2026 MOPM多體學及精準醫學聯合會議_海報投稿通過名單

Society	No.	Presenter's Chinese Name	Presenter's English Name	Abstract Title
台灣蛋白體學會（TPS）	**TPS-001**	包容	Jung, PAO	Proteome-Wide Identification of Sphingosine-1-Phosphate-Binding Proteins Using a Liposome–Proteome Microarray Platform
	TPS-002	何佳都	Jia-Jun, He	LncHIFCAR Impairs Antigen Presentation and Downregulates MHC class I in Pancreatic Ductal Adenocarcinoma
	TPS-003	吳元傑	Yuan-Jie Wu	High-Throughput Protein Analysis Cell Lysate via Protein G Oriented Antibody Microarrays
	TPS-004	李永國	Yung-Kuo Lee	Nuclear Co-accumulation of Galectin-3 and OCT4 Defines a Niche-associated Stemness State in Colorectal Cancer
	TPS-005	阮陳國全	NGUYEN TRAN QUOC TOAN	Profiling Antibody Signatures in Autoimmune Uveitis Using Escherichia coli Proteome Microarrays
	TPS-006	周廷禎	Ting-Chen Chou	Material Design and Capture Performance of a Water-Soluble Aldehyde-Capturing Kit: Formaldehyde as a Model Analyte
	TPS-007	徐祥芠	Hsiang Chih, Hsu	Development of a SWATH-MS-Based Quantitative Proteomic Strategy for the Analysis of Glioblastoma Tissues
	TPS-008	祝令儀	Ling-Yi Jhu	An Optimized High-Throughput Serum Proteomics Workflow for Deep Profiling and Clinical Phenotyping of COPD
	TPS-009	馬丞毅	Cheng-Yi Ma	Single-Microliter Serum Proteomics Reveals Nutritional State-Dependent Protein Dynamics Following High-Intensity Interval Training
	TPS-010	風山	Son Hoang	Identification of Cross-Reactive Human Proteins Elicited by SARS-CoV-2 Vaccine-Induced Antibodies
	TPS-011	張芷榆	Chih-Yu Chang	Placental Proteomic Profiling Identifies Molecular Signatures Associated with Biological Heterogeneity in Gestational Diabetes Mellitus
	TPS-012	張俊毅	Chong Jun Yi	Multi-Omic Profiling of Colorectal Cancer Reveals Distinct Tumor Features across Consensus Molecular Subtype Phenotypes
	TPS-013	張凱富	Kai-Fu Chang	Pyroptosis-Related Molecular Heterogeneity Predicts Prognosis and Immune Microenvironment Remodeling in Colon Adenocarcinoma
	TPS-014	莫靖宇	Ching-Yu Mo	Functional Regulation of mTOR through Binding of Intracellular Lipopolysaccharide
	TPS-015	許博凱	Bo-Kai Hsu	Comprehensive Volatile Profiling of Honey by HS-SPME/GC-MS for Batch-to-Batch and Geographic Origin Differentiation
	TPS-016	陳沁暉	Chin-Huei Chen	Quantitative Proteomics Unveils Manzamine A-Mediated Mitochondrial Dysfunction and Oxidative Stress in Ovarian Cancer Cells
	TPS-017	陳佳玟	Chia-Wen, Chen	HS-SPME-GC/MS-based analytical platform for plasma metabolite profiling in antiphospholipid syndrome
	TPS-018	陳榆蓁	Chen YuZhen	Repurposing Bazedoxifene, a Selective Estrogen Receptor Modulator, for Clear Cell Renal Cell Carcinoma through Phos-phoproteomic Profiling
	TPS-019	章安琪	Olivia Tjoa	Investigating The Oncogenic Role of RIM2 in Pancreatic Ductal Adenocarcinoma (PDAC)
