







Joint 12th AOHUPO, 8th AOAPO, 3rd **T-HUB** Global Summit in Conjunction with 13th CNHUPO Congress

第12届AOHUPO大会暨第8届AOAPO大会暨 π -HuB国际大科学计划 第三届全球峰会暨第13届CNHUPO大会





Deep Insight, Confident Discovery.

Al-Driven Software | Advanced Lab Services

Software



PEAKS Studio

Complete Desktop Solution for Bottom-up **Discovery & Targeted Proteomics**



PEAKS Glycan Finder

Sensitive and Accurate Solution for Glycopeptidomics & Glycomics with Structural Resolution



Comprehensive Proteoform Characterisation by Top-down MS and Intact Deconvolution



High-throughput & Multi-user Server-based **Discovery Proteomics Solution**



PEAKS®AB

Automated Desktop Solution for Antibody and Protein de novo Sequencing



Solution for Polyclonal Antibody de novo Sequencing



t Tel: 021-60919891

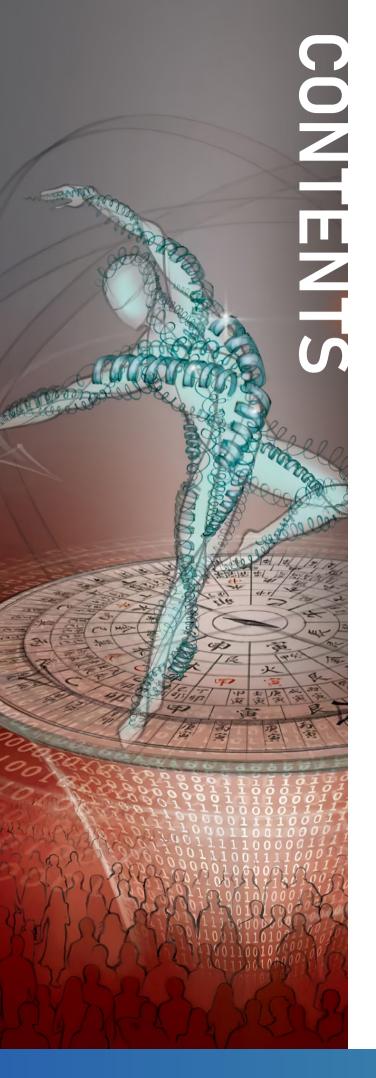




🚨 202-140 Columbia St W Waterloo, Ontario N2L 3K8 Canada



EN: www.bioinfor.com CN: www.deepproteomics.cn



- 02 Welcome Message
- 03 Organization Committee
- 05 Congress Information
- 09 Program at a Glance
- 11 Congress Agenda
- 14 Pre-Congress Training Courses
- 17 Satellite Symposiums Program
- 21 The 1st π-HuB Industry Conference
- 22 Plenary Session Program
- 24 Parallel Sessions Program
- 46 Industry Seminars
- 49 List of Posters
- 63 Exhibition
- 64 Sponsorship

Welcome Message

欢迎致辞

Dear Friends and Colleagues,

It is with great pleasure that we welcome you to the **Joint 12th AOHUPO**, 8th **AOAPO**, 3rd π-HuB Global Summit, and 13th CNHUPO Congress, to be held in Guangzhou, China, from October 11 to 14, 2025. This year marks a particularly special occasion: for the first time in 13 years, the AOHUPO Congress and the CNHUPO Congress are once again held together in China. This reunion symbolizes the strong ties and growing collaboration between the Asia–Oceania proteomics community and the Chinese proteomics society, creating a unique platform for international dialogue and partnership.

The theme of this congress is "Navigating the Protein Universe: Toward New Biology and Precision Medicine". Nearly 200 leading scientists, clinicians, and industry innovators from more than 20 countries and regions will gather in Guangzhou, together with nearly 2,000 participants. Through 30+ thematic forums and special sessions, the congress will highlight cutting-edge progress in proteomics—from fundamental research and advanced technologies to data science, clinical applications, and industrial translation. This meeting is also dedicated to inspiring the next generation: young scientists and students will have the opportunity to present their work and engage directly with world-renowned experts, while industry partners will showcase their latest innovations, fostering dialogue across academia, healthcare, and biotechnology.

We extend our heartfelt gratitude to the π -HuB Project, AOHUPO, AOAPO, CNHUPO, and our global partners for their invaluable support. Our special thanks also go to **Southern Medical University** and all the co-organizers, exhibitors, and partners—your contributions have made this gathering possible.

By the Pearl River, the stage is set for an inspiring academic exchange. In Guangzhou—a city of openness and innovation—the global proteomics community will come together. We look forward to welcoming you and hope this congress will spark new scientific progress while leaving every participant with meaningful experiences and lasting memories.

Warm regards,

Chairs of the Joint 12^{th} AOHUPO, 8^{th} AOAPO, 3^{rd} π -HuB Global Summit in conjunction with the 13^{th} CNHUPO Congress



Fu-Chu He Honorary Chair



Ruedi Aebersold Honorary Chair



Terence Poon
Co-Chair



Ping Xu Co-Chair



Li Ma Co-Chair









Organization Committee 会议组织机构

■ Sponsors and Organizers | 组织单位

Sponsors The π-HuB organization

> Asia Oceania Human Proteome Organisation (AOHUPO) Asia Oceania Agricultural Proteomics Organization (AOAPO)

China Human Proteome Organization (CNHUPO)

主办单位 π-HuB 计划国际组织(筹)

亚太人类蛋白质组组织

亚洲大洋洲农业蛋白质组组织

中国人类蛋白质组组织

Southern Medical University Organizers

> National Center for Protein Sciences (Beijing) State Key Laboratory of Medical Proteomics

International Academy of Phronesis Medicine (Guangdong)

Guangdong Provincial Key Laboratory of Chinese Medicine Pharmaceutics

承办单位 南方医科大学

> 国家蛋白质科学中心(北京) 医学蛋白质组全国重点实验室 广东智慧医学国际研究院 广东省中药制剂重点实验室

Honorary Chairs 大会名誉主席

Fu-Chu He (贺福初) Ruedi Aebersold

Co-Chairs 大会主席

Terence Poon Ping Xu (徐平) Li Ma (马骊)

Scientific Committee 学术委员会

Chien-Sheng Chen Zhong-Yi Cheng (程仲毅) Xing Chen (陈兴) Stuart Cordwell Yu-Ju Chen Max Ching Ming Chung Tian-Nan Guo (郭天南) Fu-Chu He (贺福初) Angus Grey Can-Hua Huang (黄灿华) Yasushi Ishihama Si-Min He (贺思敏) Shin Kawano Kyung-gon Kim Ho Jeong Kwon Qingsong Lin Teck Yew Low Hao-Jie Lu(陆豪杰) Mark Molloy Kazuyuki Nakamura Young-Ki Paik

Dinh Minh Pham Chantragan Srisomsap Phiphobmongkol

Terence Poon Ghasem Hosseini Salekdeh Shantanu Sengupta Richard Simpson Tri Agus Siswoyo Rui-Jun Tian(田瑞军)

Xu-Chu Wang(王旭初) Catherine C L Wong(黄超兰) Ping Xu(徐平)

3rd π-HuB Global Summit in Conjunction with 13th CNHUPO Congress

Eizadora T. Yu

Li-Hua Zhang (张丽华)

Xiao-Bo Yu(于晓波)

Shamshad Zarina

Organizing Committee 组织委员会

Dong-Bo Bu(卜东波)

Hao Chi (迟浩)

Qing-Feng Du(杜庆锋)

Feng Ge (葛峰)

Gui-Xue Hou(侯桂雪)

Xian-Zhang Huang(黄宪章)

Ying Jiang(姜颖)

Jia-Lin Liu(刘嘉琳)

Hao-Jie Lu (陆豪杰)

Yong-Zhan Nie (聂勇战)

Tie-Liu Shi (石铁流)

Min-Jia Tan (谭敏佳)

Zhi-Xin Tian (田志新)

Guan-Bo Wang(王冠博)

Tong Wang (王通)

Han Wen (温翰)

Lu Xie (谢鹭)

Jing-Hua Yang(杨静华)

Ming-Liang Ye (叶明亮)

Xiao-Bo Yu (于晓波)

Kai Zhang (张锴)

Wei-Qi Zhang (张维绮)

Fang-Qing Zhao(赵方庆)

Lei Zheng (郑磊)

Cheng Chang (常乘)

Lun-Zhi Dai(戴伦治)

Qun Fang (方群)

Xue-Jiang Guo (郭雪江)

Yue Hua(华玥)

Chen-Xi Jia (贾辰熙)

Ren Lai (赖仞)

Xiao-Yun Liu (刘小云)

Li Ma (马骊)

Wei-Jie Qin (秦伟捷)

Wen-Qing Shui (水雯菁)

Sheng-Ce Tao (陶生策)

Ying-Chun Wang (汪迎春)

Heng-Liang Wang(王恒樑)

Xiao-Wen Wang (王晓文)

Xu-Na Wu (武旭娜)

Xue-Feng Xing (邢学锋)

Ping-Fang Yang(杨平仿)

Zi-Lu Ye (叶子璐)

Wen-Feng Zeng (曾文锋)

Li-Hua Zhang(张丽华)

Yan Zhang (张延)

Qian Zhao (赵倩)

Hong-Ying Zhong(钟鸿英)

Jing Chen (陈静)

Chun-Hui Deng (邓春晖)

You-He Gao (高友鹤)

Yue-Shuai Guo (郭曰帅)

Can-Hua Huang(黄灿华)

He-Wei Jiang (江河伟)

Le-Yuan Li(李乐园)

Zhen Liu (刘震)

Qing-Wei Ma(马庆伟)

Wen-Guang Shao (邵文广)

Yao-Ting Sun (孙耀庭)

Rui-Jun Tian (田瑞军)

Chu Wang (王初)

Hong Wang (王洪)

Xu-Chu Wang (王旭初)

Bin Xiao (肖斌)

Jing Yang (杨靖)

Hui Ye (叶慧)

Xin-Pei Yi (伊心培)

Chun-Hui Zhang (张春辉)

Ling-Qiang Zhang (张令强)

Yao-Yang Zhang (张耀阳)

Qun Zhao (赵群)

Hu Zhou (周虎)

Secretary General 秘书长

Tian-Nan Guo (郭天南)

Teck Yew Low

Executive Secretary-General 执行秘书长

Qing-Feng Du(杜庆锋) Xiao-Bo Yu (于晓波)

Ping-Fang Yang(杨平仿)

Jing Yang(杨靖)

Liu-Jun Tang(唐刘君)

■ Secretariat │ 秘书处

Yan Wang(王琰)

Wei Dong(董微)

Chao-Nan Li(李超男)

Li-Qin Qian(钱丽琴)

Shao-Hui Huang(黄少慧)

Zi-Wei Huang(黄紫微)

Xue-Feng Xing (邢学锋) Xuan Zheng(郑璇)

Lu-Fang Shao(邵璐芳)

Dong Han (韩冬)

Qiong Hu(胡琼)

Nian-Zi Luo(罗年子)

国家蛋白质科学中心•北京 **National Center for Protein Sciences • Beijing**

Address: No. 38. Life Science Park Road.

Changping District, Beijing, China

地址:北京市昌平区科学园路 38号







Congress Information 会议信息

■ Theme | 会议主题

Navigating the Protein Universe: Toward New Biology and Precision Medicine 探索蛋白质宇宙: 迈向新生物学和精准医学

■ Venue | 会议地址

Baiyun International Convention Center, Guangzhou, Guangdong Province, China 白云国际会议中心,中国•广东省•广州

■ Website | 会议网址

http://www.aohupo2025.com http://cnhupo.org.cn

■ Language │ 会议语言

English/Chinese 英文 / 中文

■ Conference Rooms | 会场分布

Plenary Lecture Rooms 主会场

1. Oriental Hall, 2nd Floor, Block 3 东方厅(10.12) 2. Lingnan Convention Hall, 2nd Floor 岭南大会堂(10.13-14)

The 3rd π-HuB Global Summit and the 1st π-HuB Industry Conference: Qinghe Hall, 1st Floor, Block 1 π-HuB 计划全球峰会,π-HuB 计划首届产业大会: 清和厅,一号楼 1 层

Parallel Session Rooms 分会场

- 1. Maoming Hall, 1st Floor 茂名厅
- 3. Meizhou Hall, 1st Floor 梅州厅
- 5. Shantou Hall, 2nd Floor 汕头厅
- 2. Jieyang Hall, 1st Floor 揭阳厅
- 4. Shenzhen Hall, 2nd Floor 深圳厅

Training Classroom 技术培训教室

MaxQuant Training Courses: Maoming Hall, 1st Floor MaxQuant 技术培训教室: 茂名厅 PEAKS Online Training Courses: Jieyang Hall, 1st Floor PEAKS Online 技术培训教室: 揭阳厅 Al for Protein Science Training Courses: Jieyang Hall, 1st Floor Al 及蛋白质组学应用培训教室: 揭阳厅

Deep Visual Proteomics Training Courses: Maoming Hall, 1st Floor

深度可视化蛋白质组学培训教室: 茂名厅

CNHUPO Council Meeting CNHUPO 理事会会场

Shenzhen Hall, 2nd Floor 深圳厅

AOHUPO Council Meeting AOHUPO 理事会会场

Lingnan Convention Hall VIP Lounge, 2nd Floor 岭南大会堂贵宾室

AOAPO Council Meeting AOAPO 理事会会场

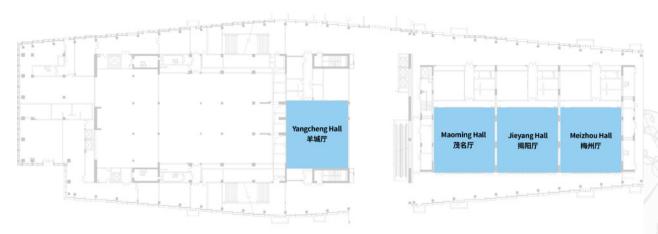
Lingnan Convention Hall VIP Lounge, 2nd Floor 岭南大会堂贵宾室

Poster 墙报 Exhibition 展厅

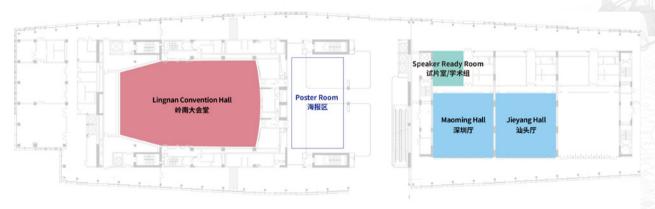
1st Floor, Block 2 二号楼一层 2nd Floor, Lingnan Convention Hall 岭南大会堂

Speaker Ready Room 试片室 / 学术组

Accessory Room of Shenzhen Hall, 2nd Floor 二层深圳厅副厅



Floor Plan of the First Floor of Block 2 2号楼一层平面图



Floor Plan of the Second Floor of Block 2 2号楼二层平面图

Catering Location 用餐地点

	10.12	10.13	10.14
Lunch 午餐	Pearl River Hall D, 1 st Floor 珠江厅 D 区,一层		
Dinner 晚餐	Oriental Hall, 2 nd Floor Pearl River Hall D, 1 st Floor 东方厅,二层 珠江厅 D 区,一层		
VIP Reception		Qinghe Hall, 1 st Floor 清和厅,一层	

WiFi: Free WiFi is accessible in Baiyun International Convention Center.

无线网络:会议中心全面覆盖免费无线网络,助您联动世界

Media Support 媒体支持:

http://www.dxy.cn http://www.ebiotrade.com http://www.bioart.com.cn http://www.pharmatable.com









Welcome to Joint 12th AOHUPO, 8th AOAPO, 3rd π-HuB Global Summit in Conjunction with 13th CNHUPO Congress. All congress activities and exhibition are in the Baiyun International Convention Center.

Registration and Information

The registration desk is located in the lobby of Block 3, Baiyun International Convention Center.

Opening Time:

Oct, 9-10 08:30 - 20:00 Oct. 11-14 08:30 - 20:00

Registered Delegates are Entitled to:

Opening Ceremony, Welcome Reception and Closing Ceremony Attendance to Sessions Entrance to Exhibition All Congress Documents Coffee Breaks

Name Badges and Tickets

For security purposes, delegates and exhibitors must wear their name badges during the congress. Entrance to the meeting room will be limited to badge holders only.

Staff Brigade

A team of enthusiastic students will be at your service. During the congress hours, they will provide hospitality support and steward services. They will also serve in most of the meeting rooms as technical assistants and can be easily recognized by their marks of VOLUNTEER.

Program Changes

The organizers cannot accept liability for any changes in the program due to external or unforeseen circumstances.

Oral Presentations

Only LCD projectors are used for oral sessions. Speakers must go to the Speaker Ready Room at least one day prior to their talks to load their

powerpoint file onto the congress computers. The Speaker Ready Room is the accessory room of Shenzhen Hall. The room will keep opening with a technician present during the following time slots:

Oct. 9 14:00 - 18:00

Oct. 10 08:00 - 18:00

Oct. 11 08:00 - 18:00

Oct, 12 08:00 - 18:00

Oct. 13 08:00 - 18:00

Oct. 14 08:00 - 18:00

Poster Presentations

Refer to the poster numbers in this program for board assignments. Authors are expected to supply scotch tape to mount their posters. Posters must be in place by 16:00 on Oct 12 at the Poster Area and removed at 18:00 on Oct 14. To assure all attendees to have time for viewing posters, please do not remove posters ahead of the designed time. All the posters have the opportunities to join the competition of the CNHUPO 2025 Excellent Poster Award. 10 posters will be awarded in the Closing Ceremony.

Duplication, Recording

Without permission from authors, taking photographs, audio-taping, video-recording, digital taping and any other form of duplication are strictly prohibited in the session rooms and poster areas.

■ Mobile Phones

Participants are kindly requested to turn off their cell phones or keep the cell phones in vibration state when entering the congress rooms and in the poster area.

Smoking Policy

In the Baiyun International Convention Center, smoking is prohibited. Smoking is only permitted in a few designated areas outside the building.

Time

Guangzhou is 8 hours ahead of Greenwich Mean Time.

Weather

October is a delightful month for weather condition in Guangzhou. Typically, it is comfortably warm with lower humidity, making the beginning of the pleasant autumn season. Temperature during the conference in Guangzhou is 22-30.

Make sure to carry an umbrella because there may be showers during the conference.

■ Water

It is not recommended to directly drink the water from the tap in your hotel room or at the congress area. If you want to drink cold water, it is best to order or buy bottled water, mineral or distilled water. Hotels generally provide an electrically heated kettle to boil water from the tap in your room. Some hotels also provide a special tap in the lavatory that delivers a flow of purified water for drinking.

This advice also applies to your pre-congress or post-congress travel in other cities in China.

Voltage, Socket and Plugs

The electrical current in China is 220-volts, 50Hz, AC. Hotels generally provide wall sockets in every room, accommodating both the standard "Flat blade attachment plug (Type A)" and common "Oblique flat blades with ground (inverted V) plug (Type I)" as well as the not-so-common "Round pin attachment plug (Type C)".

Currency

The local currency is the RMB. Visa and Master Card are accepted at the Registration Desk. Foreign currency will not be accepted. You can pay with cash in RMB or credit card. The amount debited from your account will vary due to fluctuations in the exchange rate. There is normally a 4% additional bank charge. Participants can exchange their currencies at airports, major hotels and banks in China. The exchange rate will be given daily by the Bank of China. Currently, 1

USD can be exchanged for about 7.1 RMB yuan. All currency exchange receipts should be saved in case participants want to exchange RMB back to their own currency. Banks may demand to see the original exchange receipt.

Emergencies

If you or any other delegate is unwell, an accident or any other emergency occurs, while at the venue, please contact the Registration Desk or any staff member.

Lost Property

If you see any unattended parcel, please report to one of the congress staff members. If you lose anything at the venue, please enquire at the Registration Desk.

Insurance

The congress organizers recommend participants to possess travel, property medical or other necessary insurances before coming to China. The Congress Organizers cannot be held responsible for the costs resulting from personal accidents or property loss during the congress.

