and a private ZJTD dataset. Among various classifiers, the Random Forest (RF) classifier achieved optimal performance, obtaining an accuracy of 98.46% (specificity 99.39%, sensitivity 97.33%) on

		MODMA and 93.56% (specificity 95.14%, sensitivity 91.61%) on ZJTD, surpassing existing methods that utilize more channels. These results indicate that the fused features from the 8-channel EEG may serve as potential biomarkers for depression detection. Furthermore, this framework offers an accurate, practical, and efficient solution for auxiliary screening of depression, demonstrating significant potential for clinical application.
Online1-11	KB0147 12:30-12:45	Design of an Integrated Model for Deep Causal Interpretation and Evolutionary Prediction of Zika Virus Mutations **Sony Kanhaiyalal Ahuja**, Deepti Deepak Shrimankar, and Aditi Rajratna Durge Visvesvaraya National Institute of Technology (VNIT) Abstract: Identifying genetic changes that elevate Zika Virus (ZIKV) virulence is vital for epidemic forecasting and vaccine development. Traditional phylogenetic and regression methods map variation but seldom pinpoint mutations driving phenotypic change. We present an integrated deep-learning and simulation framework that tracks ZIKV's sequence-to-consequence trajectory. A Spatio-Temporal Generative Adversarial Network (ST-GANet) learns region–time–mutation patterns to reveal evolutionary hotspots. A Causal Mutation Gradient Mapper (CMGM) then estimates each mutation's directional influence on virulence. A Viral–Host Interaction Transformer (VHIT) predicts how prioritized mutations alter Envelope and NS1 protein–receptor binding. Using transcriptomes from infected human brain progenitor cells, a Pathogenicity Potential Simulation Engine (PPSE) models resulting intracellular signaling disruptions. An Evolutionary Route Planner (ERP) identifies fitness-maximizing mutational paths under immune pressure. Together, these modules reveal how subtle sequence changes can reshape epidemiological risk and support real-time flavivirus molecular surveillance.
Online1-12	KB1019 12:45-13:00	Biofabrication of Zinc Oxide Nanoparticles Using Streptomyces Cyaneofuscatus **Manar Kamal Saad Abdelnabi** Egypt Japan University of Science and Technology (E-JUST) Abstract: This study demonstrates a green, cost-effective, and biocompatible method for synthesizing zinc oxide nanoparticles (ZnONPs)

		using the cell-free filtrate of Streptomyces cyaneofuscatus as a natural reducing and stabilizing agent. The biosynthesized ZnONPs showed good stability (−26.6 mV), a hexagonal wurtzite crystal structure, and particle sizes suitable for functional applications (81–190 nm). The successful microbial fabrication of high-purity ZnONPs highlights the method's potential for scalable, environmentally friendly production of ZnONPs for applications in biomedical, agricultural, and environmental technologies.
Online1-13	KB0119-A 13:00-13:15	Optimization of Antimicrobial Activity of Cobalt Oxide (Co_3O_4) Nanoparticles Via Modulation of Synthesis Temperature **Muhammad Shoaib Ashraf** and Shihab Uddin King Fahad University of Petroleum and Minerals Abstract: Antibiotic resistance is accelerating faster than the discovery of new drugs, emphasizing the need for alternative antimicrobial strategies. Transition-metal oxide nanomaterials offer a complementary approach, yet how synthesis parameters govern biological activity remains insufficiently defined. Here,we synthesized Co_3O_4 nanoparticles by thermal decomposition of $Co(NO_3)_2{\cdot}6H_2O$ at 320, 420, 520, and 620 °C, then structurally characterized (XRD to confirm spinel Co_3O_4; electron microscopy to assess nanoscale morphology/aggregation). Antibacterial performance was evaluated against against Escherichia coli, Micrococcus luteus, Bacillus subtilis, and Bacillus cereus by agar well diffusion assay using water-dispersed suspensions (1–3 mg mL^{-1}). Activity was selective for Gram-negative E. coli, with no inhibition observed for the Gram-positive strains across all conditions. Against E. coli, the zone of inhibition depended on both synthesis temperature and dose, showing a non-monotonic trend. Co_3O_4 prepared at 520 °C showed maximum activity and zone of inhibition diameter of 31.8 mm at 1 mg mL^{-1} was observed (representative values: 30.5 mm at 320 °C/1 mg mL^{-1}; 29.0 mm at 420 °C/1 mg mL^{-1}; 27.6 mm at 620 °C/3 mg mL^{-1}). At 520 °C, Co_3O_4 attains an optimal crystallinity–morphology balance that preserves abundant Co^{2+}/Co^{3+} redox sites and oxygen vacancies, maximized the ROS generation and membrane interactions, whereas at 620 °C, particle aggregation reduce the effective active surface and antimicrobial efficacy. These results indicate that intermediate synthesis temperature optimizes antibacterial performance against E. coli, likely via temperature-tuned surface reactivity, and that higher concentration or higher temperature alone does not guarantee stronger inhibition. This temperature–performance relationship

		provides a practical way for optimizing Co_3O_4 nanoparticle adjuncts for targeting Gram-negative infections.

Note

Note