	TPS-020	彭冠傑	Peng Kuan Chieh	Spatial Optimization of Cas9-Donor Tethering via Monomeric Streptavidin (mSA)-Biotin Interaction for Enhanced Homology-Directed Repair
	TPS-021	楊佳麟	Jia-Yi Yang	Establishment of a Scalable Food Proteome Microarray Platform for Profiling Diet-Associated Antibody Signatures in Schizophrenia Spectrum Disorders
	TPS-022	廖奕安	Yi-An Liao	Metabolomics-Driven Reconstruction of Tumor-Intrinsic Metabolic Networks for Early Detection in Colorectal Cancer
	TPS-023	熊建瑋	Chien-Wei Hsiung	Cardiac Extracellular Vesicle Proteomics Identifies Mitochondrial and Contractile Dysfunction in Carbon Monoxide Poisoning and Their Reversal by Hyperbaric Oxygen Therapy
	TPS-024	劉子琪	Tzu-Chi Liu	Deciphering the Protein Targets of Amyloid-beta with Escherichia coli Proteome Microarrays
	TPS-025	劉思辰	Ssu-Chen Liu	Identification of Key Mediators of Aging Skeletal Muscle–Induced Monocyte Aging
	TPS-026	蔡淳伊	Chun-Yi Tsai	Identification of A Candidate Cytokine Associated with BM-MSC-Mediated Metastatic Reprogramming in Lung Cancer
	TPS-027	蕭愛瑾	Ai-Li Hsiao	Functional Characterization of CDK18 in Clear Cell Renal Cell Carcinoma Progression
	TPS-028	簡聖明	Sheng-Ming Chueh	Tracing Adipokine Transfer by SILAC Proteomics Identifies Adipocyte-Derived Drivers of Colorectal Cancer Progression
	TPS-029	羅以筑	Yii-Jwu Lo	Immunometabolic Remodeling of the Tumor Microenvironment by GIPR/GLP-1 Receptor Co-agonism in Colorectal Cancer
	TPS-030	**Alia**	Alia	Evaluation of an Optimized Reductive Amination-Based Ultra-High-Performance Liquid Chromatography Coupled with Tandem Mass Spectrometry (UHPLC-MS/MS) Method for the Quantification of Arginine, ADMA, SDMA, Citrulline, and Ornithine
	TPS-031	**Dahlak Daniel Solomon**	Dahlak Daniel Solomon	Integrative Bulk, Single-Cell, and Spatial Transcriptomics Reveal an OGFOD3-High Stress-Adapted Malignant State in Glioblastoma
	TPS-032	**Hana Natasha Christiadi**	Hana Natasha Christiadi	Quantitation of Primary Biogenic Amines (Histamine, Tyramine, Putrescine, and Cadaverine) in Fermented Beverages via Isotopic Formaldehyde Reductive Amination and LC-MS/MS
	TPS-033	**Neethu Palekkode**	Neethu Palekkode	Integrative Analysis Reveals Lysosomal Acid Phosphatase 2 as a Biomarker of Glioma Progression and Immune Remodeling
	TPS-034	**Sachin Kumar**	Sachin Kumar	Multi-Omics Profiling Reveals L-Glutamine Transport-Associated Metabolic Adaptation and Temozolomide Resistance in Glioblastoma
	TPS-035	**Samantha Christy Lie**	Samantha Christy Lie	Development and Validation of a Reductive Amination LC-MS/MS Method for the Simultaneous Determination of S-Adenosylhomocysteine (SAH), Homocysteine, and Methionine as Biomarkers Associated with Cardiovascular Disease.