Hotlines

Phone number

110 Police

114 Local Telephone Number Inquiry

117 Time Inquiry

119 Fire

120 Ambulance

121 Weather Forecast

122 Traffic Police









Program at a Glance

	10.10 (Fri.)	10.11 (Sat.)	10.12	(Sun.)	10.13	(Mon.)	10.14	(Tue.)
DATE	All Day	All Day	AM	PM	AM	PM	AM	PM
MaxQuant Pre-Congress Training Courses		II 09:00-17:00						
PEAKS Online Pre-Congress Training Courses	Jieyang Hall	09:00-17:00						
The π-HuB Project Global Summit and the 3 rd Council Meeting		Qinghe Hall 09:00-18:00	Qinghe Hall 09:00-12:00					
Deep Visual Proteomics Training Courses			Maoming Hal	l 09:00-13:30				
Al for Protein Science Training Courses			Jieyang Hall	09:00-12:30				
AOHUPO Young Scholar Forum			Shenzhen Hall 08.45-12:00					
Flash Talk and Rising Star Symposium			Meizhou Hall 09:00-12:00					
Opening Ceremony				Oriental Hall 15:00-15:40				
Plenary Lectures				Oriental Hall 15:40-17:40	Lingnan Convention Hall 08:30-09:45	Lingnan Convention Hall 16:40-17:55	Lingnan Convention Hall 08:30-09:45	Lingnan Convention Hall 16:30-17:30
Welcome Reception				Oriental Hall 18:30-20:00				
CNHUPO Council Meeting					Shenzhen Hall 07:30-08:20			
Poster Viewing/Coffee Break					2 nd Floor 09:45-10:10	2 nd Floor 16:00-16:40	2 nd Floor 09:45-10:10	2 nd Floor 16:00-16:30
PS 1: Emerging Proteomics Technologies					Lingnan Convention Hall 10:10-12:10			
PS 2: Native Mass Spectrometry and Structural Biology					Shenzhen Hall 10:10-12:15			
PS 3: Single Cell Proteomics					Shantou Hall 10:10-12:20			
PS 4: Understudied Proteomics and Peptidomics					Maoming Hall 10:10-12:10			
PS 5: Artificial Intelligence and Education					Jieyang Hall 10:10-12:00			
PS 6: Proteomics-Driven Precision Medicine (A)					Meizhou Hall 10:10-12:10			
AOHUPO Council Meeting						Lingnan Convention Hall VIP Lounge 12:30-14:00		
Industry Seminars: Bioinformatics Solutions Inc. (BSI)						Lingnan Convention Hall 12:30-13:30		
Industry Seminars: Syncell Inc.						Maoming Hall 12:30-13:30		
Industry Seminars: TECAN						Jieyang Hall 12:30-13:30		
Industry Seminars: Thermo Fisher Scientific						Meizhou Hall 12:30-13:30		
Industry Seminars: Evosep						Shenzhen Hall 12:30-13:30		

	10.10 (Fri.)	10.11 (Sat.)	10.12	(Sun.)	10.13	(Mon.)	10.14	(Tue.)
DATE	All Day	All Day	АМ	РМ	АМ	РМ	АМ	PM
Industry Seminars: Gene Company Limited & Covaris						Shantou Hall 12:30-13:30		
Industry Seminars: Bruker Corporation						Yangcheng Hall 12:30-13:30		
PS 7: Chemoproteomics and Drug Discovery						Lingnan Convention Hall 14:00-16:15		
PS 8: Proteomics of Model Systems						Shenzhen Hall 14:00-16:00		
PS 9: Spatial Proteomics						Shantou Hall 14:00-16:10		
PS 10: Modernization of Traditional Chinese Medicine						Maoming Hall 14:00-15:40		
PS 11: Computational and Al Proteomics (A)						Jieyang Hall 14:00-16:00		
The 1 st π-HuB Industry Conference						Qinghe Hall 13:30-17:00		
VIP Reception						Qinghe Hall 18:30-20:00		
PS 12: Proteomics Beyond Mass Spectrometry							Lingnan Convention Hall 10:10-12:10	
PS 13: Computational and Al Proteomics (B)							Shenzhen Hall 10:10-12:10	
PS 14: Advances in Agricultural Proteomics							Shantou Hall 10:10-12:10	
PS 15: Body Fluid Proteomics							Maoming Hall 10:10-12:15	
PS 16: Proteomics-Driven Precision Laboratory Medicine							Jieyang Hall 10:10-12:15	
PS 17: Post-translational Modifications							Meizhou Hall 10:10-12:25	
AOAPO Council Meeting								Lingnan Convention Hall VIP Lounge 12:30-14:00
Industry Seminars: Olink Proteomics								Maoming Hall 12:30-13:30
Industry Seminars: Beijing Qinglian Biotech Co., Ltd.								Meizhou Hall 12:30-13:30
Industry Seminars: SCIEX CHINA								Jieyang Hall 12:30-13:30
Industry Seminars: Illumina								Lingnan Convention Hall 12:30-13:30
Industry Seminars: Novogene Co., Ltd.								Shenzhen Hall 12:30-13:30
PS 18: Cross-species proteomics								Lingnan Convention Hall 14:00-16:00
PS 19: Proteomics of the Microbes								Shenzhen Hall 14:00-15:55
PS 20: Proteomics Marries other Omics								Shantou Hall 14:00-15:50
PS 21: Proteomics-Driven Precision Medicine (B)								Maoming Hall 14:00-16:10
PS 22: Proteome Dynamics								Jieyang Hall 14:00-16:15
Closing Ceremony								Lingnan Convention Hall 16:30-18:00









Congress Agenda I

Time	Event	Venue
Oct 9, 2025		
08:30-18:00	Registration (Participants in Pre-Congress Training Course)	Lingnan Hotel (Block 1) Lobby
Oct 10, 2025		
09:00-17:00	MaxQuant Pre-Congress Training Courses (Day 1)	Maoming Hall
09:00-17:00	PEAKS Online Pre-Congress Training Courses (Day 1)	Jieyang Hall
08:30-18:00	Registration (π-HuB Project Global Summit Representative)	Lingnan Hotel (Block 1) Lobby
Oct 11, 2025		
09:00-17:00	MaxQuant Pre-congress Training Courses (Day 2)	Maoming Hall
08:00-16:50	PEAKS Online Pre-congress Training Courses (Day 2)	Jieyang Hall
08:30-18:00	Registration (All Participants)	Block 3 Lobby
09:00-18:00	The π-HuB Project Global Summit and the 3 rd Council Meeting (Day 1)	Qinghe Hall
Oct 12, 2025		
09:00-12:00	The π-HuB Project Global Summit and the 3 rd Council Meeting (Day 2)	Qinghe Hall
09:00-13:30	Deep Visual Proteomics Training Courses	Maoming Hall
09:00-12:30	Al for Protein Science Training Courses	Jieyang Hall
08:45-12:00	AOHUPO Young Scholar Forum	Shenzhen Hall
09:00-12:00	Flash Talk and Rising Star Symposium	Meizhou Hall
15:00-17:40	Opening Ceremony and Plenary Lectures (4)	Oriental Hall
18:30-20:00	Welcome Reception	Oriental Hall
Oct 13, 2025		
07:30-08:20	CNHUPO Council Meeting	Shenzhen Hall
08:30-09:45	Plenary Lectures (3)	Lingnan Convention Hall

Time		Venue	
09:45-10:10	Poster View	ving/Coffee Break	2 nd Floor
		PS 1: Emerging Proteomics Technologies	Lingnan Convention Hall
		PS 2: Native Mass Spectrometry and Structural Biology	Shenzhen Hall
10:10-12:20	Parallel	PS 3: Single Cell Proteomics	Shantou Hall
	Sessions	PS 4: Understudied Proteomics and Peptidomics	Maoming Hall
		PS 5: Artificial Intelligence and Education	Jieyang Hall
		PS 6: Proteomics-Driven Precision Medicine (A)	Meizhou Hall
12:30-14:00	AOHUPO C	Council Meeting	Lingnan Convention Hall VIP Lounge
		Bioinformatics Solutions Inc. (BSI)	Lingnan Convention Hall
		Syncell Inc.	Maoming Hall
	Industry Seminars	TECAN	Jieyang Hall
12:30-13:30		Thermo Fisher Scientific	Meizhou Hall
		Evosep	Shenzhen Hall
		Gene Company Limited & Covaris	Shantou Hall
		Bruker Corporation	Yangcheng Hall
		PS 7: Chemoproteomics and Drug Discovery	Lingnan Convention Hall
	Parallel	PS 8: Proteomics of Model Systems	Shenzhen Hall
14:00-16:00	Sessions	PS 9: Spatial Proteomics	Shantou Hall
		PS 10: Modernization of Traditional Chinese Medicine	Maoming Hall
		PS 11: Computational and Al Proteomics (A)	Jieyang Hall
13:30-17:00	The 1 st π-HuB Industry Conference		Qinghe Hall
16:00-16:40	Poster Viewing/Coffee Break		2 nd Floor
16:40-17:55	Plenary Lec	ctures (3)	Lingnan Convention Hall
18:30-20:00	VIP Recept	ion	Qinghe Hall







Time		Venue		
Oct 14, 2025				
08:30-09:45	Plenary Led	ctures (3)	Lingnan Convention Hall	
09:45-10:10	Poster Viev	2 nd Floor		
		PS 12: Proteomics Beyond Mass Spectrometry	Lingnan Convention Hall	
		PS 13: Computational and Al Proteomics (B)	Shenzhen Hall	
10:10-12:20	Parallel Sessions	PS 14: Advances in Agricultural Proteomics	Shantou Hall	
	Sessions	PS 15: Body Fluid Proteomics	Maoming Hall	
		PS 16: Proteomics-Driven Precision Laboratory Medicine	Jieyang Hall	
		PS 17: Post-translational Modifications	Meizhou Hall	
12:30-14:00	AOAPO Council Meeting		Lingnan Convention Hall VIP Lounge	
		Olink Proteomics	Maoming Hall	
		Beijing Qinglian Biotech Co., Ltd.	Meizhou Hall	
12:30-13:30	Industry		SCIEX CHINA	Jieyang Hall
	Seminars	Illumina	Lingnan Convention Hall	
		Novogene Co., Ltd.	Shenzhen Hall	
		PS 18: Cross-species proteomics	Lingnan Convention Hall	
	Parallel	PS 19: Proteomics of the Microbes	Shenzhen Hall	
14:00-16:00	Sessions	PS 20: Proteomics Marries other Omics	Shantou Hall	
		PS 21: Proteomics-Driven Precision Medicine (B)	Maoming Hall	
		PS 22: Proteome Dynamics	Jieyang Hall	
16:00-16:30	Poster Viev	ving/Coffee Break	2 nd Floor	
16:30-18:00	Plenary Led	Lingnan Convention Hall		

Pre-Congress Training Courses

MaxQuant Workshop

Oct 10-11, 2025 09:00-17:00 (Maoming Hall)

Time		Session
Oct 10, 2025		00001011
09:00-09:45	MaxQuant DDA Workflow	
09:45-10:30	DDA Label Free Quantification	V
	·	
10:30-11:00	Coffee Break	
11:00-11:45	MaxQuant DDA Tutorial I	
11:45-12:30	MaxQuant DDA Tutorial II	
12:30-13:30	Lunch Break	
13:30-14:15	Output Tables	16/1/00
14:15-15:00	Perseus Introduction	
15:00-15:30	Coffee Break	
15:30-16:15	Perseus Basic Tutorial I	
16:15-17:00	Perseus Basic Tutorial II	
17:00	Question Session	
Oct 11, 2025		
09:00-09:45	MaxDIA I	
09:45-10:30	MaxDIA II	
10:30-11:00	Coffee Break	
11:00-11:45	MaxQuant DIA tutorial	
11:45-12:30	Single-Cell Proteomics	
12:30-13:30	Lunch Break	
13:30-14:15	Metadata in Proteomics	,
14:15-15:00	PTMs I	
15:00-15:30	Coffee Break	
15:30-16:15	PTMs II	Q.
16:15-17:00	PTMs Analysis	
17:00	Question Session	









PEAKS Online Training Workshop

Oct 10-11, 2025 09:00-17:00 (Jieyang Hall)

Time	Session
Oct 10, 2025	
09:00-09:45	Deep Learning-based De Novo Sequencing and Database Search for In-depth and High- throughput Proteomics
09:45-10:30	Confident PTM and Sequence Variants Profiling
10:30-11:00	Coffee Break
11:00-11:45	Multi-omics Enabled Immunopeptidome with Higher Accuracy and Sensitivity
11:45-12:30	Stream-lined Proteomics Workflow with DIA
12:30-13:30	Lunch
13:30-14:15	Uncover Dark Peptidome/Proteome from DIA Data with PEAKS
14:15-15:00	Cloud-based Scalable Data Analysis of Large Cohort Proteomics
15:00-15:30	Coffee Break
15:30-17:00	Hands-on & Question Session
Oct 11, 2025	
09:00-09:45	TMT and SILAC Data Analysis
09:45-10:30	PEAKS GlycanFinder Walkthrough-Glycan Profiling with Structural Resolution
10:30-11:00	Coffee Break
11:00-11:45	Deep Proteoform Profiling with Intact, Top-Down and Bottom-Up
11:45-12:30	Hands-on
12:30-13:30	Lunch
13:30-14:15	Peptide De Novo Sequencing
14:15-15:00	Protein De Novo Sequencing
15:00-15:30	Coffee Break
15:30-17:00	Hands-on & Question Session

Al for Protein Science Workshop

Oct 12, 2025 09:00-12:30 (Jieyang Hall)

Chair: Lu Xie, Menghuan Zhang, Cheng Chang

Time	Speaker and Title
09:00-09:40	Mingfei Han National Center for Protein Sciences (Beijing), China Title: Introduction to Proteomic Data Resources and Multi-Omics Analysis Strategies
09:40-10:20	Qun Dong Dalian University of Technology, China Title: Statistical Analysis and Annotation of Clinical Cohort Proteomics Quantification Data
10:20-10:30	Coffee Break
10:30-11:10	Jun Xia Hong Kong University of Science and Technology (Guangzhou), China Title: Spectra Al: Towards Building Proteomic Mass Spectrum Foundation Models and Beyond
11:10-11:50	Menghuan Zhang Tongji University, China Title: The Application of Large Models in Protein Post-Translational Modification Research
11:50-12:30	Yongge Li Al For Science Institute, Beijing, China Title: A Review of Frontier Technologies in Omics-Based Large Models

Deep Visual Proteomics Workshop

Oct 12, 2025 09:00-13:30 (Maoming Hall)

Time	Session
09:00-09:20	Introduction to DVP – Principles, Pipeline, and advantages
09:20-09:40	Tissue Slides Preparation – Sectioning, staining, and imaging
09:40-10:30	Al-based Cell Segmentation and Region-Selective Sampling – Tools and Contour Processing
10:30-10:50	Coffee Break + Q&A Networking
10:50-11:20	Laser Microdissection Workflow – Precision Cutting and Sample Collection
11:20-11:40	Low-input Sample Preparation & HPLC-MS/MS Acquisition
11:40-12:10	Data Quality Control and Data Analysis in DVP
12:10-12:30	Applications & Case Studies
12:40-13:30	Working Lunch + Q&A & Networking

Satellite Symposiums Program

卫星会报告日程

AOHUPO Young Scholar Forum

Oct 12, 2025 08:45-12:00 (Shenzhen Hall)

Host: Qian Zhao, Yao Zhang, Wanting Liu, Jingyi Hou

Time	Speaker and Title
08:45-09:00	Yafeng Zhu Sun Yat-sen University, China Title: Mining Dark Proteome: shedding lights on unannotated human proteins
09:00-09:15	Yang Yang Hong Kong Polytechnic University, China Title: Proteogenomic Profiling Reveals Small ORFs and Functional Microproteins in Activated T Cells
09:15-09:30	Ayaka Yoshida National Institute of Health Sciences, Ministry of Health, Labour and Welfare, Japan Title: Proteomics-Based Study on Expression Dynamics of a Novel Biomarker Candidate in Interstitial Lung Disease Rat Models
09:30-09:45	Penchatr Diskul-Na-Ayudthaya Chulabhorn Research Institute, Thailand Title: Identification of Metastatic Breast Cancer Biomarkers by Integrative Transcriptome and Proteome Analyses
09:45-10:00	Joan Catherine A. Chua Marine Science Institute, University of the Philippines Diliman, The Philippines Title: Philippine Teredinibacter Turnerae Leverage Multiple Polysaccharide Utilization Loci for Pectin Catabolism
10:00-10:15	Surbhi Bihani Indian Institute of Technology Bombay, India Title: Pan-Respiratory Virus Protein Microarray Reveals Diminished IgG Responses to Non-SARS-CoV-2 Viruses Post-Pandemic
10:15-10:30	Coffee Break
10:30-10:45	Na Li Institute of Biophysics, Chinese Academy of Sciences, China Title: Single-Position Peptide Clustering Strategy for Peptidomics Reveals Novel Disease Biomarkers and Dysregulated Proteolytic Characteristics

Time	Speaker and Title
10:45-11:00	Ming Li Hubei University, China Title: Research on Peptidogenomics of Rice Under Abiotic Stress and Construction of a Tissue-Specific Peptide Database
11:00-11:15	Jing Zhang Jinan University, China Title: Functional Study of uPE1s on Chromosome 20 in Colorectal Cancer
11:15-11:30	Zhao Peng Central China Normal University, China Title: Prediction of Human smORF-Encoded Peptides and Their Interacting Proteins
11:30-11:45	Hamizah Shahirah Hamezah Universiti Kebangsaan Malaysia, Malaysia Title: Alterations of Proteome Profiles in the Aged Rats Brain
11:45-12:00	Yimeng Qiao Hong Kong University of Science and Technology, Hong Kong, China Title: Spatial-GTPformer: A Generative Model for Translating Spatial Transcriptomics to Proteomics





Flash Talk and Rising Star Symposium

Oct 12, 2025 09:00-12:00 (Meizhou Hall)

Chair: Zilu Ye, Lili Niu

Time	Speaker and Title
09:00-09:10	Mowei Zhou Zhejiang University, China Title: Informing Enzyme Design via Native Top-Down Mass Spectrometry
09:10-09:20	Xiaoyuan Hu Guangxi University, China Title: Proteomic Investigation into the Mechanisms of Aluminum Exposure-Induced Developmental Toxicity in Mice
09:20-09:30	Lei Gu Suzhou Institute of Systems Medicine, Chinese Academy of Medical Sciences, China Title: Dual-Spray Tandem LC System Improves MS Utilization and Throughput in MS-based Proteomics
09:30-09:40	Shouxiang Zhang La Trobe University, Australia Title: Global analysis of Endogenous Protein Disorder in Cells
09:40-09:50	Wenbin Jiang Xiamen University, China Title: AbNovoBench: A Comprehensive, Standardized, and Reliable Benchmarking System for Evaluating Monoclonal Antibody De Novo Sequencing Analysis
09:50-10:00	Liujia Qian Westlake University, China Title: Rationale Prediction of Drug Combinations Based on Large-Scale Perturbation Proteomics
10:00-10:10	Jiayi Shen Shanghai Jiao Tong University, China Title: A Machine Learning–Enabled Urinary Protein Signature for the Accurate Diagnosis of Preeclampsia: Discovery and Multi-Center Validation
10:10-10:30	Coffee Break
10:30-10:40	Liang Yue Westlake University, China Title: Spatial Distribution of the Proteome in Human Body and Cancers
10:40-10:50	Ting Yu Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: Solvent-Induced Partial Cellular Fixation Approach Enables Proteome-Wide Decoding of Drug Targets And Drug-Induced Downstream Biochemical Pathways in Living Cells