	TPS-036	李妮容	Ni-Rong Li	Verification of Serological Lung Adenocarcinoma Protein Markers Using Liquid Chromatography Multiple Reaction Monitoring Mass Spectrometry
	TPS-037	林俊錞	Chun-Chi Lin	Discovery of Chemical Markers in Spoiled Eggs Using Mass Spectrometry-Based Untargeted Metabolomics
	TPS-038	林曉芯	Yu-Hsin Lin	Comprehensive Profiling of Human Hair Metabolome Using Mass Spectrometry
	TPS-039	林逸軒	YuXuan, Lin	Hair Exposome Features Associated with Alzheimer's DiseaseRelated Neurocognitive Disorder Using High Resolution Mass Spectrometry-based Untargeted Approaches
	TPS-040	張志瑋	Chih-Wei Chang	Characterization of the Human Hair Metabolome for Long-Term Chemical Exposome Monitoring Using High-Resolution Mass Spectrometry-Based Suspect Screening
	TPS-041	莊曉妮	Man-Ni Zhuang	Comprehensive Profiling of Human Urinary Mercapturic Acid Conjugates Associated with Exposure to Reactive Chemical Species Using Enzymatic Deacetylation and High-Resolution Mass Spectrometry
	TPS-042	陳語宇	Pei-Yu Chen	Discovery of Chemical Markers for Fish Freshness during Storage Using Mass Spectrometry-Based Untargeted Metabolomics Analysis
	TPS-043	新心妤	XIN-YU JIN	Investigation of Hair Metabolome Alterations in Animal Models of Alzheimer's Disease Using Mass Spectrometry
	TPS-044	蔡東宸	DONG-CHEN TSAI	Discovery of Chemical Composition Changes in Black Garlic Processing Using Untargeted Mass Spectrometry-Based Metabolomics
台灣生物資訊與系統生物學會（TBSB）	**TBSB-001**	王珮昀	Pei-Yun Wang	Integrative Temporal RNA and ATAC Profiling Uncovers Nuclear NORAD as a Regulator in Maintaining Epigenetic Concordance of DNA Repair Processes Upon Radiation Exposure
	TBSB-002	江皓宇	Chiang Hao-Yu	Evaluating Spatial Pattern Preservation in Histology-Based Gene Expression Prediction for Breast Cancer
	TBSB-003	吳秉容	Bing-Rong Wu	Modeling Protein Modification States for Intraprotein Posttranslational Modification Crosstalk Prediction
	TBSB-004	李文凱	WenKai Lee	NETS: Network Topology-based Single-Sample Gene Set Scoring
	TBSB-005	曹廷瑋	Ting-Wei Tsao	An Interactive Multi-Crop Platform Integrating Genomic, Phenomic, and GWAS Data to Accelerate Marker Discovery for Breeding
	TBSB-006	梁禎智	Chen Chi Liang	Deviation from a Healthy Multi-Omics Network Discriminates Cognitive Impairment in Older Adults: A Normative Graph Autoencoder Approach
	TBSB-007	陳芯崴	Hsin-Wei Chen	Inferring Small Extracellular Vesicle-Mediated Cell-Cell Communication from Spatial Transcriptomics with Graph Transformers
	TBSB-008	陳卿鄱	Dan-Yi Chen	KuyMamba: An Explainable Multi-Label Framework for Eight Lysine PTM Types
	TBSB-009	黃亭嘉	Ting-Jia Huang	Gene Panel Selection Governs the Total-RNA Contribution to Histology-Based Spatial Expression Prediction in Colorectal Cancer
	TBSB-010	裴友勝	You Sheng Paik	Pan-Cancer Spatial Transcriptomics Study Reveals Tumor Microenvironment Signatures Associated with Immunotherapy Response
	TBSB-011	蔡丞睿	Cheng-Ruei Tsai	CardioSketch: An Automated Software Tool for ECG Delineation and Feature Extraction
	TBSB-012	蔡佳緝	Jia-Jin Tsai	WQFC: Quantitative Molecular Feature Comparison of Caenorhabditis elegans Gene Lists
	TBSB-013	蔡宗芸	Zong-Yun Tsai	Integrated Analysis of Gut–TMA Microbial Remodeling and Host Metabolic Responses During Canagliflozin Treatment
	TBSB-014	蔡芷琳	Chih-Lin Tsai	Deciphering Molecular Mechanisms of Jing-Wu Formula and Tung-Yi Formula in Depressive and Bipolar Disorders through Network Pharmacology
	TBSB-015	賴偉承	Wei-Cheng Lai	Detection of Mutations from Tumor-Only Whole Exome Sequencing Data
	TBSB-016	謝誌喆	Chih-Hung Hsieh	Characterizing Aberrant Polyadenylation Sites and Their Impact on Post-Transcriptional Regulation Across the Four Molecular Subgroups of Medulloblastoma
	TBSB-017	鍾秉諺	Ping-Yen Chung	Deep Learning for Mandibular Canal Segmentation in Cone-Beam Computed Tomography Using Annotation-Defined Regions of Interest
	TBSB-018	蘇軒廣	SU, HSUAN KUANG	Cross-Hospital Evaluation of Mass Spectral Representations for OxacillIn Resistance Prediction in Staphylococcus aureus
台灣基因醫學暨生物標記學會（TGMBS）	**TGMBS-001**	毛芷儀	CHIYI-MAO	Expression and Localization Analysis of Human TIAM2 in Colorectal Cancer Tissues
	TGMBS-002	王平宸	Chien-Yi Wang	GLUT 1 Inhibition Sensitizes Hyperglycemic Colorectal Cancer to 5-Fluorouracil
	TGMBS-003	王郁涵	Yu-Han Wang	YAP1 3'UTR Shortening Promotes Oxaliplatin Resistance Through Lipid Accumulation in Colorectal Cancer
	TGMBS-004	王翊婷	Wang Yi-Ting	Developing an Efficient Antiviral Drug Screening Platform through Membrane-Tethered Protease Expression System
	TGMBS-005	吳郁涵	Yuh-Harn Wu	Overexpression of ZBTB10 Leads to the Development of Castration-Resistant Prostate Cancer
	TGMBS-006	宋禹蔚	Yu-Jui,Sung	Maximizing oxaliplatin's impact on EGFR+colorectal cancer through targeted extracellular vesicles
	TGMBS-007	宋麗芬	Rangsinee Songphim	A targeted long-read sequencing approach for accurate determination of copy number in the survival motor neuron 1/2 genes
	TGMBS-008	李冠圃	Kuan Ting Li	Obesity-Centered Genetic Architecture of Metabolic Syndrome: Causal Inference And Risk Prediction for Type 2 Diabetes
	TGMBS-009	沈倢	Chieh Shen	Deciphering Fibroblast Plasticity in PDAC: A Single-Cell and Spatial Landscape of the IL-13/Collagen Axis
	TGMBS-010	林羚恩	Chin-En Lin	FL3 Modulates Epigenetic Silencing of NKG2D Ligands to Enhance NK Cell Responses in Urothelial Carcinoma
	TGMBS-011	林倚頡	Lin, Yi-Jing	Bioinformatic Analysis of Extracellular Matrix and M2-like Macrophage Signatures in Relation to Anti-PD-1 Response in Melanoma
	TGMBS-012	林逸宣	Yi-Syuan Lin	A Reciprocal Positive Feedback Loop Between RP11-732A21.3 and YAP1 Regulates E-Cadherin Expression in Colon Cancer
	TGMBS-013	邱廣惠	Guang-Huei Chiou	Genome-Wide Association Study of Androgen Deprivation Therapy Response and Survival in Patients with Metastatic Prostate Cancer