Time	Speaker and Title
10:50-11:00	Beirong Zhang Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: In Vivo XL-MS Enables Large-Scale Mapping of Protein-Protein Interaction Networks in Cells
11:00-11:10	Pengzhi Mao Institute of Computing Technology, Chinese Academy of Sciences, China Title: pLink3: Unified Analysis of Large-Scale Crosslinking Proteomics Data
11:10-11:20	Rui Sun Westlake University, China Title: ProteinTalks: An Al Virtual Cell Foundation Model Extended to Clinical Application
11:20-11:30	Zhen Dong Westlake University, China Title: Filter-Aided Expansion Proteomics for Spatial Analysis of Single Cells and Organelles in FFPE Tissues
11:30-11:40	Changying Fu Southern University of Science and Technology, China Title: Deciphering Ectodomain Shedding of Membrane Proteins in Pancreatic Cancer: Mechanisms and Functional Implications
11:40-11:50	Tingpeng Yang Peng Cheng Laboratory, China Title: π-HelixNovo2: Making Accurate Online De Novo Peptide Sequencing Available to All
11:50-12:00	Siyu He Sichuan University, China Title: Global Analysis of Protein Modifications Reveals Faecalibacterium-mediated PRDX6 Acetylation Protecting Against Primate Gut Inflammaging





The 1st π-HuB Industry Conference

Oct 13, 2025 13:30-16:50 (Qinghe Hall)

Time	Session
13:30-14:00	Registration & Welcome Reception
14:00-14:10	Opening Address
14:10-14:20	Official Announcement Ceremony: π-HuB Park
14:20-14:40	Keynote Presentations: π-HuB Ecosystem Strategy & π-HuB Park Planning Report
14:40-15:30	Signing Ceremony: Partnerships with Global Leading Enterprises and Key Projects
15:30-16:15	Innovation Launch: New Technology and Product Launches, Initiative of the International Pathology Center
16:15-16:45	Closing Remarks
16:45-16:50	Event Concludes

Post-Event: Networking Session-Dinner

Plenary Session Program | 大会报告日程

Time	Speaker and Title
Oct 12, 2025	
Chair: Ming Li,	Connie R Jimenez, Hui Zhang, Albert Heck
15:40-16:10	Ruedi Aebersold Academician of the German National Academy of Sciences Leopoldina ETH Zurich, Switzerland Title: The Adaptable Modular Proteome Specifies Cellular States
16:10-16:40	Zihe Rao Academician of the Chinese Academy of Sciences, Tsinghua University, China Title: Pathogen and Public Health
16:40-17:10	Jun Ma Academician of the Chinese Academy of Sciences Sun Yat-sen University Cancer Center, China Title: Research on Immunotherapy for Nasopharyngeal Carcinoma
17:10-17:40	Fuchu He Academician of the Chinese Academy of Sciences National Center for Protein Sciences (Beijing), China Title: π-HuB: Proteomic Navigator of The Human Body
Oct 13, 2025	
Chair: Mark Mo	olloy

08:30-08:55	Albert Heck Academician of the Royal Netherlands Academy of Arts and Sciences Utrecht University, the Netherlands Title: Touching Upon the Millions of Hidden Treasures in the Plasma Proteome
08:55-09:20	Aiping Lyu Foreign Academician of Academia Europaea, Hong Kong Baptist University, China Title: Proteomics-Powered Innovation in Modernizing Traditional Chinese Medicine: A Case Study of Oridonin
09:20-09:45	Wen Gao Academician of the Chinese Academy of Engineering Pengcheng Laboratory, China Title: Pengcheng CloudBrain Series and Application Exploration of Pengcheng Mind Large Model







Time	Speaker and Title
Chair: Wei Wu	
16:40-17:05	K. W. Michael Siu Fellow of the Royal Society of Canada Shandong Provincial Public Health Clinical Center, China Title: Clinical Application of Mass Spectrometry-Based Proteomics
17:05-17:30	Ho Jeong Kwon Yonsei University, South Korea Title: Organelle-Targeted Chemical Proteomics: Toward Precision Metabolic Therapy
17:30-17:55	Connie R. Jimenez Amsterdam University Medical Center, the Netherlands Title: Clinical (Phospho) Proteomics for Precision Medicine
Oct 14, 2025	
Chair: Yasushi	i Ishihama
08:30-08:55	Ming Li Fellow of the Royal Society of Canada University of Waterloo, Canada Title: Al for MS: From Small Data to Large Data and Back to Small Data
08:55-09:20	Uwe Völker Universitätsmedizin Greifswald, Germany Title: Multiomics Analyses of Population-Based Cohorts - The study of Health in Pomerania (SHIP) as an Example
09:20-09:45	Hui Zhang Johns Hopkins University, USA Title: Clinical Proteomics: Technologies and Applications
Chair: Teck Ye	w Low
16:30-17:00	Chris Sander Harvard Medical School, USA Title: Reducing the Cancer Burden using Proteomic Profiles - Combination Therapy and Early Detection
17:00-17:30	Matthias Mann Academician of the German National Academy of Sciences Leopoldina Max Planck Institute of Biochemistry, Germany Title: MS-Based Proteomics Enters the High-Throughput Era

Parallel Sessions Program

分会报告日程

Session 1: Emerging Proteomics Technologies

Oct 13, 2025 10:10-12:10 (Lingnan Convention Hall)

Organizers: **Haojie Lu, Chu Wang, Minjia Tan, Weijie Qin** Co-Chairs: **Chu Wang, Yasushi Ishihama, Minjia Tan**

Time	Speaker and Title
10:10-10:30	Yasushi Ishihama Kyoto University, Japan Title: Ultrahigh-Throughput Proteomics with Robust NanoLC/MS/MS with Sample Preparation
10:30-10:50	Qingsong Lin National University of Singapore, Singapore Title: Acoustically Enhanced Protein Extraction Facilitates Proteomic Analysis of FFPE KRAS-Mutant Colorectal Cancer Tissues
10:50-11:05	Qun Fang Zhejiang University, China Title: Microfluidic Single-Cell Proteomics and Multi-Omics Analysis
11:05-11:20	Ying Zhang Fudan University, China Title: Chemical Proteomics Toolbox for Global Mapping of Ligandable Surfaceome and Viral Receptors
11:20-11:35	Jie Zheng Shanghai Jiao Tong University, China Title: High Resolution HDX-MS Fuels Structural Proteomics: From DDA to DIA ETD
11:35-11:50	Wei Qin Tsinghua University, China Title: Spatiotemporally Resolved Proteomics Enabled by in Vivo-Compatible Proximity Labeling Methods
11:50-12:00	Hartmut Schlüter University of Hamburg, Germany Title: Tissue Sampling & Homogenization with Nanosecond- & Picosecond Infrared Laser Systems for Improved Proteomics
12:00-12:10	Weidi Xiao Peking University Chengdu Institute, China Title: An Automated Proteomic Platform for Extracellular Vesicles: Development and Clinical Applications



Session 2: Native Mass Spectrometry and Structural Biology

Oct 13, 2025 10:10-12:15 (Shenzhen Hall)

Organizers: Guanbo Wang, Hongying Zhong, Wenqing Shui, Qun Zhao

Co-Chairs: Fan Liu, Hongying Zhong, Richard Simpson

Time	Speaker and Title
10:10-10:30	Fan Liu Leibniz Institute for Molecular Pharmacology, Germany Title: Building 3D Cellular Architecture by Cross-Linking Mass Spectrometry
10:30-10:50	Leonard Foster University of British Columbia, Canada Title: Single-Cell Lipidomics and Proteomics of the Same Cells to Understand Astrocyte Biology
10:50-11:05	Fangjun Wang Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: Ultraviolet Photodissociation Mass Spectrometry Captures the In-Solution Functional Conformation Dynamics of Proteins
11:05-11:20	Wenqing Shui ShanghaiTech University, China Title: Conformational Dynamics of GPCR Signaling Complexes Revealed by Structural MS
11:20-11:35	Xiaoyun Liu Peking University, China Title: Bacterial Strategies to Evade Septin-Mediated Cell-Autonomous Immunity
11:35-11:50	Gongyu Li Nankai University, China Title: Chemical Measurement and Molecular Intervention of Disease-Associated Protein Aggregation
11:50-12:05	Guanbo Wang Peking University, China Title: Resolving Structural Heterogeneity of Natural Proteins from Biological Samples Using Single-ion Super-Resolution Mass Spectrometry
12:05-12:15	Jiayue Sun Kyoto University, Japan Title: Oxidation-Induced Structural Destabilization of βB2-Crystallin: Mechanistic Insights into Trp59/Trp151-Dependent Oligomerization and Cataract Pathogenesis

Session 3: Single Cell Proteomics

Oct 13, 2025 10:10-12:20 (Shantou Hall)

Organizers: Qun Fang, Zilu Ye

Co-Chairs: Max Ching Ming Chung, Xianting Ding, Zilu Ye

Time	Speaker and Title
10:10-10:30	Lihua Zhang Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: Multi-Omics Analysis for Single Cells
10:30-10:50	Xianting Ding Shanghai Jiao Tong University, China Title: Single-Cell Spatial Temporal Proteomics and Clinical Applications
10:50-11:10	Weijie Qin National Center for Protein Sciences (Beijing), China Title: New Technologies for Spatial, Cellular, and Subcellular Resolution Proteomics Research
11:10-11:25	Xuejiang Guo Nanjing Medical University, China Title: Single-cell Proteomics Reveals Complex Translational Regulation during Gametogenesis
11:25-11:40	Fan Yang Tencent Life Sciences Laboratory, China Title: Enhancing Proteomics Data Analysis with Al
11:40-11:55	Chen Li Shanghai Jiao Tong University, China Title: Comparative Proteomic Landscapes Elucidate Human Preimplantation Development and Failure
11:55-12:10	Yun Yang International Academy of Phronesis Medicine (Guang Dong), China Title: Towards High-Throughput and High-Sensitivity MS-Based Single-Cell Proteomics
12:10-12:20	Mo Hu Changping Laboratory, China Title: Asymmetric Protein Abundance among Blastomeres of Pre-Implantation Mouse Embryos Revealed by Single-Cell Proteomics









Session 4: Understudied Proteomics and Peptidomics

Oct 13, 2025 10:10-12:10 (Maoming Hall)

Organizers: Tieliu Shi, Yaoyang Zhang, Chenxi Jia, Wenguang Shao, Qian Zhao

Co-Chairs: Chenxi Jia, Christopher Overall, Qian Zhao, Yaoyang Zhang

Time	Speaker and Title
10:10-10:30	Anthony Purcell Monash University, Australia Title: The Plasma Immunopeptidome - Insights into Tumour Antigen Evolution and Treatment Response
10:30-10:50	Christopher M Overall University of British Columbia, Canada Title: There is No Dark Side of the Proteome As a Matter of Fact, It's All Dark
10:50-11:05	Aifu Lin Zhejiang University, China Title: Micropeptides Derived from ncRNA: Unveiling a Hidden Functional Proteome in Tumor Biology
11:05-11:20	Cuihong Wan Central China Normal University, China Title: Landscape of Novel smORFs and Their Encoded-Peptides Predicted from Crop Genomes
11:20-11:35	Gong Zhang Jinan University, China Title: Structural and Functional Insights of Human Understudied Proteome
11:35-11:50	Jing Li Shanghai Jiao Tong University, China Title: Integrated Proteogenomics Uncovers Human Microproteins in Gastric Cancer
11:50-12:00	Honggang Huang COFCO Nutrition and Health Research Institute, China Title: Development and Application of Multi-Omics (Peptidomics + Lipidomics) Strategies for Adulteration Detection in Peanut Oil Authentication Study
12:00-12:10	Baozhen Shan Bioinformatics Solutions Inc, Canada Title: An Al-Driven De Novo-Based Multi-Omics Platform for Discovering Cancer-Specific Non-Canonical HLA-I Peptides

Session 5: Artificial Intelligence and Education

Oct 13, 2025 10:10-12:00 (Jieyang Hall)

Organizers: Li Ma, Chunhui Zhang, Yue Hua, Cheng Chang Co-Chairs: Cheng Chang, Chunhui Zhang, Shaohui Huang

Time	Speaker and Title
10:10-10:25	Hua Sun Peking University, China Title: Reshaping Higher Education and Promoting Teacher Development in the Digital and Intelligent Era
10:25-10:40	Lei Chen Hong Kong University of Science and Technology (Guangzhou), China Title: The New Era of Artificial Intelligence: The Innovation of Large Models and Opportunities for Future Education
10:40-10:55	Jing Tian Zhujiang Hospital, Southern Medical University, China Title: Artificial Intelligence–Empowered Clinical Skills Education and Evaluation
10:55-11:10	Xuming Ji Zhejiang Chinese Medical University, China Title: The Practice and Collaborative Application of Traditional Chinese Medicine Mentorship Platforms and AI - based Courses
11:10-11:25	Chunhui Zhang Southern Medical University, China Title: Exploring the Practice of Building Subject Models Based on Generative AI and Sharing Teaching Wisdom
11:25-11:40	Xiaoyong Hu South China Normal University, China Title: Integrating Artificial Intelligence into Higher Education: Cultivating New - Type Teachers and Innovating Talent - Training Models
11:40-12:00	Arunima Singh Nature Methods, USA Title: Publishing in Nature Methods and Pursuing an Editorial Career









Session 6: Proteomics-Driven Precision Medicine (A)

Oct 13, 2025 10:10-12:10 (Meizhou Hall)

Organizers: Yongzhan Nie, Ying Jiang, Hong Wang

Co-Chairs: Ed Nice, Hong Wang, Jie Li

Time	Speaker and Title
10:10-10:30	Kyunggon Kim Asan Institute for Life Sciences, South Korea Title: Application of Spatial Proteomics for Discovery of Biomarker and Drug Target
10:30-10:50	Phillip Robinson The University of Sydney, Australia Title: ProCan® - Adding Proteomics to Genomics for Precision Oncology
10:50-11:10	Bing Zhang Baylor College of Medicine, USA Title: Decoding PTM Patterns to Gain Functional Insights into Pathogenic Missense Variants
11:10-11:25	Min-Sik Kim Daegu Gyeongbuk Institute of Science and Technology, South Korea Title: Multi-Omics Analysis of Autism Spectrum Disorders
11:25-11:40	Christoph W. Turck Kunming Institute of Zoology, Chinese Academy of Sciences, China Title: Molecular Pathway Illumination for Psychiatric Disorders - from Animal Models via Omics to Biosignatures
11:40-11:55	Y. Eugene Chin Zhejiang Provincial People's Hospital, China Title: Lysine Post-translational Modifications in Diversity
11:55-12:10	Ruibing Chen Tianjin University, China Title: Harnessing Proteome Thermostability to Characterize dsRNA Binding Proteins

Session 7: Chemoproteomics and Drug Discovery

Oct 13, 2025 14:00-16:15 (Lingnan Convention Hall)

Organizers: Mingliang Ye, Kai Zhang, Hui Ye Co-Chairs: Ben Collins, Hui Ye, Kai Zhang

Time	Speaker and Title
14:00-14:20	Bernd Wollscheid ETH Zurich, Switzerland Title: Precision Medicine, Drug (target) Discovery and Creating Novel Cancer Medicines
14:20-14:40	Ben Collins Queen's University Belfast, UK Title: Scaling Up Proteomics Tools for Targeted Protein Degrader Development
14:40-14:55	Chu Wang Peking University, China Title: Real-Time Isotopic Signature Targeted Profiling
14:55-15:10	Kai Zhang Tianjin Medical University, China Title: ACSS2 Coupled with KAT7 Regulates Histone β-Hydroxybutyrylation to Enhance Transcription
15:10-15:25	He Huang Shanghai Institute of Materia Medica, Chinese Academy of Sciences, China Title: Identification and Pathological Function Study of Lactyl-CoA Synthetase
15:25-15:40	Gang Li Institute of Chemical Biology, Shenzhen Bay Laboratory, China Title: Scaling Covalent Ligand Discovery via Library-versus-Proteome Screening
15:40-15:55	Hui Ye China Pharmaceutical University, China Title: TRAP: A Universal Chemoproteomic Strategy for Mapping Ligand-Target Interactions
15:55-16:05	Haiteng Deng Tsinghua University, China Title: Identification of Aging Biomarkers and Development of Anti-Aging Interventions
16:05-16:15	Nan Chen ChomiX Biotech Co., Ltd, China Title: Chemoproteomic Discovery and Preclinical Development of FAP-Targeted Radiopharmaceuticals via a Novel Covalent Small-Molecule Ligand







Session 8: Proteomics of Model System

Oct 13, 2025 14:00-16:00 (Shenzhen Hall)

Organizers: Ren Lai, Lingqiang Zhang, Feng Ge, Xiaowen Wang

Co-Chairs: Giuseppe Palmisano, Ren Lai

Time	Speaker and Title
14:00-14:20	Ren Lai Kunming Institute of Zoology, Chinese Academy of Sciences, China Title: Venomics of Animal Venoms and Their Applications for Drug Development
14:20-14:40	Dong Yang National Center for Protein Sciences (Beijing), China Title: Multi-Omics Analysis Demonstrates the Pivotal Role of Tardigrade-Specific Genes in Developing Extremotolerant Capability
14:40-15:00	Xiaozhe Zhang Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: Structural Characterization, Target Discovery, and Rational Modification of the Neuroprotective Peptide Bidentatide
15:00-15:15	Mingqiang Rong Hunan Normal University, China Title: Deep Mining of Bioactive Peptides from Spider Venom via Multi-Omics Approaches
15:15-15:30	Shilong Yang Northeast Forestry University, China Title: Thermal Switch Mechanisms of Temperature-dependent Sex Determination in Turtles
15:30-15:45	Wenliang Zhou Southern Marine Science and Engineering Guangdong Laboratory, China Title: Integrative Multi-Omics Approaches Facilitate the Evolutionary Research of Venom in Scorpaeniformes
15:45-16:00	Zhijian Cao Hubei University of Technology, China Title: Molecular Mechanism and Evolution of the Itch Induced by Fungal Defensins

Session 9: Spatial Proteomics

Oct 13, 2025 14:00-16:10 (Shantou Hall)

Organizers: Ruijun Tian, Fangqing Zhao, Guixue Hou, Yaoting Sun

Co-Chairs: Phillip Robinson, Ruijun Tian, Yaoting Sun

Time	Speaker and Title
14:00-14:20	Angus C Grey University of Auckland, New Zealand Title: Comparative Proteomics and Spatial Metabolomics of Ocular Lens Glucose Transport: Implications for Tissue Transparency and Diabetic Cataract
14:20-14:40	Zexian Liu Sun Yat-sen University Cancer Center, China Title: Spatial Architecture of the Immune-Tumor Battlefield Determines Therapeutic Response and Prognosis in Nasopharyngeal Carcinoma
14:40-14:55	Minrui Liang Huashan Hospital, Fudan University, China Title: Big Data to Small Target: Spatial Multi-Omics in Autoimmune Disease
14:55-15:10	Changying Fu Southern University of Science and Technology, China Title: Deciphering Ectodomain Shedding of Membrane Proteins in Pancreatic Cancer: Mechanisms and Functional Implications
15:10-15:25	Chuanyu Liu BGI Research, China Title: Stereo-cell: Spatial Enhanced-Resolution Single-Cell Sequencing
15:25-15:40	Jinyang Qian Zhejiang University, China Title: Identification and Characterization of Cell Niches in Tissue from Spatial Omics Data at Single-cell Resolution
15:40-15:50	Lin Zhu Hong Kong Baptist University, Hong Kong, China Title: Integrative Spatially Resolved Proteomic and Metabolomic Imaging Reveals Synovitis Endotypes Implicated in Osteoarthritis Progression
15:50-16:00	Andreas Metousis Max Planck Institute of Biochemistry, Germany Title: Deep Visual Proteomics Reveals Early Drivers of Ovarian Cancer Development
16:00-16:10	Jingfang Bian Hong Kong Polytechnic University, Hong Kong, China Title: Development of a Laser Capture Microdissection-Guided Spatial Proteomics Platform for Layer-Resolved Retinal Proteome in Ocular Study









Session 10: Modernization of Traditional Chinese medicine

Oct 13, 2025 14:00-15:40 (Maoming Hall)