	TGMBS-014	范若涵	FAN,JO-HAN	Engineered Anti-EphA2 Extracellular Vesicles as Tumor-targeted Nanocarriers to Improve Oxaliplatin Delivery in Pancreatic Cancer
	TGMBS-015	張在堯	Zai-Yao chang	Tumor-selective Activation of IFNγ–gallmaxsib Enhances Antitumor Efficacy and Reduces Systemic Toxicity
	TGMBS-016	張慕申	Mu-Shen Chang	A Protease-Responsive CAR-T Platform for Safer CD19-Targeted Immunotherapy
	TGMBS-017	陳宇彤	Yu-Tung Chen	Tumor-associated protease-activated anti-CD47 antibody precisely maintains phagocytic ability of macrophages with minimal effect on healthy tissue
	TGMBS-018	陳幸儀	Hsing-Yi Chen	Seminal Exosomal LCN2 as a Noninvasive Biomarker for Predicting Sperm Retrieval Failure in Non-Obstructive Azoospermia
	TGMBS-019	陳怡臻	Yi-Chen Chen	Development of Protease-Activated Receptor 4 (PAR4) Inhibitory Antibodies to Reduce Thrombosis with Minimal Bleeding Risk
	TGMBS-020	陳泓宇	Hung-Yu Chen	Dissecting the Mechanisms of Placental-Derived Mesenchymal Stem Cell Exosomes on Collagen Production in Human Dermal Fibroblasts
	TGMBS-021	陳琮明	Tsung-Ming Chen	FGF9 reduced oxidative stress through NRF2/GPX3 axis to attenuate osteoarthritis progression
	TGMBS-022	曾名謙	Ming-Chieh Tseng	Transcriptional Regulation of POU3F2 by EBF3 and Its Association with Cell Proliferation in MYCN-Amplified IMR-32 Neuroblastoma Cells
	TGMBS-023	黃筠媛	huang yun jie	MMP-Responsive Pro-IFNα/Nivolumab for Conditional Activation and Enhanced Antigen Presentation in Melanoma
	TGMBS-024	葉宜橙	Yi-Chen, Yeh	Identification of Ubiquitin-Conjugating Enzyme E2C (UBE2C) as a Prognostic Biomarker and Functional Driver in Cholangiocarcinoma
	TGMBS-025	劉柏均	Po-Chun Liu	Analyzing the prognosis of sessile serrated lesions and exploring the mechanisms of their carcinogenesis process using machine learning and multi-omics studies
	TGMBS-026	劉恩碩	Liu En-Shuo	Protease-activated Pro-CD3×CD20 bispecific antibody selectively unleashes T-Cell cytotoxicity against B-Cell lymphomas and improves safety
	TGMBS-027	蔡亦涵	Yi-Han Tsai	Constructing canine anti-PD-L1 antibody to enhance the efficacy of treatment for canine melanoma
	TGMBS-028	蔡亞娟	Tsai Ya-chuan	NUDT16L1 Suppresses Primary Cilliogenesis to Regulate Lipid Metabolism and Chemoresistance in Pancreatic Cancer
	TGMBS-029	戴昱菁	Yu-Jing Tai	Autonomous VEGF-C Signaling Reprograms Glutamine Metabolism to Maintain Cellular Redox Balance and Prevent Ferroptosis in PDAC
	TGMBS-030	謝理格	Li-Ger, Hsieh	A Mitophagy-derived Signature Enables Prognostic Stratification and Identifies Novel Therapeutic Vulnerability in Acute Myeloid Leukemia
	TGMBS-031	羅紫芸	Tzu Yun Lo	Development of a Preimplantation Genetic Test for Facioscapulohumeral Muscular Dystrophy
	TGMBS-032	鄭伊辰	I-Chen Cheng	Bacisterol Sorting Signal Combined Recombinant Protein as a Therapeutic Protein Delivery Strategy to Bypass Blood Brain Barrier (BBB) and Enhances Target Selectivity for Glioblastoma Multiforme (GBM) Treatment.
	TGMBS-033	王香穎	Wang Xiang Ying	Genome-Wide Association Study of Genetic Susceptibility to Neonatal Jaundice in Taiwanese Han Chinese
台灣演化與計算生物學會（TSECB）	**TSECB-001**	尤毓淮	Yu-Huai Yu	Predicting Host-Pathogen Protein-Protein Interactions Using Siamese Hybrid CNN-Transformer Model and Transfer Learning
	TSECB-002	江偉立	Wye-Lup Kong	Profiling maize embryonic leaf development and discovering new genes using high-resolution spatial long-read isoform sequencing
	TSECB-003	凱文麗	Wannaporn Utvichai	Whole-genome shotgun metagenomics pipeline validation and preliminary results for metagenomic characterization of gut microbiota in obesity-associated colorectal cancer
	TSECB-004	李祥宇	Li Shiang Yu	Development of an Integrated Analysis Platform for Cancer Somatic Variants and Biomarkers Based on Next-Generation Sequencing Data
	TSECB-005	李冠瑋	Bin-Wei Lee	From protein-DNA complex structures to regulatory variant interpretation: mapping structure-derived binding sites onto clinically annotated positions in the human genome
	TSECB-006	林劭庭	Shaoting Lin	OrchidBase 7.0: An integrated Multi-Omics Platform Advancing Orchid Genomics and Evolutionary Science
	TSECB-007	苑欣佑	Hsin-Yo Yuan	Predicting Target-Gene Change Along RNA Velocity-Defined Transitions Resolves Stage-Specific Regulatory Programs
	TSECB-008	張鈞量	JUN-LIANG CHANG	A Label-Efficient Pipeline for Harvesting Cup-like Blast Phenotypes in NPM1/FLT3 - Associated AML
	TSECB-009	陳雨彤	Yu Tung, Chen	Attention-based Synergistic Drug Combination Prediction via Multi-View Knowledge-Aware Graph Cross-Contrastive Learning and Gene Ontology-driven Cell Line Encoding
	TSECB-010	陳彥嘉	Yan-Jia Chen	Construction of an Integrated Pangenome and Transcriptome Analytical Platform for Dendrobium: Insights from 26 Species Comparative Genomics
	TSECB-011	陳昱丞	YuCheng Chen	Molecular Mimicry Epitope Finder: An Integrated Platform for Pathogen–Human Molecular Mimicry Discovery
	TSECB-012	陳家萱	Jia-Syuan Chen	SynPatternApp: A Multi-Scale Comparative Genomics Framework for Flexible Synteny Visualization, Quantitative Evolutionary Indexing, and Automated Pattern Recognition
	TSECB-013	曾得恩	Te-Yen,Tseng	A Feature-to-Image Convolutional Neural Network Framework for Microbiome Classification and Cross-Dataset Prediction
	TSECB-014	黃庭羽	Ting-yun, Huang	A Deep Learning Pipeline for Automated Interpretation of MYC-FISH Images
	TSECB-015	黃敦楷	Dun-Kai Huang	Exploring Antibiotic Resistance in Mycobacterium Intracellulare in Taiwan
	TSECB-016	黃東國	NG SHANG-KOK	DarkneseMine: A Single-Cell Multi-Omics Framework for Systematically Discovering Hidden Regulation in Non-Differentially Expressed Genes
	TSECB-017	楊玉峰	Yu-Feng Yang	AI-Predicted Spatial Drug Sensitivity from H&E Histopathology via Adversarial Cross-Domain Alignment of Cancer Pharmacogenomics and Spatial Transcriptomics in Colorectal Cancer
	TSECB-018	葉秉霖	FENG LIN,YE	Development of an Integrated Database Platform for Duck Genome Annotation, Functional Analysis, and Cross-Species Comparison
	TSECB-019	廖秉恺	Bin Hsin Liou	Development of a Multi-Omics Deep Learning Model to Predict Histone Modification Signals Across Developmental Stages in Drosophila melanogaster
	TSECB-020	蔡昕偉	Hsin-Wei, Tsai	Cross-Species Identification of Cell-Type-Specific Active Cis-Regulatory Modules via Deep Transfer Learning
	TSECB-021	戴萊恩	Ryan Rey M. Daga	Chromatin Contacts and Histone Modification Profiles Predict Evolutionary Conservation Across Gene Loci and Species