Organizers: Qingfeng Du, Chunhui Deng, Xiaomin Sun, Xuefeng Xing Co-Chairs: Songqi He, Junshan Liu, Xiaomin Sun, Lei Gao, Shenhai Gong

Time	Speaker and Title
14:00-14:20	Zhihong Jiang Macau University of Science and Technology, China Title: Glycomic Analysis of Glycoproteins in Traditional Chinese Medicine
14:20-14:40	Xiaohe Xiao Chinese PLA General Hospital, China Title: Multi-Omics-Supported Strategies and Methods for Evaluating the Safety and Efficacy of Traditional Chinese Medicine
14:40-15:00	Zhongqiu Liu Guangzhou University of Chinese Medicine, China Title: Development and Practice in the Integrated Methodologies for the Effectiveness of Chinese Herbs and Their Combined Formulae
15:00-15:20	Jinghua Yang The First Affiliated Hospital of Zhengzhou University, China Title: Disease-Associated Protein Variants and Their Applications
15:20-15:40	Jigang Wang Institute of Chinese Materia Medica, China Academy of Chinese Medical Sciences, China Title: Chemical Biology Studies on Targets and Mechanisms of Traditional Chinese Medicine

Session 11: Computational and Al Proteomics (A)

Oct 13, 2025 14:00-16:00 (Jieyang Hall)

Organizers: Lu Xie, Hao Chi, Wenfeng Zeng, Han Wen Co-Chairs: Henning Hermjakob, Lu Xie, Wenfeng Zeng

Time	Speaker and Title
14:00-14:20	Henning Hermjakob European Bioinformatics Institute, UK Title: Reactome 4: Pathways Reimagined – Dynamic Visualisation and Intelligent Chat
14:20-14:40	Juan Antonio Vizcaino European Bioinformatics Institute, UK Title: The PTMeXchange Project: Making PTM-Data FAIR and AI-Ready
14:40-15:00	Robert Winkler National Laboratory for Genomics of Biodiversity, Mexico Title: Public Money, Public Code, and Public Data in Proteomics
15:00-15:15	Zilu Ye Institute of Systems Medicine, Chinese Academy of Medical Sciences, China Title: Single-Cell Proteomics Meets Al: Opportunities and Challenges
15:15-15:30	Peijie Zhou Peking University, China Title: Towards Al Virtual Cell Through Dynamical Generative Modeling of Single-cell Omics Data
15:30-15:40	Hao Chi Institute of Computing Technology, Chinese Academy of Sciences, China Title: Advancing Computational Proteomics: Large-scale Scoring Models and the pFind Platform
15:40-15:50	Hong Li Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences, China Title: Computational Methods for Spatial Proteomics
15:50-16:00	Menghuan Zhang Tongji University, China Title: Biologically Structured Deep Learning for Context-Specific Inference of Kinase-Substrate Networks









Session 12: Proteomics Beyond Mass Spectrometry

Oct 14, 2025 10:10-12:10 (Lingnan Convention Hall)

Organizers: Shengce Tao, Xiaobo Yu, Hewei Jiang Chairs: Limsoon Wong, Shengce Tao, Xiaobo Yu

Time	Speaker and Title
10:10-10:30	Chiensheng Chen National Cheng Kung University, Chinese Taipei Title: A Next-Generation Proteome Microarray: Wafer-Based Mechanistic Proteomics
10:30-10:50	Limsoon Wong National University of Singapore, Singapore Title: Proteomics Beyond Cataloguing
10:50-11:10	Zhengming Chen University of Oxford, UK Title: Harnessing the Power of Proteogenomics in Population Biobanks to Advance Precision Health
11:10-11:30	Shuangjia Zheng Lingang Laboratory, China Title: Drugging Undruggable Targets with Generative Models
11:30-11:45	Shengce Tao Shanghai Jiao Tong University, China Title: Antibody Reactome: From Protein Microarray to PhIP-seq
11:45-12:00	Xiaobo Yu National Center for Protein Sciences (Beijing), China Title: Advances in Non-mass spectrometry Proteomics Technology
12:00-12:10	Zheng Ser A*STAR Institute of Molecular and Cell Biology (A*STAR IMCB), Singapore Title: Structural Proteomics and Modelling Identifies Key Interacting Residue and Compact Conformation of Dengue NS2B-NS3 Complex

Session 13: Computational and Al Proteomics (B)

Oct 14, 2025 10:10-12:10 (Shenzhen Hall)

Organizers: Lu Xie, Hao Chi, Wenfeng Zeng, Han Wen Co-Chairs: Yasset Perez-Riverol, Hao Chi, Han Wen

Time	Speaker and Title
10:10-10:30	Wilson Wen Bin Goh Nanyang Technological University, Singapore Title: Harnessing Al-Driven Proteome Analytics to Transform Mental Health Management: A Singapore Perspective
10:30-10:50	Yasset Perez-Riverol European Bioinformatics Institute, UK Title: Quantms: A Hub for high-quality proteomics data to power AI development
10:50-11:10	Shin Kawano Kitasato University, Japan Title: jPOST and JPDM: Attempts to Collect Metadata
11:10-11:25	Mingliang Ye Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: Glyco-Decipher and PELSA-Decipher Facilitate Proteome-Wide Identification of Site-Specific Glycoforms and Ligand-Target Proteins
11:25-11:40	Cheng Chang National Center for Protein Sciences (Beijing), China Title: A Foundation Model for Decoding Dark Proteome through Self-Supervised Learning
11:40-11:50	Wenfeng Zeng Westlake University, China Title: FennOmix-MHC: A Foundation Model for Peptide–HLA Representation Learning and Shared Epitope Discovery
11:50-12:00	Jianhui Liu Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: Microbial Resource Mining Based on Computational Proteomics
12:00-12:10	Yongge Li Al For Science Institute, Beijing, China Title: Dynamical Foundation Models for Biology: A Neural ODE Case Study on Proteomics







Session 14: Advances in Agricultural Proteomics

Oct 14, 2025 10:10-12:10 (Shantou Hall)

Organizers: Pingfang Yang, Xuchu Wang, Yingchun Wang, Xuna Wu

Co-Chairs: Setsuko Komatsu, Shaojun Dai

Time	Speaker and Title		
10:10-10:30	Setsuko Komatsu Fukui University of Technology, Japan Title: The Growth of Soybean under Salt Stress Is Modulated in Simulated Microgravity Conditions		
10:30-10:50	Sixue Chen University of Mississippi, USA Title: Unraveling the Molecular Choreography of C3 to CAM Transition in Common Ice Plant Using Multi-Omics		
10:50-11:10	Wolfram Weckwerth University of Vienna, Austria Title: From Pangenomics to Panomics–Al-Assisted Causal Modelling of the GxE Equation		
11:10-11:20	Kun Wang Wuhan University, China Title: Decoding Plant Translational Regulation with eRibo-Seq: From Initiation Site Switching to Conserved Operon-Like Modules		
11:20-11:30	Xiaojian Yin Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, China Title: Identification of Key Proteins and Elucidation of Their Regulatory Mechanisms in Tanshinone and Terpenoid Biosynthesis		
11:30-11:40	Feng Ge Institute of Hydrobiology, Chinese Academy of Sciences, China Title: Lysine Acetylation and Its Regulatory Enzymes in Cyanobacteria		
11:40-11:50	Yanmei Chen China Agricultural University, China Title: Functional Proteomics Reveals Protein Kinase Networks Orchestrating Maize Abiotic Stress Responses		
11:50-12:00	Kaiguang Yang Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: In Vivo Profiling of Light-Dependent Protein Interactions and Conformational Changes in Spinach by Cross-linker Delivery Coupled with Mass spectrometry		
12:00-12:10	Guochen Qin Peking University, China Title: The Proteomic Landscape and Homeolog Expression Patterns in Polyploid Wheat		

Session 15: **Body Fluid Proteomics**

Oct 14, 2025 10:10-12:15 (Maoming Hall)

Organizers: Youhe Gao, Tong Wang, Xuejiang Guo, Yueshuai Guo

Co-Chairs: Robert Winkler, Tong Wang, Xuejiang Guo

Time	Speaker and Title
10:10-10:25	Youhe Gao Beijing Normal University, China Title: Recent Progress on Urine Biomarkers
10:25-10:45	Chen Ding Fudan University, China Title: Proteomics-Centered Multi-Omics Study of Tumors
10:45-11:05	Bo Situ Nanfang Hospital, Southern Medical University, China Title: Circulating Bacterial Extracellular Vesicles: Detection and Clinical Applications
11:05-11:20	Wei Sun Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences, China Title: China Urine Multi-Omic Analysis
11:20-11:35	Lili Niu Institute of Chemical Biology, Shenzhen Bay Laboratory, China Title: Integrative Plasma Proteomics and Genomics for Biomarker and Drug Target Identification
11:35-11:50	Shuxuan Tang Beijing Ditan Hospital, Capital Medical University, China Title: Urinary Proteome Profiling: A Study to Reveal Pregnant Process and Predict Early Drug Efficacy
11:50-12:05	Wei Sun Beijing Qinglian Biotech Co., Ltd, China Title: Comprehensive Solution for Mass Spectrometry-based High-throughput Deep Plasma Proteomics Using Nano-Magnetic Beads
12:05-12:15	Jihong Tang Hong Kong University of Science and Technology, Hong Kong, China Title: Proteomic Classification and Clonal Evolution of IDH-Mutant Astrocytoma through Panomics Integration

Session 16: Proteomics-Driven Precision Laboratory Medicine

Oct 14, 2025 10:10-12:15 (Jieyang Hall)

Organizers: Li Ma, Lei Zheng, Bin Xiao, Jie Zhan Co-Chairs: Xianzhang Huang, Bin Xiao, Jie Zhan

Time	Speaker and Title
10:10-10:30	Yizhou Jiang Fudan University Shanghai Cancer Center, China Title: Molecular Subtyping and Precision Treatment of Triple-Negative Breast Cancer
10:30-10:50	Lei Zheng Nanfang Hospital, Southern Medical University, China Title: Research Methods and Diagnostic and Therapeutic Value of Extracellular Vesicles
10:50-11:10	Youhe Gao Beijing Normal University, China Title: The Foundation of Precision Medicine and Personalized Medicine, Is Based on Omics Data of Urine
11:10-11:30	Lin Bai Shanghai General Hospital, Shanghai Jiao Tong University, China Title: Tumor Marker Discovery and Diagnostic Applications Based on Pan-Cancer Plasma Proteomic Profiling
11:30-11:50	Bing Gu Guangdong Provincial People's Hospital, China Title: Interdisciplinary Collaboration Promotes the Development of Precision Laboratory Medicine
11:50-12:05	Wenbo Cheng Suzhou Institute of Biomedical Engineering and Technology, Chinese Academy of Sciences, China Title: Developing Domestic Wide Mass Range TQ-MS for Clinical Proteomics
12:05-12:15	Arka Ray Indian Institute of Technology Bombay, Powai, Mumbai, India Title: Pan-Respiratory Virus Protein Microarray Reveals Diminished IgG Responses to Non-SARS-CoV-2 Viruses Post-Pandemic

Session 17: Post-translational Modifications

Oct 14, 2025 10:10-12:25 (Meizhou Hall)

Organizers: Jinghua Yang , Yan Zhang, Zhixin Tian, Jialin Liu

Co-Chairs: Hui Zhang, Jialin Liu, Zhongyi Cheng

Time	Speaker and Title		
10:10-10:30	Giuseppe Palmisano University of São Paulo, Brazil Title: Comprehensive Characterization of Protein Glycosylation in Host-Pathogen Interaction		
10:30-10:45	Zhixin Tian Tongji University, China Title: Structural N-glycoproteomics and Applications		
10:45-11:00	Huali Shen Fudan University, China Title: N-glycosylation in Alzheimer's Disease: Panoramic Characterization and Mechanistic Exploration through Ultra-Deep Glycoproteomics		
11:00-11:15	Zhongyi Cheng Jingjie Bio, China Title: Innovative Proteomics Research in Precision Oncology		
11:15-11:30	Xia Zou Shanghai Jiao Tong University, China Title: Comprehensive Characterization of the O-GalNAc Glycoproteome in Complex Biological Tissues		
11:30-11:45	Yue Zhai National Translational Center for Molecular Medicine, Air Force Medical University, China Title: The Pan-Modifications: Identify Metabolically Responsive PTM Neoantigens and Their Autoimmune Response Mechanisms		
11:45-12:00	Shisheng Sun Northwest University, China Title: High-Resolution Glycoproteomics for Structural and Functional Interpretation of Site-specific Glycans		
12:00-12:15	Yixuan Xie Fudan GBA Institute for Precision Medicine, China Title: Integrating Metabolic Glycan Phenotype Manipulation with Affinity Purification for a Systematic Exploration of Glycoprotein Interaction Networks		
12:15-12:25	Jinjun Gao Peking University Shenzhen Graduate School, China Title:Advancing Proteomics Strategies for Investigating Protein Post-translational Modification		









Session 18: Cross-species proteomics

Oct 14, 2025 14:00-16:00 (Lingnan Convention Hall)

Organizers: Weiqi Zhang, Jing Yang, Jing Chen, Jing Lu

Co-Chairs: Weiqi Zhang, Pingfang Yang

Time	Speaker and Title	
14:00-14:20	Ping Zheng Kunming Institute of Zoology, Chinese Academy of Sciences, China Title: Naïve Pluripotency and Genomic Stability are Coordinated in Mouse Embryonic Stem Cells by a Novel Pluripotency Regulator Zfp998	
14:20-14:40	Xiangjiang Zhan Institute of Zoology, Chinese Academy of Sciences, China Title: Qinghai-Tibet Plateau Adaptation of a Top Predator-Saker Falcons	
14:40-15:00	Hongjie Yao Guangzhou Laboratory, China Title: Capturing R-loops at Base-Pair Resolution Reveals Clustered R-Loops Activating Gene Expression and YMCAG-Contained R-Loops Inducing DNA Damage	
15:00-15:20	Guoji Guo Zhejiang University, China Title: Mapping and Modeling Cell Landscapes at Single-Cell Level	
15:20-15:40	Lili Zhou Nanfang Hospital, Southern Medical University, China Title: Proteomics and Metabolomics: Discovering the Eye of Storm in Kidney Diseases	
15:40-16:00	Weiqi Zhang China National Center for Bioinformation and Beijing Institute of Genomics, Chinese Academy of Sciences, China Title: Deciphering Aging Mechanisms and Developing Interventions Based on Aging Clocks	

Session 19: Proteomics of the Microbes

Oct 14, 2025 14:00-15:55 (Shenzhen Hall)

Organizers: **Hengliang Wang, Qingwei Ma, Xiaoyun Liu, Leyuan Li** Co-Chairs: **Hengliang Wang, Paola Roncada, Qingwei Ma, Xiaoyun Liu**

Time	Speaker and Title
14:00-14:20	Paola Roncada University "Magna Græcia" of Catanzaro, Italy Title: The study of Microbiome in the Era of Global Health
14:20-14:40	Tim Van Den Bossche Ghent University, Belgium Title: Improving Metaproteomics Data Analysis with the Ghent Metaproteomics Toolbox
14:40-15:00	Liang Qiao Fudan University, China Title: DIA Metaproteomics in Microbiome Research
15:00-15:20	Kai Cheng Quadram Institute, UK Title: MetaPilot: A One-Stop Platform for Comprehensive Metaproteomics Data Analysis
15:20-15:35	Yao Zhang National Center for Protein Sciences (Beijing), China Title: Precision Proteogenomics Unmasks Mycobacterium Tuberculosis Species-Specific Dark Proteins and Novel Causal Diagnostic Biomarkers
15:35-15:45	Yingying Sun Westlake University, China Title: Population-Based Metaproteomics Reveals Functional Associations between Gut Microbiota and Phenotypes
15:45-15:55	Luman Wang Peking University, China Title: A Practical Guide to Experimental Design and Power Analysis for Metaproteomics Studies







Session 20: Proteomics Marries other Omics

Oct 14, 2025 14:00-15:50 (Shantou Hall)

Organizers: Canhua Huang, Hu Zhou, Xinpei Yi Co-Chairs: Anthony Purcell, Hongxiu Yu, Ling Lin

Time	Speaker and Title
14:00-14:20	Fernando Corrales National Center for Biotechnology, Spain Title: Proteomics Study of Progressive Familial Intrahepatic Cholestasis 3 (PFIC3)
14:20-14:35	Zeping Hu Tsinghua University, China Title: Deciphering Disease-Specific Metabolic Reprogramming through Innovative Metabolomics and Multi-Omics
14:35-14:50	Rui Liu Sichuan University, China Title: Metabolic Enzymes Function as Cellular Sensors for Radiation-Induced Damages
14:50-15:05	Hongxiu Yu Fudan University, China Title: SIRT7 Regulates T-cell Antitumor Immunity through Modulation BCAA and Fatty Acid Metabolism
15:05-15:20	Yang Wang Jinan University, China Title: Acetylation of Cyclin Dependent Kinases in Cancer
15:20-15:35	Ling Lin Zhongshan Hospital, Fudan University, China Title: Multi-Omics Profiling Reveals Mitochondrial Metabolic Remodeling in Foam Cell Formation
15:35-15:50	Yang Zhao National Institute of Metrology, China Title: Proteomics Data Quality Control and Deep Analysis for Precision Oncology

Session 21: Proteomics-Driven Precision Medicine (B)

Oct 14, 2025 14:00-16:10 (Maoming Hall)

Organizers: Yongzhan Nie, Ying Jiang, Hong Wang

Co-Chairs: Hong Wang, Mark Baker

Time	Speaker and Title
14:00-14:20	Chantragan Srisomsap Phiphobmongkol Chulabhorn Research Institute, Thailand Title: Proteomics-Driven Insights into Cancer Biomarkers Discovery
14:20-14:40	Terence Poon University of Macau, China Title: Data Quality Challenges in Precision Medicine
14:40-15:00	Teck Yew Low Sunway University, Malaysia Title: Unveiling the Distinct Microproteome Across Cancer Progression
15:00-15:20	Mark Molloy The University of Sydney, Australia Title: Proteomics of Colorectal Liver Metastases
15:20-15:35	Shuncheng Li Western University, Canada Title: Ultra-Deep Phosphoproteomics and Kinomics- Applications in Cancer Research and Precision Medicine
15:35-15:50	Jinghua Yang The First Affiliated Hospital of Zhengzhou University, China Title: Proteoformics by Pan-modifications & Human Diseases
15:50-16:00	Xiaohui Liu SJTU Technical Center of Clinic-Omics, China Title: A Multidimensional Proteomic Analysis of Brain Metastases (BrMs) and Gliomas
16:00-16:10	Daryl Chin A*STAR Institute of Molecular and Cell Biology (A*STAR IMCB), Singapore Title: Cell-Surface Proteomics Reveals a Novel Candidate Immunotherapeutic Target in Microsatellite-Stable Colorectal Cancer









Session 22: Proteome Dynamics

Oct 14, 2025 14:00-16:15 (Jieyang Hall)

Organizers: Lihua Zhang, Zhen Liu, Lunzhi Dai Co-Chairs: Lihua Zhang, Pouya Faridi, Yansheng Liu

Time	Speaker and Title
14:00-14:20	Wei Wu Agency for Science, Technology and Research, Singapore Title: Going Beyond Personal in the Quest for Neoantigens
14:20-14:40	Pouya Faridi Monash University, Australia Title: The Trans Effect of Driver Mutations on the Tumour Antigenic Landscape
14:40-15:00	Yansheng Liu Yale School of Medicine, USA Title: Proteome and Phosphoproteome Turnover Atlas: From In Vitro to In Vivo
15:00-15:20	Nguan Soon Tan Nanyang Technological University, Singapore Title: A Multi Organomics Map Reveals Complementary Metabolic Rewiring by GLP 1 and Dietary Reversion Using the MASLD Mouse Model
15:20-15:35	Zhen Liu Nanjing University, China Title: Cracking the Glyco-Code
15:35-15:50	Qun Zhao Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China Title: Large-Scale Mapping of Dynamic Protein Complexes in Cells by in Vivo Crosslinking Mass Spectrometry
15:50-16:05	Lunzhi Dai Sichuan University, China Title: Internal Standard–Assisted Profiling of Protein Modifications in Low-Input Samples
16:05-16:15	Miaohsia Lin National Taiwan University, Chinese Taipei Title: Layer-Resolved Proteomic Profiling of the Cornea After Trigeminal Denervation

Industry Seminars

Bioinformatics Solutions Inc. (BSI)

Oct 13, 2025 12:30-13:30 (Lingnan Convention Hall)

Speaker: Anthony Purcell, Professor, Monash University

Title: Advances in DIA and its Applications in Immunopeptidomics

Speaker: Hui Ye, Professor, China Pharmaceutical University

Title: Chemoproteomics-Empowered Target Discovery

Speaker: *Chenxi Jia*, *Professor*, *National Center for Protein Sciences (Beijing)*Title: PEAKS Studio Enables an In-Depth Analysis of the Neurochemical Signaling

Syncell Inc.

Oct 13, 2025 12:30-13:30 (Maoming Hall)

Speaker: Jung-Chi Liao, PhD, Founder & CEO

Title: Optoproteomics: Unbiased Spatial Proteomics at Disease-Associated Sites

Thermo Fisher Scientific

Oct 13, 2025 12:30-13:30 (Meizhou Hall)

Topic: Bringing light to discovery

Speaker: *Haiteng Deng*, *Professor*, *Tsinghua University*Title: Finding the Fountain of Youth by Mass Spectrometry

Speaker: Zilu Ye, Principal Investigator, Institute of Systems Medicine, Chinese Academy of Medical Sciences

Title: End-to-end High-Throughput Single-Cell Proteomics

Speaker: Yue Xuan, Ph.D, MBA, Senior Global Product Marketing Manager, Chromatography and Mass

Spectrometry, Thermo Fisher Scientific
Title: Bringing Light to Discovery

Evosep

Oct 13, 2025 12:30-13:30 (Shenzhen Hall)

Topic: Next Generation LC-MS Based Proteomics - New Standards and Future Performance Requirements

Speaker: Prof. Matthias Mann

Title: Missing - will Send You this Hopefully Tomorrow

Gene Company Limited & Covaris

Oct 13, 2025 12:30-13:30 (Shantou Hall)

Speaker: Hu Zhou, Deb Bhattacharyya, Jong Bae Park

Title: Complexities Addressed - Better Sample Prep for Protein Analysis









Tecan

Oct 13, 2025 12:30-13:30 (Jieyang Hall)

Speaker: Xiaofang Zhang, TECAN product manager

Title: Automated Solutions for Proteomics Sample Preparation and Case Studies

Bruker Corporation

Oct 13, 2025 12:30-13:30 (Yangcheng Hall)

Speaker: Prof. Hui Zhang, Johns Hopkins University

Prof. Jinghua Yang, First Affiliated Hospital of Zhengzhou University

Daniel Hornburg Ph.D., Bruker

Title: Bruker 4D-Proteomics with TIMS and PASEF: Go Deeper, Faster, and more Confidently —from Tissue to

Single Cell, from Peptides to Proteoforms —Only on TimsTOF

Olink Proteomics

Oct 14, 2025 12:30-13:30 (Maoming Hall)

Topic: Advancing Proteomics Together - Synergistic tools with PEA and Mass Spectrometry

Speaker: Prof. Zhengming Chen

Title: Pioneering the Future of Precision Medicine Driven by Biological Big Data

Speaker: Jun Fu

Title: Comprehensive Proteomics: Olink × Astral Zoom DIA

Speaker: Jin Xiao

Title: From Insight to Impact: Olink Proteomics in Biomarker Translation

Beijing Qinglian Biotech Co., Ltd.

Oct 14, 2025 12:30-13:30 (Meizhou Hall)

Topic: End-to-End Solution for Clinical Body Fluid Cohort Biomarker Research

Speaker: Yan Wang, Senior Product Manager

Title: Innovative Technology and Applications of Automated Proteomics Prep Platforms

Speaker: Sisi Geng, Ph.D., Bioinformatics R&D Director

Title: Advanced Proteomics Bioinformatic Solutions & Cloud Platform

SCIEX CHINA

Oct 14, 2025 12:30-13:30 (Jieyang Hall)

Topic: Expanding the Boundaries of Proteomics Analysis with Advanced Mass Spectrometry Technologies

Speaker: Prof. Liang Qiao, Fudan University

Title: Deep Coverage N-glycoproteomics based on the ZenoTOF system

Speaker: Dr. Patrick A Pribil, SCIEX

Title: Redefining Sensitivity in Accurate Mass Spectrometry with the SCIEX ZenoTOF 8600 System

Illumina

Oct 14, 2025 12:30-13:30 (Lingnan Convention Hall)

Speaker: Leming Shi, Professor and Director of International Human Phenome Institutes (Shanghai)

Title: Reproducibility of Quantitative Multiomic Data: A Prerequisite for Precision Medicine

Speaker: Krishna Morampudi, Associate Director, Illumina

Title: Illumina Protein Prep Solution: Launch the Next Era of Proteomics

Novogene Co., Ltd.

Oct 14, 2025 12:30-13:30 (Shenzhen Hall)

Speaker: Prof. Xia Shen

Title: From Proteome to Complexome: Unveiling the Next Frontier in Proteogenomics

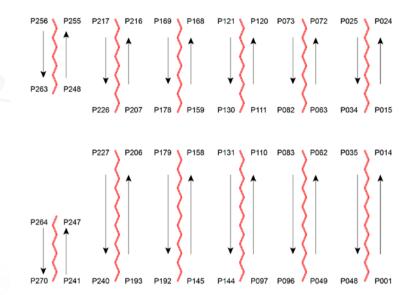








List of Posters I



Number	Title	Author
P001	"All-in-one" Single-Cell Proteomic Analysis of Protein Alterations in Human Oocytes Undergoing In Vitro Aging	Shen Zhang
P002	A Comprehensive Landscape of the Human Body Fluid N-glycoproteome	Fei Cai
P003	A Functionally Tunable Magnetic Nanochains Platform for N-glycoproteomic Analysis of Extracellular Vesicles from Ultratrace Biofluids	Mingyang Li
P004	A High-Density Antibody Array Enables Proteome-Scale Profiling of Post-translational Modifications	Ying Luo
P005	A Machine Learning–Enabled Urinary Protein Signature for the Accurate Diagnosis of Preeclampsia: Discovery and Multi-Center Validation	Jiayi Shen
P006	A methionine/aspartate-rich Nonapeptide Delineated from N-terminal Region of Nucleophosmin Protein Effectively Antagonizes Cadmium Toxicity	Daoran Liu
P007	A Multidimensional Proteomic Analysis of Brain metastases (BrMs) and Gliomas	Xiaohui Liu
P008	A new Platform for Detecting the Novel Protein Post-translational Modification of Lactylation Based on High-density Antibody Array	Panning Wang
P009	A Novel and Efficient DNA Mini-Column-Based Method for High-Throughput Proteomic Sample Preparation in 96-Well plates	Ying Zhang
P010	A Novel Effector for Ambient Particulate Matter Induced Hepatic Metabolic Reprogramming: Site-Specific Cysteine Oxidation on Carnitine Palmitoyltransferase II	Zuowei Xu

Number	Title	Author
P011	A Practical Guide to Experimental Design and Power Analysis for Metaproteomics Studies	Luman Wang
P012	A Protein-Centric Strategy Coupled with Match-Between-Run Glycoproteomics Enables Discovery of Robust Site-Specific Glycan Biomarkers for Hepatocellular Carcinoma	Lei Liu
P013	A Robust and Streamlined Sample Preparation Workflow for in Vivo Single-cell Proteomics via SPRINT	Wenbo Dong
P014	A Scalable Experimental–Computational Pipeline for Linear and Conformational Antibody Epitope Discovery	Zigan Sha
P015	A Thermal Proteome Profiling Reveals Meltome Upon NLRP3 Inflammasome Activation	Jian Wang
P016	A Rapid and Efficient Preparation Method for Phosphoproteomic of FFPE Samples	Liangyu Chen
P017	AbNovoBench: A Comprehensive, Standardized, and Reliable Benchmarking System for Evaluating Monoclonal Antibody De Novo Sequencing Analysis	Wenbin Jiang
P018	ACSS2 Coupled with KAT7 Regulates Histone β-hydroxybutyrylation to Promote Transcription and Tumor Cell Growth	Siyu Wang
P019	Activity-Based Protein Profiling Identifies Immune-Regulatory Targets of Indole- 3-carboxaldehyde	Jingzhuo Chen
P020	Advancing Proteomics Strategies for Investigating Protein Post-translational Modifications	Jinjun Gao
P021	AllerMap: High-Throughput, Epitope-Resolved IgE Profiling for Precision Allergy Diagnosis and Intervention	Wenjing Du
P022	Alterations of Proteome Profiles in the Aged Rats Brain	Hamizah Shahirah Hamezah
P023	An Al-driven De Novo-based Multi-omics Platform for Discovering Cancer- specific Non-canonical HLA-I Peptides	Baozhen Shan
P024	An Integrated Workflow Combining Selective Precipitation and SPE for Deep Top-Down Proteomics Profiling of the Human Serum Proteome	Ning Liu
P025	APPLE-MS: An Affinity Purification-mass Spectrometry Method Assisted by PafA-Mediated Proximity Labeling	Shihan Luo
P026	Artificial InteLligence-drivEn Autoantibody Reactome Analysis SysTem, ALERT	Bomiao Yu
P027	Associations of Plasma Proteomic and Polygenic Profiling with Incident Psoriasis Risk: A Prospective Cohort Study	Jingyi Fan
P028	Asymmetric Protein Abundance Among Blastomeres of Pre-implantation Mouse Embryos Revealed by Single-cell Proteomics	Mo Hu







Number	Title	Author
P049	Cross-species Atlas of Thyroid Aging and Intervention Strategies	Yingrui Wang
P050	Deciphering Drought-Induced Proteomic Shifts in Banana (Musa acuminata Colla cv. Berangan)	Lau Su Ee
P051	Deciphering Ectodomain Shedding of Membrane Proteins in Pancreatic Cancer: Mechanisms and Functional Implications	Changying Fu
P052	Deciphering Plant-Insect Molecular Interplay: Mass Spectrometry-Driven Discovery of Elicitor Perception Complexes and Effector-Mediated Defense Suppression	Xueying Chen
P053	Deciphering the Mechanism of Interactions Between Polyubiquitin Chains and Caspase Activation and Recruitment Domains using Protein-polymer-engineering-assisted Native Mass Spectrometry	Qingrong Chen
P054	Decoding Protein Glycosylation by an Integrative Mass Spectrometry-based De Novo Sequencing Strategy	Jing Gao
P055	Decoding Subcellular Spatio-temporal Landscapes of Transcriptomics and Proteomics during the Oocyte-to-Zygote Transition	Jun Zhu
P056	Deconvolution of Multiplexed Peptidoform Mass Spectra Enables High-resolution Profiling of Complex Protein Modification Patterns	Zhiyuan Cheng
P057	Deep Learning-Driven Proteomic Discovery of Novel Antimicrobial Peptides from Deep-Sea Microbiomes	Bairun Chen
P058	Deep N-Terminomics Using a Cleavable 2-Pyridinecarboxaldehyde Probe and Its Application in Colorectal Cancer Research	Xiaohan Song
P059	Deep Proteomics of Peritoneal Dialysis Effluents Unveils a Comprehensive Landscape Across Dialysis Durations	Ruolin Li
P060	Deeply Profiling the Secretome of Lung Adenocarcinoma Organoids	Wenhui Wu
P061	Development and Validation of a Novel Myeloid-Targeted Therapeutic Regimen	Yukun Wang
P062	Development of a Glycopeptide Spectrum Classification Model Based on Oxonium Ion Characteristics	Lehan Chen
P063	Development of a Laser Capture Microdissection-guided Spatial Proteomics Platform for Layer-resolved Retinal Proteome in Ocular Study	Jennifer Bian
P064	DIA-BERT2, a DIA Software Based on Pre-trained End-to-end Transformer Models using 15,000 DIA Maps	Zhiwei Liu
P065	Differential O-glycoproteomic Analysis Regulated by GalNAc-T13 in Mouse Brains	Tao Deng
P066	Discovery of Immunotherapy Response Predictive Biomarkers for Non-small cell Lung Cancer Based on Serum Proteomics	Yao Min
P067	Dissecting Diazirine Photo-reaction Mechanism for Protein Residue-specific Cleavable Photo-cross-linking	Yida Jiang







Number	Title	Author
P068	Dual-Affinity HZIF-1Mo Microcolumn Platform for Quantitative Profiling of N-Phosphorylation in Breast Cancer Subtypes	Yechen Hu
P069	Dual-Spray Tandem LC system Improves MS Utilization and Throughput in MS-based Proteomics	Lei Gu
P070	Dynamic Proteomics and PTMomics Reveal Mycobacterial Response Mechanisms to Clinical Anti-TB Drugs and Polyphenols	Mingya Zhang
P071	Dynamics of Acetylome of Temperature-influenced Aging in Caenorhabditis Elegans	Guangxu Hu
P072	EasyDIA pipeline: Proteomics is Becoming More Automated and Intelligent	Xinrui Li
P073	Enhancing Analytical Precision in Proteogenomics through Mutation-Informed Proteomic Analysis	Yiwei Ling
P074	Evaluation of a Commercial Nanocapillary Electrophoresis Device ("ZipChip") for Top-down Proteomics of Histones	Ansgar Poetsch
P075	Exploring the Role of Axl in Chemo-Drug Resistance in Gastric Cancer Based on Multiple Proteomics	Miaomiao Tian
P076	FF tags-BiocatDEL: Biocatalytic and Chemoproteomic-Guided Discovery of PHGDH Inhibitor from DNA-Encoded Libraries Selection Platform	Yiwei Zhang
P077	Fibroblast-Linked T Cell Distribution in Glioblastoma Revealed by Multiplex Imaging	Xiaoyu Pu
P078	Filter-Aided Expansion Proteomics for Spatial Analysis of Single Cells and Organelles in FFPE Tissues	Zhen Dong
P079	Fully Automated Workflow for Solid-Phase Extraction (SPE)-Based Sample Preparation with Positive Pressure Enabling High-Throughput Proteomics	Yini Pan
P080	Fully Functionalized Fragments for Integrated Antiviral Screening and Host Target Identification	Jianpiao Cai
P081	Genetic Link Between Metabolic Syndrome and Coronary Artery Disease: Insights From Genome-Wide Cross-Trait Analysis	Pengcheng Yi
P082	Genetic Mapping of Lifespan and Mitochondrial Stress Response in C. Elegans	Xiaoxu Li
P083	Global Analysis of Endogenous Protein Disorder in Cells	Shouxiang Zhang
P084	Global Analysis of Protein Modifications Reveals Faecalibacterium-mediated PRDX6 Acetylation Protecting Against Primate Gut Inflammaging	Siyu He
P085	Global Characterization of Mouse Testis O-glycoproteome Landscape During Spermatogenesis	Xia Zou
P086	Global Methylation Profiling by Selective Release of Methylated Sites from Immobilized Tryptic Peptides	Mingwei Sun

Number	Title	Author
P087	Glycoproteomic Profiling and Clinical Significance of IgG and IgG Glycosylation in Arthritis Patients	Yujiao Zhao
P088	HARD: Human Autoantibody Reactome Database	Mansheng Li
P089	High-coverage, High-confidence De Novo Peptide Sequencing using Mirror Proteases and Deep Learning	Zixuan Cao
P090	High-Throughput Automated STEX Platform: A novel Approach for Antiviral Drug Target Discovery	Qiong Wu
P091	High-Throughput Discovery of Differential Subcellular Protein Localization During Chemotherapy Resistance in Triple-Negative Breast Cancer	Shijun Yang
P092	High-Throughput Discovery of Functional N-glycosylation Sites for Protein Stability by Thermal Glycoproteome Profiling	Shulei Liu
P093	High-Throughput Screening of Covalent Probes Targeting Reactive Lysines in the Human Proteome	Qihe Jiang
P094	HLA-A*02 Mono-allele Specific Immunopeptidome	Ping Wu
P095	Hypothermic oxygenated Machine Perfusion (HOPE) Mitigates Hepatic Cold Ischemia-reperfusion Injury in Donation After Circulatory Death (DCD) Livers by Modulating Glutathionylation-mediated Glycerophospholipid Metabolism	Lele Zhang
P096	Identification of Metastatic Breast Cancer Biomarkers by Integrative Transcriptome and Proteome Analyses	Penchatr Diskul-Na- Ayudthaya
P097	Identification of SIRT3 as an Eraser for Histone H3K9 Lactylation by Antibody- mediated Proximity Labeling Chemoproteomics	Mingzhe Li
P098	Identification of TNR as a Hippocampal Marker of Novelty Seeking Behavior with Integrated Quantitative Proteomics and Systems Genetics Approaches	Jiahui Liu
P099	In Vivo XL-MS Enables Large-Scale Mapping of Protein-Protein Interaction Networks in Cells	Beirong Zhanç
P100	In Situ Formaldehyde Cross-linking Mass Spectrometry Analysis by Real- time Isotopic Signature Targeted Profiling	Tianyu Feng
P101	Informing Enzyme Design via Native Top-Down Mass Spectrometry	Mowei Zhou
P102	Integrated Approach of Ascites Secretome and Single-cell Cross-tissue Mapping Reveals Paracrine Regulatory Protein Targets in HGSOC Metastasis	Ting Chen
P103	Integrated Multi-Omics Analysis Reveals the Impact of Vaginal Microbiota on the Microenvironment During Cervical Precancerous Progression	Jianxvjie Zheng
P104	Integrating Environmental Metaproteomics into Multi-Omics Frameworks to Support Efficient Exploration of Hydrothermal Vent Microbiota	Weiyi Li







Number	Title	Author
P105	Integrating Multi-omics Strategies Reveals Novel Genetic risk loci of Diabetes- Associated Fibrosis	Yu Ma, Enhui Wang, Quanting Yin, Zhiwei Liu, Fuyi Xu
P106	Integrative Multi-omics Analyses Reveal the Global Regulation Network of the Microalga Nannochloropsis Oceanica Under Nitrogen Stress Adaptation	Can Xu
P107	Integrative Proteomic and Post-Translational Modification Analysis Reveals Metastasis-Associated Regulatory Networks in Pancreatic Cancer Cell Lines	Jie Song
P108	Integrative Spatially Resolved Proteomic and Metabolomic Imaging Reveals Synovitis Endotypes Implicated in Osteoarthritis Progression	Lin Zhu
P109	Integrative Transcriptomic and Proteomic Analysis Reveals DAO-mediated Mechanisms of Idiopathic Pulmonary Fibrosis	Hui Liu
P110	Investigation on the Breast Milk N-glycoproteome in Gestational Diabetes Mellitus	Shuai Zhu
P111	Label Free Quantification using the Orbitrap Astral: a perspective from the Mass Spectrometer Maintainer	Jianfeng Zheng
P112	Lactylation Proteomics in Brain Organoids-on-a-chip Reveals ZIKV Microcephaly Mechanisms	Yu Wang
P113	Large-Scale Analysis of Autoantibody Reactome in Lung Cancer Cohorts with Immunotherapy-Related Adverse Events	Ruimin Liu
P114	Large-scale Analysis of Autoantibody Reactome in Mice that Experienced Microgravity and Radiation	Lining Wu
P115	Large-Scale Glycoproteome Analysis Reveals Inverted Distribution of Neu5Gc and Neu5Ac in Mouse Liver tissues and Cell Lines	Jialin Liu
P116	Large-scale Proteomic Analysis of Intercellular Protein Complex	Jiangnan Zheng
P117	Layer-Resolved Proteomic Profiling of the Cornea After Trigeminal Denervation	Miao-Hsia Lir
P118	Low-input Citrullinomics and Deep Learning Reveal Insights into Rheumatoid Arthritis Onset, Treatment Response and Autoantigens	Meng Hu
P119	Macrophages Undergo a Metabolic Switch from Glycolysis to Fatty acid Metabolism Through GAPDH Carboxyethylation	Kefei Wu
P120	MALDI-TOF MS-Based Serum Peptidome Analysis for Biomarker Discovery in Feline Chronic Gingivostomatitis	Sekkarin Ploypetch
P121	Mapping the Substrate Landscape of Lysine Acetoacetylation Through Chemical Proteomics	Yanan Zhenç
P122	Mass Spectrometric Characterization of Synthetic Acylated Peptides	Wangya Yang