	TSECB-022	戴睿紘	Jui-Hung, Tai	Genomic Origin Tracing of SARS-CoV-2: Lessons from Taiwan's Third Outbreak and Its Cryptic Transmission
	TSECB-023	蘇梅玉	Angela Merici Giannetta Surya	Development of a Rapid Pathogen Identification Platform Integrating Real-Time Nanopore Sequencing and Machine Learning-Based Analysis
	TSECB-024	鍾文旺	Wen-Yu Chung	eDNA Workbench: A Lightweight, Interactive Tool for Environmental DNA Analysis and Visualization
台灣精準醫學會（TPMMS）	**TPMS-001**	白昀必	Bai, Yun-Bi	From Hematologic Clues to Genomic Interpretation: A Case of Suspected MYH9-Related Disorder in an Infant
	TPMS-002	吳念	Wu Nian	Association between Differences in Dysmenorrhea Phenotypes and Genome-wide DNA Methylation Profiles
	TPMS-003	呂家慧	Jia-Huei Lyu	Multiplex ligation-dependent probe amplification for copy number analysis of survival motor neuron genes
	TPMS-004	呂家慧	Jia-Huei Lyu	Distribution of FMR1 Gene CGG Repeat Sizes in the Taiwanese Population Evaluated by CGG Repeat-Primed PCR
	TPMS-005	洪國勝	Kuo-Sheng Hung	Uncovering Genetic Susceptibility Loci Associated with Anti-Ro Antibody Levels in Taiwanese Patients with Primary Sjögren's Syndrome
	TPMS-006	梁庭樑	Ting Chen-Liang	Predicting Next-Week Container Index from Routine Weekly Dengue Vector Surveillance Data in Kaohsiung, Taiwan
	TPMS-007	陳品均	Pin-Jiun Chen	From Case Diagnosis to Gene-Editing Horizons: CRISPR-Cas9 Therapeutics for Angelman Syndrome
	TPMS-008	陳寬寬	Chi-Kuan Chen	Lung Deep Precancerous Gene Screen (LDGS): A Deep Airway Secretion-Based Platform for Precision Lung Cancer Risk Stratification
	TPMS-009	黃永琪	Huang, Yung-Chi	Multi-Omics Profiling Reveals Adipocyte–Tumor Crosstalk and Metabolic Reprogramming in colRCC Progression
	TPMS-010	魏瑄萱	Hsuan-Hsuan Wei	Tracing the Biochemical Path: A Personalized Approach to Primary Hyperparathyroidism in Pregnancy
台灣臨外體學會（TSEV）	**TSEV-001**	高皓軒	Hao-Hsuan, Kao	Machine learning-guided blood exosome proteomics defines a five-protein liquid biopsy score for T2DM complication stratification
	TSEV-002	張靜卉	Ching-Hui, Chang	Integrated Blood Inflammatory Indices and Urinary Extracellular Vesicles for Risk Stratification in Upper Tract Urothelial Carcinoma
	TSEV-003	許禾臻	Ho-Chen Hsu	SCAP-Derived Extracellular Vesicles Promote Hair Growth in a Murine Model
	TSEV-004	黃品皓	Pin-Hao Huang	AiOmics: An automated LLM-integrated transcriptomics analysis platform with retrieval-augmented generation
	TSEV-005	黃品皓	Pin-Hao Huang	Machine learning-guided blood exosome proteomics defines a five-protein liquid biopsy score for T2DM complication stratification
	TSEV-006	葉宇瑄	Yu-Hsuan Yeh	The Functional Intrinsically Disordered Region in Streptolysin O Modulates ESCRT-III components to Promote Exosome-Mediated Bacterial Clearance
	TSEV-007	楊書聯	Shu-Hua, Yang	Gut Health Implications of Extracellular Vesicles Derived from Benzoic Acid-Tolerance Microorganisms
	TSEV-008	簡浩原	Chien hao yuan	Hijacking the Host's Extracellular Vesicles: Route for Citrus Exocortis Viroid Systemic Movement in Tomato
	TSEV-009	楊詳翔	Jiung-Xiang Yang	MicroRNA Responses in Caco-2 Cell-Derived Exosomes to Ajl and FadA and Growth Inhibition of gut opportunistic bacteria by Next-generation prebiotic-derived extracellular vesicles

TGMBS-033 王香穎 Wang Xiang Ying Genome-Wide Association Study of Genetic Susceptibility to Neonatal Jaundice in Taiwanese Han Chinese