Number	Title	Author
P123	Mass Spectrometry-Based Spatial Multiomics Revealed Bioaccumulation Preference and Region-Specific Responses of PFOS in Mice Cardiac Tissue	Wenlong Wu
P124	MassNet: A 35-species Proteomics Corpus from 28,000 DDA-MS Files for Building Pretrained Models	Jun A
P125	MCOD: Memory Constraint for Anomaly Detection in Quantitative Proteomics Data	Jinze Huang
P126	Mechanoresponsive Proteome Remodeling Reveals Pan- Cancer Adaptation Strategies to Microenvironmental Stress	Jiawei Dai
P127	Membrane Proteome Profiling on Metastatic Pancreatic Ductal Adenocarcinoma (PDAC) Cell Line	Lim Lay Cheng
P128	Metaproteomics Reveals Community Coalescence Outcomes in Co□Cultured Human Gut Microbiota	Boyan Sun
P129	MetaSpaR-DIA: Enabling Accurate Metaproteomic DIA Analysis Independent of Spectral Libraries and Metagenomic Sequencing	Songduo Wang
P130	Mining Dark Proteome: Shedding Lights on Unannotated Human Proteins	Yafeng Zhu
P131	Molecular Imprinting of Phospholipids for Targeted Cell and Exosome Recognition	Luxi Chen
P132	MSIPep: Immunogenic Peptide Identification Pipeline Based on Immunopeptidome and Proteogenomic Strategies for tumor Antigen Discovery	Xiaoxiu Tan
P133	Multi-center Multi-omics Integration Predicts Individualized Prognosis in Medullary Thyroid Carcinoma	Yan Zhou
P134	Multi-omics Application in Kidney Cell Carcinoma	Jiaming Guo
P135	Multi-omics Elucidation of Molecular Mechanisms for Antibody Level Differences in Elderly Post-COVID-19 Infection	Guobin Han
P136	Multi-omics Integration Reveals the Genetic Architecture and Candidate Therapeutic Targets of Aortic Stenosis	Zhiwei Liu
P137	Multi-omics Knowledge Graph for Interpreting Type 2 Diabetes Mellitus Biomarkers	Shuaishuai Wu
P138	Multi-omics Profiling Uncovers SDHB as a Central Regulator of the TCA-Cardiolipin Axis in Atherogenic Foam Cells	Ling Lin
P139	Multi-omics Studies Reveal Combined Traditional Chinese and Western Medicine Treatments Accelerate Systemic Recovery in AECOPD	Xinglin Zhou
P140	Mycobacterial PstP Impairs Host RNA Alternative Splicing by Dephosphorylation of Spliceosome RBMX at S189	Tianxian Liu
P141	Neuron–Tumor Crosstalk Drives Glioblastoma Recurrence Revealed by Integrated Multi-Omics	Fei Zheng







Number	Title	Author
P142	New Liquid Junction Interface in Capillary Electrophoresis-Mass Spectrometry for Top-down Proteomics Applications	Mengting Zhang
P143	Noninvasive Biomarker Discovery for Hepatitis B Virus-related Liver Disease Based on High-throughput Extracellular Vesicle Proteomics	Fengzhang Wang
P144	Not Aging But Calorie Restriction Strongly Affects Protein Oxidation in Heart and Brain Mitochondria	Shipan Fan
P145	OmicsEase: An Al-based Proteomic Data Analysis Learning and Practice Platform	Wenhao Shi
P146	OmixNetExplorer: Integrative Construction and Stability Assessment of Multi- Layer Biological Networks	Zhanlong Mei
P147	OmniProt V2 Powered by LingBot: A Magnetic Nanoparticle-Based Automated Workflow for Deep Plasma Proteomics from 10 µL Samples	Liqin Qian
P148	OpenLink: Explore Unexpected Chemical Crosslinking Peptides	Jinyang Li
P149	Optimization of Enzymatic Digestion Conditions for Microscale Mammalian Cell Samples Based on Trifluoroacetic Acid Lysis	Ye Tian
P150	Optimization of the Routine Approach for Label-Free Single-Cell Proteomics Using timsTOF Pro2 MS	Liying Chen
P151	OSaMPle Workflow for Salivary Metaproteomics Analysis Reveals Dysbiosis in Inflammatory Bowel Disease Patients	Jinhui Yuan
P152	Oxidation-Induced Structural Destabilization of βB2-Crystallin: Mechanistic Insights into Trp59/Trp151-Dependent Oligomerization and Cataract Pathogenesis	Jiayue Sun
P153	P130 Regulates Macrophage Polarization Through Mitochondrial Metabolism Reprogramming	Jinfang Liu
P154	PAC-PELSA: Peptide-Centric Local Stability Assay for Rapid and Sensitive Drug Target Identification in Limited Samples	Jiaqin Chen
P155	Pan-Protein Modification Omics Reveals Novel Serum Biomarkers and Complement Therapeutic Targets in Membranous Nephropathy	Chunli Wei
P156	Pan-Respiratory Virus Protein Microarray Reveals Diminished IgG Responses to Non-SARS-CoV-2 Viruses Post-Pandemic	Surbhi Bihani, Arka Ray
P157	Peptide-based Disruption of Disease-relevant Protein-protein Interactions as a Novel Strategy for Autophagy Restoration	Jungmin Ha
P158	Philippine Teredinibacter turnerae leverage multiple Polysaccharide Utilization Loci for Pectin Catabolism	Joan Catherine A. Chua
P159	Phosphoproteomic and Acetylomic Characterization of Colorectal Cancer Cells Treated with Kinase Inhibitors	Lei Zhao

Number	Title	Author
P160	PiSPA: Automated Single-Cell Proteomics for CTC Heterogeneity and Migration Studies	Yu Wang
P161	pLink3: Unified Analysis of Large-Scale Crosslinking Proteomics Data	Pengzhi Mao
P162	Pmultiqc: An open-source, Lightweight, and Metadata-oriented QC Reporting Library for MS-proteomics	Qixuan Yue, Mingze Bai
P163	Population-based Metaproteomics Reveals Functional Associations Between Gut Microbiota and Phenotypes	Yingying Sun
P164	Potential Compensatory Mechanism for ESBLs and Carbapenemase Production in Klebsiella Pneumoniae: Insights from Data-independent Acquisition Proteomics	Haowen Jiang
P165	Preventive Maintenance and Daily Operation Protocol for the Orbitrap Astral	Beiyi Chen
P166	ProExplorer: An Interactive Platform for Comprehensive Analysis of Protein Modifications and Their Functional Implications	Chenxia Li
P167	Proteomic Analysis Reveals Modulation of Key Proteins in Follicular Thyroid Cancer Progression	Xue Cai
P168	Profiles of Changes in the Early-Stage Proteome and Phosphoproteome during LPS-Induced Macrophage Polarization	Wanmeng Li
P169	Protein-level Batcheffect Correction Enhances Robustness in MS-based Proteomics	Qiaochu Chen
P170	ProteinTalks: An Al Virtual Cell Foundation Model Extended to Clinical Application	Rui Sun
P171	Proteogenome and Peptidogenome Atlas of Ginseng Enhance the Understanding of Gene Product Function in Medical Plant	Baojin Zhou
P172	Proteogenomic Profiling Reveals Small ORFs and Functional Microproteins in Activated T Cells	Yang Yang
P173	Proteogenomic Reannotation of Mycobacterium avium Reveals Novel Species- Specific ORFs Enabling Enhanced Strain Discrimination	Yuwei Zhang
P174	Proteome-wide Detection and Analysis of Translation Errors in Human Cancer	Danqing Shen
P175	Proteomic Analysis Reveals the Effect of Mitragynine Supplementation in Rat Model of LPS-Induced Neuroinflammation	Zhanqing Luo
P176	Proteomic Classification and Clonal Evolution of IDH-mutant Astrocytoma Through Pan-omics Integration	Jihong Tang
P177	Proteomic Investigation into the Mechanisms of Aluminum Exposure-Induced Developmental Toxicity in Mice	Xiaoyuan Hu
P178	Proteomic Investigation into the Molecular Mechanisms of Bacterial Response to Erythromycin Stress	Chenchen Mao
P179	Proteomic Landscape of Renal Tissue in Diabetic Kidney Disease	Yingying Ling







Number	Title	Author
P180	Proteomic Profiling of Cerebrospinal Fluid Uncovers Distinctive Pathophysiological Changes and Potential Biomarkers in Pediatric Tubercular Meningitis	Jing Wei
P181	Proteomic Profiling of Mouse Ovarian Tissues Undergone Cryopreservation	Wenxuan Hou
P182	Proteomic Profiling Reveals Regional Network Dysregulation in Alzheimer's Disease Pathogenesis	Tian Chen
P183	Proteomics Profiling of Small Cell Lung Cancer Patients Reveals Embryonic Developmental Pathways as Prognostic Markers via Dedifferentiation Reversal	Haonan Gu
P184	Proteomics Study on Both of Liver and Brain Combined with Mendelian Randomization Identifies Key Proteins Affected by YL0919	Yudai Yang
P185	ProteomicsAnalyzer: A Scalable and Integrated Platform for Robust Multi-Source Proteomics Data Harmonization, Differential and Functional Analysis	Yan Ren
P186	Proteomics-based Genetic Analyses Identify Causal Endophenotypes at Cell- type Resolution and Prioritize Drug Targets for Chronic Pancreatitis	Yahui Wang
P187	Proteomics-Based Study on Expression Dynamics of a Novel Biomarker Candidate in Interstitial Lung Disease Rat Models	Ayaka Yoshida
P188	Proteomics-Driven Target Deconvolution of D36, a Natural Product-Derived Anti-Acute Myeloid Leukemia Agent	Jingwen Liu
P189	Protocol for Structural Analysis of Amyloid Fibrils using Hydrogen/deuterium Exchange Mass Spectrometry	Qian Meng
P190	Proximal Proteomics Reveals a Landscape of Human Nuclear Condensates	Feng Liu
P191	Quantification of Multiple β-Amyloid Isoforms in Cerebrospinal Fluid Using Cation Exchange Chromatography Coupled with Mass Spectrometry	Shuhui Gao
P192	Quantitative Analysis of Albumin Redox State Variations with Age via Tandem Mass Spectrometry	Meng Han
P193	Quantitative Chemoproteomics Reveals Dopamine's Protective Modification of Tau	Youjia Wang
P194	Quantitative Glycoproteomic Analysis Reveals High Prevalence and Functional Roles of Atypical N-Glycosylation in Plasma and Trastuzumab	Siyuan Kong
P195	Quantitative Glycoproteomics Reveals MPO Glycoforms and ECM–Lysosome Dysregulation in Gallbladder Cancer	Haiyang Li
P196	Quantitative Screening Towards Hemoglobin Subunits in the Thalassemia Carriers of Pregnant Women using Target Proteomics	Yixi Cai
P197	Quantms-rescoring and Multiple Search Engines Consensus Identification Enables Deep Proteome Coverage Across Label Free, Multiplex, Immunopeptidomics, and Phosphoproteomics Experiments	Chengxin Dai
P198	Rapid Single-Cell Proteomics using Nanoconfined Enzyme Reactors on a Microscale Digital Microfluidics Platform	Hang Li

Number	Title	Author
P199	Rational Prediction of Drug Combinations Basedon Large-scale Perturbation Proteomics	Liujia Qian
P200	Region-resolved Proteomic Dissection of Aging Mouse Heart Uncovers the Protective Role of FTL1 and SPERINA3K in Cardiac Aging	Jingnan Huang
P201	Screening and Validation of Serum Biomarkers for Diagnosis of Mycobacterium Tuberculosis Infection	Huan Qi
P202	Screening of Aβ-interacting Neuropeptides using a Native MS-centric Pipeline and Analysis of the Molecular Mechanism	Yaoyao Bian
P203	Shared Genetic Architecture between Type 2 Diabetes and Cardiovascular traits	Quanting Yin
P204	Silicon-rhodamine-enabled Identification (SeeID) for Near-Infrared Light Controlled Proximity Labeling In Vitro and In Vivo	Hongyang Guo
P205	Simple, Fast and Highly Efficient One-or Two-step Proteomic Pretreatment for Microgram-level FF and FFPE Tissues	Chupin Wei
P206	Single-cell Omics Analysis of Ovarian Cancer Ascites Based on 10x RNA-seq and IBT-16plex Labeling	Weiran Chen
P207	Single-nucleus Proteomics of Human Neurons for Alzheimer's Disease Research via SPRINT	Ruicheng Ge
P208	Site-specific N-glycoproteomic analysis of serum glycoproteins and its application in intrahepatic cholangiocarcinoma biomarker discovery	Jun Li
P209	Solvent-induced Partial Cellular Fixation Approach Enables Proteome-wide Decoding of Drug Targets and Drug-induced Downstream Biochemical Pathways in Living Cells	Ting Yu
P210	Spatial Distribution of the Proteome in Human Body and Cancers	Liang Yue
P211	Spatial Phosphoproteomic Profiling of Murine Heart Reveals Region-Specific Functions via Optimized TiO ₂ Enrichment	Dan Zhao
P212	Spatial Proteomics Analysis onto the FFPE Samples of Esophageal Squamous Cell Carcinoma Treated with Neoadjuvant Therapy	Ping Feng
P213	Spatial-GTPformer: A Generative Model for Translating Spatial Transcriptomics to Proteomics	Yimeng Qiao
P214	Spatially-resolved TRAP for In Situ Characterization of Drug Target Landscapes	Chunyu Li
P215	Spatiotemporal Profiling of Modification-specific Proteome Secretion Uncovers an Itaconation-activated tyrosine Kinase	Wenjie Lu
P216	Spatiotemporally Resolved Mapping of Extracellular Proteomes via in Vivo- compatible TyroID	Zijuan Zhang







Number	Title	Author
P217	Stereochemical Modifications Drive Structural Transformations and Functional Alterations in Tau Protein	Weida Qin
P218	Structural and Site-specific N-glycoproteomic Analysis Reveals Distinct Glycan Structure Alterations in Clear Cell Renal Cell Carcinoma	Yingjie Zhang
P219	Structural Characterization, Target Discovery, and Rational Modification of the Neuroprotective Peptide Bidentatide	Xiaozhe Zhang
P220	Structural Proteomics and Modelling Identifies Key Interacting Residue and Compact Conformation of Dengue NS2B-NS3 Complex	Zheng Ser
P221	Subcellular Proteome Dynamics Reveal Anti-inflammatory Drug Mechanisms	Yanan Yang
P222	Systematic Evaluation of Evosep One system For Ultra High-throughput Proteomics	Xinyao Yu
P223	Systematic Profiling of SHC1 Complexes in Living Cells with Proximity Labeling	Peng Zhang
P224	Target Identification of Vanillic Acid in the Regulation of Intestinal Epithelial Ferroptosis via PISA-proteomics	Jiahui Ni
P225	Temporal Proteomic Remodeling During DLD-1 Cancer Stem Cell Induction Reveals Stage-Specific Network Dysregulation	Yacheng Wang
P226	Tetrazine-phenol Probe for Hydrogen Peroxide-independent APEX2 Proximity Labeling in Living Animals	Boyi Chen
P227	The Effect of Moringa Oleifera Leaves Extract on Cognitive Changes and Protein Modulation in Lipopolysaccharide (LPS)-Induced Neuroinflammation Rats	Chenyu Zhou
P228	The Functional Landscape of the Human Ubiquitinome	Julian van Gerwen
P229	The Invasive Progression Characteristic of Papillary Thyroid Microcarcinoma is Unveiled by Spatial Proteomics	Jun Luo
P230	The Study of RNA-protein Interactions Based on Proteome Thermal Stability Shift Induced by RNA Degradation	Yi Liu
P231	The Urinary Proteome in Aging Mouse Models Reflects Changes in the Cerebral Cortex	Mengzhen He
P232	Thermal Proteome Profiling Reveals G6PD as a Target of the Diterpenoid Lathyr ol in A549 Cells	Zhaoxuan Li
P233	Time-resolved Proteomic Profiling Reveals TRAIL-induced Dynamic Signaling Networks in Non-small Cell Lung Cancer Cells	Yi Zhong
P234	Total-sync Ultra-content Microscopic Opto-biotinylation Enables High-sensitivity Hypothesis-free Subcellular Protein Discovery	Jiaojiao Jin

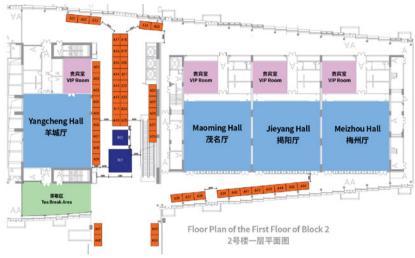
Number	Title	Author
P235	Towards Unmanned Proteomics Data Generation: A Fully Automated Sample-to- Data System for Proteomic Experiments	Dongxue Wang
P236	Transformer-based De Novo Peptide Sequencing Methods: A Comprehensive Benchmarking on Monoclonal Antibody	Jiajia Xu
P237	Transforming Single-cell Proteomics to High Throughput via SPRINT System	Zhen Liu
P238	Tumor Neoantigens Identified via High-efficiency Immunopeptidomics Trigger Potent Cytotoxicity Against Hepatic Carcinoma Cells	Kexin Ding
P239	Ultra-Sensitive Quantitative Proteomics: Achieving Deep Coverage with ZT Scan DIA at Sub-Nanogram Loadings on ZenoTOF 8600	Song Yang
P240	Uncovering PROTAC Sensitivity and Efficacy by Multidimensional Proteome Profiling: A Case for STAT3	Yuying Suo
P241	USP14 and UCHL5 Synergistically Deubiquitinate PKCα and Translocate NF-κB to Promote the Progression of Anaplastic Thyroid Cancer	Bing Han
P242	VistaProX™: A Comprehensive Platform for High-Resolution Spatial Proteomics and Workflow Standardisation	Huaping Li
P243	Whole-Cell Proteome, and Phospho-proteome, Nascent Proteome, Ribosomal Proteome Reveal Cellular Dynamics and Adaptation During Heat Stress	Jiawei Dai
P244	XA-Novo: An Accurate and High-throughput Mass Spectrometry-based De Novo Sequencing Technology for Monoclonal Antibodies and Antibody Mixtures	Yueting Xiong
P245	π-HelixNovo2: Making Accurate Online De Novo Peptide Sequencing Available to All	Tingpeng Yang
P246	π-MultiOmics: A Unified Workflow for Integrated Genome, Transcriptome, Proteome, and Phosphoproteome from a Single Sample	Shuyi Feng
P247	π-NovoQC: An End-to-end Platform for De Novo Peptide Quality Control and Quantification	Zhendong Liang
P248	π-SPECFormer: A Foundation Model for Decoding the Dark Proteome through Self-Supervised Learning	Tianze Ling
P249	π-UrinePro: A ZASP-Based Standardized Workflow for Urinary Proteomics	Qingjing Chen







Exhibition



Booth	Company		
B01	Bioinformatics Solutions Inc. (BSI)		
B02	ProteinT (Tianjin) Biotechnology Co., Ltd		
A01-A02	Illumina		
A03	Fujifilm Wako (Guangzhou) Trading Corporation		
A04	Nanomics Biotechnology		
A05	Novogene Co., Ltd.		
A06	Opentrons Labworks Inc,		
A07	Beijing Jm Instrument Co., Ltd		
A08	Shenzhen BayOmics Biotechnology Co., Ltd		
A09	Shanghai Bioprofile Technology Co., Ltd		
A10	Shanghai Omicsolution Co., Ltd.		
A11	Suzhou Motif Biotech Co., Ltd.		
A12	Wuhan Metware Biotechnology Co., Ltd.		
A13-A14	Jingjie PTM Biolab (Hangzhou) Co. Inc PTM Bio LLC		
A15	Proteoformics Biotechnology Co., Ltd.		
A16	Secretech		
A17	Lc-Bio Technologies (Hangzhou) Co., Ltd.		
A18	Olink Proteomics		
A19-A20	Thermo Fisher Scientific		
A21	Evosep		
A22	Hangzhou Neuchan Biotech Co., Ltd.		
A23	SCIEX CHINA		
A24	Anhui Guoping Pharmaceutical Co., Ltd.		

Booth	Company
A25	Gene Company Limited Covaris
A26	TECAN
A27	Shanghai Easymass Co., Ltd.
A28	ProteoEdge
A29-A30	Westlake Omics (Hangzhou) Biotechnology Co., Ltd.
A31	Molecular Machines & Industries GmbH
A32	Shanghai Biotree Biotech Co., Ltd.
A33	Alamar Biosciences
A34	ACX Instruments Ltd.
A35	ProteomicsEra Medical Co., Ltd.
A36-A37	Bruker Corporation
A38	Shanghai OE Biotech Co., Ltd.
A39	Shenzhen Wininnovate Biotech Co., Ltd.
A40	Beijing Qinglian Biotech Co., Ltd.
A41	Shanghai Applied Protein Technology Co., Ltd.
A42	Hangzhou Micrometer Biotech Co., Ltd.
A43	Beijing Shengxia Proteins Scientific Ltd
A44	Beijing Qinglian Biotech Co., Ltd.
A45	ChomiX Biotech Co., Ltd.
A46	National Center for Protein Sciences · Beijing
A47	Nanjing EVLiXiR Biotechnology Co., Ltd.
A48	BGI Tech Solutions Co., Ltd.
A49	Agilent Technologies Inc.
A50	International Academy of Phronesis Medicine (Guangdong)

Sponsorship |













































































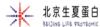


































Note:	
vote.	
ALL STATE OF THE S	<u></u>



展位号: A50



The 1st π-HuB Industry Conference

π-HuB Park 产业园官宣

大会亮点

首度官宣

π-HuB的顶层产业逻辑、产业园发展规划及核心产业模块布局, 描绘协同共生的创新生态全景

现场签署

与全球头部企业的重磅战略合作协议,π-HuB产业园一期孵化器 企业入驻,以及生态伙伴建设,共同谱写合作新篇章

集中亮相

颠覆性的新技术、新产品,见证产学研融合创新力量



2025年10月13日 14:00-17:00



会议地点

广东省广州市 白云国际会议中心・清和厅



、 东智慧医学国际研究院(IAPM)

联系方式

联系人: 罗老师

联系电话: 18826052417

邮箱: 1365628751@qq.com

官网: https://www.pi-hub.org.cn/

公众号二维码:





MT8000

mindray迈瑞

全实验室智能化流水线

畅行检验高质路

强效能

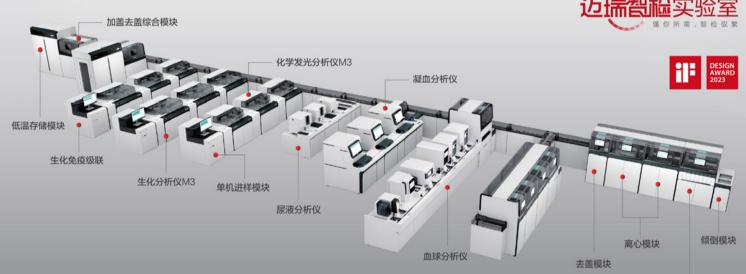
- 精巧设计,极致空间管理
- 三合一进出样设计
- 四轨超万速
- 多设备在轨直连

融生态

- 多元拓展, 促进生态融合
- 多学科联合, 助力医院高质量发展
- 区域数据集成,中心化运营管理

智流程

- 多维智慧流程, 为样本检验保驾护航
- 急诊全程优先, 样本实时监控
- 多模态样本质量管理
- 单屏远程操控整条流水线



进出样(含混匀)模块





- 最大离心力4300g 单批次最大装载量80管 具有智能自动平衡功能 支持多模块拓展功能 支持血清余量、 血清质量拍照识别功能



- 模块速度850管/小时
 旋转去盖方式可以减少气溶胶的产生
 具备气溶胶过滤和紫外线消毒功能以防止生物污染
 支持多模块拓展



- 每条轨道处理速度3600管/小时采用4轨道结构,可灵活超车,快速掉头样品管在主轨道和分析仪前轨道上都采用单管传输轨道采用RFID技术对样本进行定位追踪





- 软件采用B/S架构, 支持移动设备(如手机)端直看 能够集中控制并管理在线仪器, 可实时监控检测标本实时状态 和标本位置以及仪器运行状态、试剂信息 开放数据接口并能与本院US和HS系统连接 提供数据接口文档



诺禾致源·精准质谱解决方案 多组学研究的核心引擎

项目经验丰富

9年深耕质谱领域 累计交付项目数5万+ 累计交付样本数100万+



自建高质量代谢数据库 NovoMet-UM 3.0

自建标准品1.5万+ Level 1 检出可达 1700+ 物质总检出可达7000+

科研产出显著

助力客户文章发表项目860+ 累计影响因子6200+



质谱 服务优势



交付智能化

全自动Falcon-MS系统 实现超高通量,保障高效且 稳定交付,年通量高达 100万例样本

全流程服务支持

依托完善的交付服务体系,提供 从方案设计到生信分析的 全流程一站式服务



Novomagic Plus云平台

界面简洁易用,交互体验更佳,多组 学分析一键关联,生信智能专家

多元化质谱检测平台





Olink[®]











代谢组

蛋白质组



北京市朝阳区酒仙桥北路甲10号院301号楼101栋 天津市武清区创业总部基地B07/B08/B09栋 广东省广州市黄埔区发源路企业加速器C6栋西梯701 上海市闵行区浦江镇临港浦江国际生命健康城9号楼









诺禾致源科服

质谱全组学解决方案

代谢组学解决方案

非靶向代谢组	类靶向代谢组	靶向代谢组		空间代谢组
HQ 非靶向代谢组 Pro 66 66 66 66 66 66 66 66 66 66 66 66 66	植物类靶向代谢组 2007 人&动物类靶向代谢组 2007 日本	N500高通量靶向代谢组 ### GM200高通量靶向代谢组 ### 短链脂肪酸 ### 氨基酸 ### 色氨酸 ### EF# EF# EF# EF# EF# EF# EF# EF# EF#	神经递质 有机酸 类固醇激素 植物激素 氧化脂质 神经酰胺	AFADESI空间代谢组 超 (20μm/50μm/100μm) MALDI-TOF空间代谢组 (20μm/50μm/100μm)
脂质组 定量脂质pro		脂肪酸 個現 中心碳相关物质 TMAO及相关代谢物	类黄酮 花青素 个性化靶向代	谢组

蛋白质组学解决方案

Olink蛋白质组解决方案

定量蛋白质组	修饰蛋白质组	定性蛋白质组	Explore 系列
Deep DIA 鍵 Rapid DIA 鍵 血液 HD Blood plus	乳酸化 227 磁酸化 227 乙酰化 227	蛋白定性修饰定性	Explore HT Explore 3072 Explore 1536
宏蛋白质组	泛素化 健养 琥珀酰化	靶向蛋白质组	Explore 384
FFPE蛋白质组	N/O-糖基化	iPRM	Reveal
外泌体蛋白质组 Label free	丙酰化 丙二酰化		Reveal ###
TMT	戊二酰化 甲基化		Target 系列
	甲蚕化		Target 96 Target 48

近2年部分高分项目文章

发表时间	发表期刊	IF	文章题目	合作单位	服务类型
2025/5/2	Bioactive Materials	20.3	Human induced pluripotent stem cell derived nanovesicles for cardiomyocyte protection and proliferation	新加坡国立大学	定量蛋白质组
2025/2/20	SCIENCE	45.8	Base-modified nucleotides mediate immune signaling in bacteria	华中农业大学	定性蛋白质组
2025/2/12	Bioactive Materials	20.3	Metal-phenolic networks specifically eliminate hypoxic tumors by instigating oxidative and proteotoxic stresses	华中科技大学同济医学院 附属协和医院	类靶向代谢组
2025/1/26	Molecular Plant	24.1	Graph-based pangenome provides insights into the structural variation and genetic basis of metabolic traits in potato	云南农业大学	类靶向代谢组
2024/12/25	Cancer Communications	24.9	Orchestrated desaturation reprogramming from stearoyl-CoA desaturase to fatty acid desaturase 2 in cancer epithelial-mesenchymal transition and metastasis	广州医科大学	脂质组
2024/12/5	CANCER CELL	44.5	Mannose metabolism reshapes T cell differentiation to enhance anti-tumor immunity	中国医学科学院北京协和 医学院	非靶向代谢
2024/11/6	Cell Metabolism	30.9	Microbiota-derived lysophosphatidylcholine alleviates Alzheimer's disease pathology via suppressing ferroptosis	首都医科大学基础医学院	非靶向代谢
2024/10/16	Cell Host & Microbe	20.6	Gut symbiont-derived anandamide promotes reward learning in honeybees by activating the endocannabinoid pathway	中国农业大学	非靶向代谢、靶向代谢组
2024/10/3	Cell Metabolism	30.9	Stress triggers irritable bowel syndrome with diarrhea through a spermidine-mediated decline in type I interferon	中山大学附属第三医院	非靶向代谢、定量蛋白质组
2024/9/18	Nature Microbiology	20.5	Taurolithocholic acid protects against viral haemorrhagic fever via inhibition of ferroptosis	中国人民解放军军事医学科 学院微生物流行病研究所	非靶向代谢组
2024/6/21	IMMUNITY	26.3	Cellular spermine targets JAK signaling to restrain cytokine-mediated autoimmunity	中国医学科学院北京协和 医学院基础医学研究所	类靶向代谢
2024/4/2	Cell Metabolism	30.9	A clinical-stage Nrf2 activator suppresses osteoclast differentiation via the iron-ornithine axis	华中科技大学同济医学院	非靶向代谢



Opentrons 全自动移液工作站

自动化您的实验全流程



多种移液器与功能模组自由组合,单通道、8通道、 96通道灵活切换,精准覆盖多元场景

2 开源生态系统

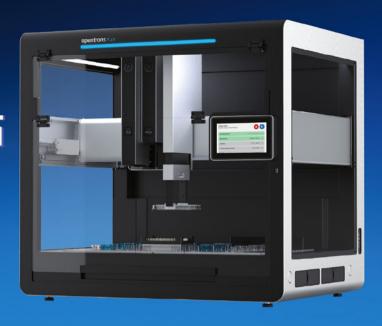
软硬件全开源架构,兼容90%市售实验耗材,支持个性化协议开发,真正实现"您的需求定义设备"

3 国际权威认证

通过FCC与CE资质认证,结合行业出厂校验金标准,确保移液精准度,实验结果可重复性达行业顶尖水平

4 全场景覆盖

集成温控、读板器、热振荡、热循环等核心功能模块, 覆盖类器官、基因组学、蛋白组学等前沿领域



· 为什么选择我们?



全球布局 国际品牌

2024年销量突破 1000台,服务遍及欧 美亚大主流实验室



全球标准 本地响应

中国区设有专属 售后团队,提供 全球品质保证 和本土化服务



物美价优普惠创新

较同级产品降低 30%使用成本 让前沿技术赋能 每个科研梦想

• 应用场景

类器官疾病建模

药物研究

合成生物学

蛋白组学

微生物学

分子育种

检验医学

基因组学



合创生物工程(深圳)有限公司

Opentrons Labworks, Inc.

が 抖音

@opentrons



www.opentrons.com.cn



180 9895 2246





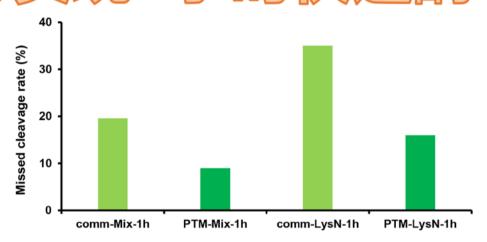
系列蛋白质组学专用

位点特异性超高活性蛋白酶产品

为大队列样本精准蛋白质组学研究提供核心工具



可实现1小时快速感动



序号	产品名称	货号	规格	特性
1	rAc-Trypsin, MS Grade	P01001	25 μg/瓶*4/包	高活性,抗自消化
2	rLys-C, MS Grade	P01002	20 μg/瓶*5/包	高活性,耐受性强
3	rGlu-C, MS Grade	P01003	20 μg/瓶	活性稳定
4	rAc-LysargiNase, MS Grade	P01004	20 μg/瓶	高活性,应用于N端组学
5	rAc-Trypsin/rLys-C Mix, MS Grade	P01005	20 μg/瓶*5/包	超高活性,耐受性佳
6	rsLys-N, MS Grade	P01006	20 μg/瓶	超高活性,耐受性强













SCIEX ZenoTOF 8600 system

质臻匠心

共谱非凡

ZenoTOF 8600 印证非凡

ZenoTOF 8600 系统实现了卓越的灵敏度,同时具备电子活化解离技术 EAD和 Zeno-trap 阱等多功能性的工作流程。该系统可提供支撑重大发现、证实生物学结论的强效数据,助力科研探索迈向新高度。

ZenoTOF 8600 系统核心优势:

- MS1 与 MS2 灵敏度提升高达 10 倍
- 高能 EAD 技术开辟全新研究路径(如 快速数据依赖采集模式)
- 拓展质量范围的 ZT Scan DIA 2.0 技术 赋能大小分子研究
- 提供数据洞察和发现的战略软件解决 方案

探索 SCIEX ZenoTOF 8600 系统的 超凡表现





10x

与 SCIEX 前代仪器相比,不同扫描模式的灵敏度提升 10 倍

SCIEX临床诊断产品线仅用于体外诊断。仅凭处方销售。这些产品并非在所有国家地区都提供销售。获取有关具体可用信息,请联系当地销售代表或查阅https://sciex.com.cn/diagnostics。所有其他产品仅用于研究。不用于临床诊断。本文提及的商标和/或注册商标,也包括相关的标识、标志的所有权,归属于AB Sciex Pte. Ltd. 或在美国和/或某些其他国家地区的各权利所有人。

© 2025 DH Tech. Dev. Pte. Ltd. MKT-36244-A

SCIEX中国

北京分公司

北京市昌平区生命科学园科学园路18号院A座一层 电话: 010-5808-1388

传真: 010-5808-1390

全国咨询电话: 800-820-3488, 400-821-3897

上海公司及中国区应用支持中心 上海市长宁区福泉北路518号1座502室

电话: 021-2419-7201 传真: 021-2419-7333 官网: sciex.com.cn 广州办公室

广州国际生物岛星岛环北路1号B2栋501、502单元

电话: 020-8842-4017

官方微信: SCIEX-China





Duo双功能数字分液仪 重新定义皮升级数字分液仪.

Duo Digital Dispenser™

进阶版D3OOe, 拓展单细胞分液功能

The evolution of D300e. Picoliter dispensing redefined, now for single cells too.

简化您的工作流 Streamline your workflow



☆ 分液精确高和速度快

Highest precision and speed



细胞分液温和 Gentle on cells







扫码关注帝肯生命科学



TECAN自动化蛋白组学样本制备工作站

TECAN automated proteomics sample preparation workstation

自动化•标准化•高通量

三重保障:数据稳、重复佳、结果更可信!

Automation • Standardization • High throughput, triple guarantee: stable data, better reproducibility, and more reliable results!

♪ 方法兼容广 Wide method compatibility

适配SP3, FASP, 胶内酶切等 Compatible with SP3, FASP, in-gel digestion, etc.

♠ 稳定更可靠 More stable and reliable

移液准、精度高,整合模块性能佳,运行无忧 Accurate pipetting, high precision, better integrated modular performance, worry-free operation.

净 操作零门槛 Zero-threshold operation

触摸屏叠加预验证流程库,上手即会

Touchscreen overlays with pre-validated workflow library, easy to use right away.

③ 效率最大化 Maximum efficiency

智能调度系统支持多项目并行处理

Intelligent scheduling system supports multi-project parallel processing.



布鲁克 4D-多组学解决方案



更深入、更快速、更可信 —— 从组织到单细胞, 从多肽到蛋白质异构体,唯 timsTOF 独有!

- 创新引领结构蛋白质组学的进步
- 创新支持大小分子多组学的一机式需求
- 创新拓展数据挖掘的纵深



全新代谢组学与蛋白质组学 双平台设备

timsMetabo™ 捕集离子淌 度质谱仪

—— 代谢组学突破,蛋白质 组学升级

搭载创新离子淌度技术, 灵敏度提升 10 倍,为代谢 组学研究及复杂样品检测 提供突破性解决方案。其 在蛋白质组学领域的表现 更是优于市售同类产品, 助力多组学研究实现更高 维度的科学发现。



布鲁克质谱

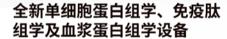
联系咨询: 400-810-1099



timsOmni™ 捕集离子淌度 质谱仪

di consulta

—— 蛋白质变体深度测序突破,复杂结构解析革新



timsUltra AIP 捕集离子淌度 质谱仪

—— 重新定义灵敏度,解锁每 一个细胞,分析每一条肽段

搭载创新 Athena 离子处理器,信号强度提升 2-3 倍,Captive Spray 离子源优化离子流,支持 PASEF 模式含独有 diagonal-PASEF,扫描速度达 300 Hz。采用 ICC 2.0 技术拓宽上样量范围,Bruker ProteoScape™集成最新 Spectronaut 20。timsUltra AIP 适用于微量样本,蛋白质和肽段鉴定量分别提升超 20%和 35%。



欧易生物科研技术服务

Shanghai O E Biotech C o . ,

国内首家代理 华东区独家

Illumina Protein Prep (IPP)

单细胞时空多组学 攀头产品

- 1. 单细胞转录组测序
 - 10x Genomics
 - 2 BD Rhapsody
 - ③ MobiNova
- (4) 10x FLEX
- 2. 单细胞核转录组测序
- 1 10x Genomics
- ② MobiNova
- 3. 单细胞及免疫组库测序
 - ① 10x Genomics
 - 2 BD Rhapsody
- ③ MobiCube
- 4. 单细胞表观组测序
 - ① 10x ATAC-sea
- ② MobiCHIP
- 5. 空间转录组
- ① 10x 冰冻样本
- ② 10x Visium CytAssist FFPE样本
- ③ 10x Visium CytAssist 冰冻样本
- ④ 10x Visium HD FFPE样本
- ⑤ 10x Visium HD 冰冻样本 57%
- ⑥ 10x Visium HD 3' poly A 冰冻样本
- ⑦ 华大Stereo-seq V1.3 冰冻样本
- 6. 空间代谢组
- 1 waters DESI
- ② AFADESI
- 7. 前沿技术 技术红利
- ① 10x Xenium Prime 5k
- ② 10x Xenium 定制探针

质谱线

- 1. 蛋白组
 - ① DIA定量蛋白质组学 DTK
 - ② Deep高深度血液蛋白质组学 DEE
 - ③ FFPE定量蛋白质组
 - ④ 标记定量蛋白质组学
 - ⑤ 超微量蛋白质组学
 - ⑥ 修饰蛋白质组学
 - ⑦ PRM靶向蛋白质组学
 - ® LC-MSMS蛋白质谱鉴定
 - ⑨ 空间蛋白质组
- 2. 代谢组
 - ① LC-MS全谱代谢组学 DTK
 - ② 双平台全谱代谢组学
 - ③ Level One 500 全谱代谢组 🏧
 - ④ Level One 1000 全谱代谢组 7000
 - ⑤ 精准靶向代谢组学
 - ⑥ GC-MS全谱代谢组学
 - ⑦ 脂质代谢组学

Olink蛋白质组

- 1. Olink Target 96
- 2. Olink Reveal

表观组

- 1. Illumina 935K甲基化芯片检测
- 2. CUT&Tag测序 DTK

中药组学

- 1. 中药复方/单方成分鉴定
- 2. 中药入血/入靶原型成分鉴定
- 3. 中药全谱代谢组
- 4. 中药空间代谢组
- 5. 网络药理学、系统药理学、分子对接

酵母文库 为荐《

- 1. 建库
 - ① 核体系酵母文库构建
 - ② 膜体系酵母文库构建
 - ③ 原核酵母文库构建
 - ④ 酵母表达文库构建
- 2. 筛库
 - ① 酵母单杂交筛选
 - ② 酵母双杂交筛选
- 3. 家族库筛选
 - ① 水稻转录因子库单/双杂交筛选
 - ② 拟南芥转录因子库单/双杂交筛选
 - ③ 水稻泛素E3文库双杂筛选
- ④ 水稻TF_E3家族文库双杂筛选

转录组

- 1. 真核转录组测序 57%
- 2. 微量转录组测序
- 3. 原核转录组测序
- 4. 全转录组测序
- 5. Small RNA测序
- 6. 实时荧光定量 PCR

基因组

- 1. 全外显子捕获测序(人、小鼠)
- 2. 全基因组重测序

微生物组

- 1.16S/18S/ITS微生物多样性测序
- 2. 二代宏基因组测序
- 3. 2bRAD-M®简化微生物组 **28**
- 4. 微生物单细胞转录组 🔤
- 5. 微生物单细胞基因组
- 6. 微生物 de novo 测序

联系我们

- 版本: 2025年9日









上海市闵行区联航路1188号25号楼欧易生物总部

market@oebiotech.com



青莲百奥完整解决方案

▶ 科研服务产品体系 以蛋白质组学为优势和核心的多组学服务平台

体液蛋白质组学

常规血浆蛋白质组

高深度血浆蛋白质组

其它体液蛋白质组

Olink靶向定量蛋白质组

特色蛋白质组学

热蛋白质组

限制性酶解-质谱分析

细胞外囊泡蛋白质组

单细胞蛋白质组

常规空间蛋白质组

全息空间蛋白质组

生物肽组

免疫肽组

微量蛋白质组

FFPE蛋白质组

宏蛋白质组

定性蛋白质组

胶条鉴定

蛋白溶液鉴定

蛋白提取鉴定

CoIP(AP-MS)鉴定

修饰位点鉴定

定量蛋白质组

LFQ定量蛋白质组

DIA定量蛋白质组

TMT定量蛋白质组

PRM定量蛋白质组

CoIP(AP-MS)定量

高级分析

生物标志物筛选

预后标志物筛选

分子分型

全蛋白质组关联分析

修饰蛋白质组

磷酸化修饰组

糖基化修饰组

泛素化修饰组

SUMO化修饰组

乙酰化修饰组

乳酸化修饰组

琥珀酰化修饰组

巴豆酰化修饰组

丙酰化修饰组

丙二酰化修饰组

戊二酰化修饰组

二羟基异丁酰化修饰组

三羟基丁酰化修饰组

棕榈酰化修饰组

二硫键组学

亚硝基化修饰组

亚磺酸化修饰组

次磺酸化修饰组

代谢组学

非靶向代谢组

非靶向脂质组

靶向代谢组

测序

转录组测序

16S/ITS测序

宏基因组测序

多组学联合

蛋白定量+蛋白修饰 蛋白修饰+蛋白修饰

蛋白质组+转录组

蛋白质组+代谢组

代谢组+16S

代谢组+转录组

细胞外囊泡表征

细胞外囊泡电镜

细胞外囊泡NTA

细胞外囊泡标志物WB

细胞外囊泡纳米流式

> 科学工具产品 一站式蛋白质组学创新平台

蛋白质组前处理试剂盒

低丰度蛋白富集磁珠试剂盒(MagicOmics DMB)

微量/通用型蛋白质组学磁珠试剂盒(MagicOmics MMB)

细胞外囊泡蛋白质组学磁珠试剂盒(MagicOmics EMB Plus)

磷酸化肽段富集试剂盒(MagicOmics PEB)

蛋白质组前处理自动化仪器平台

蛋白质组学样本前处理智能机器人Pro(MagicOmics-AP-96-Pro)

DeepResolve c18 HPLC 色谱杆

Autotip-c18 自动化除盐柱

AI智能数据分析平台



青莲百奥平台与服务优势

自主研发自动化蛋白质前处理平台



蛋白提取、富集、酶解等全流程2小时完成

同时处理96例样本,降低批次效应

(高深度) 独特纳米磁珠富集技术, 助力低丰度蛋白灵敏检测

全系列质谱检测平台

满足不同场景蛋白和代谢检测需求



Bruker timsTOF HT



Thermo Scientific™ Orbitrap Astral



Thermo Scientific™ Orbitrap Exploris™ 480



Thermo Scientific[†] O Exactive HF-X



Thermo Scientific™ Q Exactive™



Thermo Scientific™ Orbitrap Eclipse™ Tribrid™

AI智能数据分析平台BioLadder 2.0

50+分析模块,助力数据深度挖掘 售后个性化分析无忧



业务覆盖全国范围

青莲百奥业务覆盖全国170+医院、230+药企、300+科研院 校、业务涵盖临床前研究、精准医疗、伴随诊断、药物研发、 药物表征等多个方向。



170+医院



230+药企



300+科研院校

合作发表众多学界认可高质量文章

青莲百奥深度参与众多前沿研究,与中国医学科学院、中国科学院、军事医学研究院、国家蛋白质科学中心、四川大学华西医院、 浙江大学医学院等科研团队合作发表高质量SCI文章100余篇,累积影响因子1000+。

















































Endoproteinase provider for Proteomics

生命科学 蛋白组学 核心试剂



技术产品质量:

符合GMP规范 活度量化报告 批次质谱数据 技术包装品质 干冰冷链运输





国家蛋白质科学中心•北京(以下简称"凤凰中心") 是为突破我国蛋白质组学研究中技术标准不统一、数据共享程 度低等关键瓶颈而设立的生命科学领域的国家级大科学基础设施。作为中国人类蛋白质组计划的核心实施单位,凤凰中心 同时肩负医学蛋白质组学全国重点实验室及首都科技条件平台的职能。

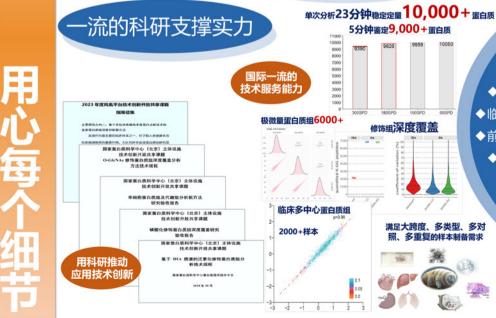
凤凰中心构建了以高通量、高分辨率、高精度的生物质谱仪为核心的蛋白质组学技术平台,以及基于"天河"超级计 算机的生物信息学平台。在院士领衔、"干人计划"专家、国家杰出青年科学基金获得者及北京市科技新星等为骨干的高 水平团队带领下,凤凰中心坚持以原始创新与集成技术创新为驱动,已建立起国际一流的蛋白质组分析技术体系,能够为 科研工作者提供涵盖样本制备、色谱分离、质谱分析及数据处理的"一站式"优质技术服务。

蛋白质组

蛋白质组

单细胞 蛋白质组

Skyline



专业的综合技术体系

全面的软硬件配置

泛素化 蛋白质组

PRM

满足大跨度、多类型、多对

蛋白质组

◆差异蛋白的发现与验证

◆翻译后修饰的探索与分析

◆微量样本与单细胞蛋白质组

◆临床大队列蛋白质组解决方案

◆前沿的定量蛋白质组分析技术

◆蛋白质组与代谢组联合分析 ◆时间/空间蛋白质组分析

◆生物信息学分析平台

◆靶向定量蛋白质组

技术服务

01 定性鉴定:

蛋白质组快速深度覆盖

02 定量分析:

Label-free蛋白质组学 DIA 蛋白质组学 TMT蛋白质组学 PRM靶向验证蛋白质组学

03 蛋白质修饰分析:

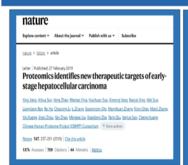
泛素化蛋白质组学 磷酸化蛋白质组学 糖基化蛋白质组学 目标蛋白质翻译后修饰

04 蛋白质药物表征分析:

二硫键解析 糖基化位点解析 糖型分析 液相色谱和质谱肽谱图 完整分子量检测



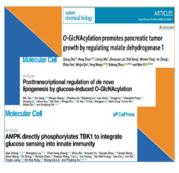
代表性合作成果

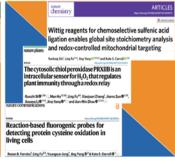
















代表性合作项目

- Chinese Human Proteome Project
- Chinese State Key Projects for Basic Research (973) (2014CBA02001)
- National Key Research and Development Project of China (2018YFA0507502, 2020YFC2002700, 2020YFE0202200,2021YFA1301600, 2021YFA1301602, 2021YFA1301603, 2021YFA1300200, 2022YFC2302900, 2023YFF1204600)
- National Natural Science Foundation of China (32271518, 32371504, 32088101,82192881, 82192881)
- Research Program of the State Key Laboratory of Proteomics(SKLP-O201704, SKLP-K201901)

国家蛋白质科学中心・北京(简称"凤凰中心"), 是国家为了解 决蛋白质组学领域技术标准不统一、数据共享度低等科研瓶颈而设立的生命科学领域的 **国家级大科学基础设施**,也是**中国人类蛋白质组计划**的核心实施单位、**医学蛋白质组学** 全国重点实验室和首都科技条件平台。

凤凰中心拥有以高通量、高分辨率、高精度定量蛋白质组技术为特色的蛋白质组学 技术平台和以高性能"天河"超级计算机为核心的生物信息学平台。在院士领衔, 人计划"学者、国家杰青、北京市科技新星为骨干的专家团队带领下,凤凰中心建立了 从蛋白质组发现研究到生物信息学分析,生物学验证和应用转化的闭环式技术服务平台。

我们愿与从事蛋白质组学、生物功能研究、生物信息学、转化医学和蛋白质药物研 发等相关创新研究的有识之士一起,推动生命科学新发现、新技术、新产品的涌现,实 现"**创造历史、引领世界**"的使命和梦想。

音自原组学技术平台 母競会組织銀

01 定性鉴定 蛋白质组快速深度覆盖

02 定量分析

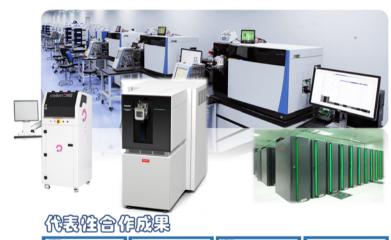
Label-free蛋白质组学 DIA 蛋白质组学 TMT蛋白质组学 PRM靶向验证蛋白质组学

03 蛋白质修饰分析

泛素化蛋白质组学 磷酸化蛋白质组学 糖基化蛋白质组学 目标蛋白质翻译后修饰

04 蛋白质药物表征分析

二硫键解析 糖基化位点解析 糖型分析 液相色谱和质谱肽谱图 完整分子量检测





Chinese Human Proteome Project
Chinese State Key Projects for Basic Research (973) (2014CBA02001)
National Key Research and Development Project of China (2018YFA0507502, 2020YFC2002700, 2020YFE0202200,2021YFA1301600, 2021YFA1301602, 2021YFA1301603, 2021YFA1300200, 2022YFC2302900, 2023YFF1204600)

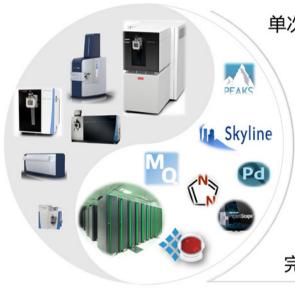
National Natural Science Foundation of China (32271518, 32371504, 32088101,82192881, 82192881) Research Program of the State Key Laboratory of Proteomics(SKLP-O201704, SKLP-K201901)

照然分配

王明超(主管): 010-61777070 管理办公室: 010-61777010

王贵宾/谢玉萍/付斌 (高级工程师) : 010-61777117 公众号: Phoenix 网站: www.ncpsb.org.cn/genee/

快速深度覆盖与定量蛋白质组



单次分析23分钟稳定定量10,000+蛋白质

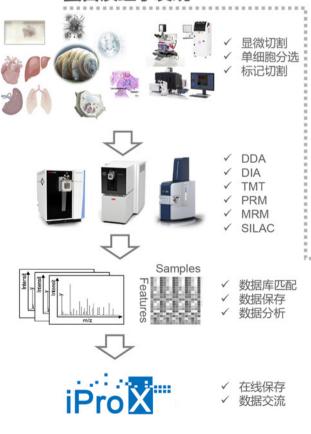
单次分析**5分钟**稳定鉴定**9,000**+蛋白质 Pg级微量样本单次定量**6000**+蛋白质 临床大队列样本(>**2000**+)解决方案 深度覆盖体液(**血浆**等)蛋白质组分析

泛素化与磷酸化修饰组深度覆盖解决方案

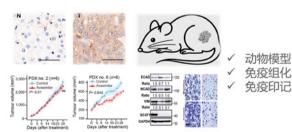
完整的单细胞、空间蛋白质组技术服务体系

从蛋白质组学发现。生物信息学解析到功能验证的全流程解决方案

蛋白质组学发现







www.ncpsb.org.cn/genee/

V/-连接完整糖肽蛋白质组 完整解析,甜蜜升级

产品优势

○ 真结构

StrucGP软件 实现真正意义上的 糖链结构解析

○ 超全面

同时获得糖链结构、 糖肽及糖链和糖基化位点 的对应关系



○ 高深度

常规全谱鉴定5000+, 超深度检测可达14000+; 定量鉴定糖肽2700+

○ 高通量

TMT/IBT标记定量 可同时对多至16个样本 进行检测

应用方向











函服务热线: 400-706-6615 □ 网址: www.bgitechsolutions.com

🖾 邮箱: info@genomics.cn 🛮 🚨 地址: 广东省深圳市盐田区梅沙街道云华路9号华大时空中心



华大科技

空间蛋白质组学

组织样本到数据全流程服务

专业博士团队指导

高性能质谱仪检测



代表文章

- Proteomic Profiling of Gastric Signet Ring Cell Carcinoma Tissues Reveals Characteristic
 Changes of the Complement Cascade Pathway. Molecular & cellular proteomics, 2021. 胃印戒细胞癌的空间蛋白质组研究
- The Comparable Microenvironment Shared by Colorectal Adenoma and Carcinoma: An
 Evidence of Stromal Proteomics. Frontiers in oncology, 2022. 结直肠癌的空间蛋白质组研究
- Routine Workflow of Spatial Proteomics on Micro-formalin-Fixed Paraffin-Embedded Tissues.
 Analytical Chemistry, 2023. 小鼠脑空间蛋白质组图谱绘制

邮箱: info@genomics.cn

热线电话: 400-706-6615

网址: www.bgitechsolutions.com

地址:广东省深圳市盐田区梅沙街道云华路9号华大时空中心



高通量 CE-SDS 蛋白分析 ProteoAnalyzer 系统



Agilent ProteoAnalyzer 系统是一种平行毛细管电泳仪器,可自动进行还原型和非还原型蛋白质样品的毛细管电泳 — 十二烷基硫酸钠 (CE-SDS) 分析。 该系统能够在短短 30 min 内对 12 个样品进行分离,省去了 SDS-PAGE 凝胶制备、染色/脱色和分析的繁琐过程,让您专注于结果。

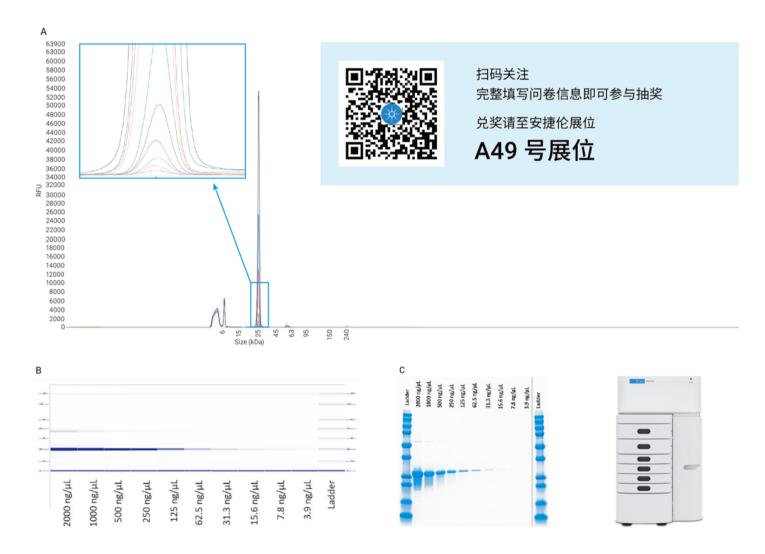


图:比较安捷伦 ProteoAnalyzer 系统和 SDS-PAGE 上分析 CAII 蛋白的连续稀释样本电泳结果。(A) ProteoAnalyzer 系统的电泳峰图叠加,在插入框中突出显示较小的浓度结果,(B) ProteoAnalyzer 系统的数字凝胶图像。(C) 相同的样品 SDS-PAGE 凝胶图。









高分辨率

~350 nm 精度 达到亚细胞器级别



高灵敏度

提供高动态范围的蛋白质组学 精确检测低拷贝数蛋白





高特异性

双光子导引光致生物 素标记



广泛样本兼容性

适用于细胞与组织样本 (FFPE 与新鲜冷冻样本)

无偏倚探索

无需依赖靶向探针或Panel,即可从 整个样本中提取全部蛋白质组信息

专题午餐会

现场为您提供精美简餐,并有惊喜抽奖,欢迎参会!



Optoproteomics: Unbiased Spatial Proteomics at Disease-Associated Sites

日期

2025年10月13日 中午12:30-13:30

地点

茂名厅



主讲人

- 新析生物科技(Syncell Inc.)创办人兼执行长
- 前中央研究院研究员、哥伦比亚大学助理教授
- 荣获 国家创新奖、科技部杰出研究奖



Brochure



Contact Us



Booth No.: B01





DeepSuite



S Deep**Proteo**

Advanced Biomarker Discovery and PTM Profiling Services



Deeplmmu

Integrated Proteogenomics Discovery Pipeline for Neoantigen Discovery



DeepGlycan

Glycan Structure Profiling for Purified Proteins and Complex Lysate Samples



M Deep AB

Antibody Sequencing, ADC Analysis, PTM and Glycan Profiling by LC-MS



Al-driven Mass Spectrometry Focus on Precision Medicine



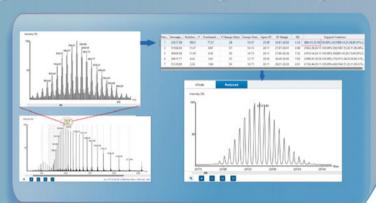
Booth No.: B01



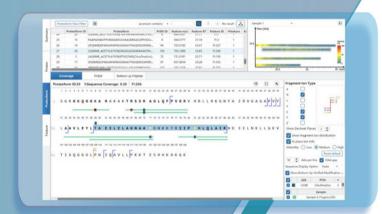


Proteoform Characterization by Multi-modal Mass Sepctrometry

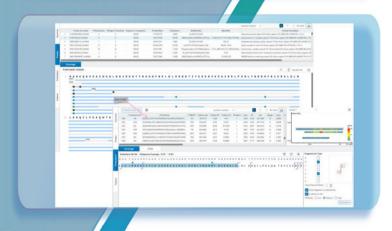
High precision spectra deconvolution



Integrate bottom up and topdown/middle-down



In-depth top-down proteome identification with open search



CONNECT WITH US





Headquarters 202-140 Columbia St w Waterloo, Ontario N2L 3K8, Canada

Lab Services 1B-1425 Strasburg Rd Kitchener, Ontario N2R 1H2,Canada







sales@bioinfor.com support@bioinfor.com