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Westlake Symposium for

AI Proteomics and Virtual Cell

AIVC Series 4

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Westlake Symposium for AI Proteomics and Virtual Cell

Location: Westlake University (Yungu Campus), Hangzhou, China
Dates: 8–9 October 2025

8 Oct, 2025 Schedule

Session 1 Proteomics

Chair: Tiannan Guo 郭天南

9:00-9:10 **Opening**
Yigong Shi 施一公 Westlake University

9:10-9:30 **AI proteomics, virtual cells, and AI proteomics competition (AIPC)**
Tiannan Guo 郭天南 Westlake University

9:30-10:00 **The adaptable, modular proteome specifies AIVC**
Ruedi Aebersold ETH Zurich

10:00-10:30 **Refreshment Break**

Chair: Yaoting Sun 孙耀庭

10:30-10:50 **AI virtual cell**
Matthias Mann Max Planck Institute of Biochemistry

10:50-11:10 **Tackling a next frontier in proteomics: de novo sequencing of endogenous antibodies**
Albert Heck Utrecht University

11:10-11:30 **TBD**
Uwe Völker Universität Greifswald

11:30-11:45 **Summary**
Tiannan Guo 郭天南 Westlake University

12:00-13:00 **Lunch**

Session 2 Biomedicine

Chair: Robert Winkler

14:00-14:20 **A global genetic interaction map of a human cell reveals conserved principles of genetic networks**
Charles Boone University of Toronto

14:20-14:40 **Deciphering human immunopeptidome by AI**
Ming Li 李明 Central China Institute of Artificial Intelligence

14:40-15:00 **Single cell imaging to study proteome dynamics in yeast**
Brenda Andrews University of Toronto

Chair: Jingyi Hou 侯婧逸

15:00-15:20 **A deep exploration of the genotype-phenotype relationship through the lens of 1,086 near telomere-to-telomere yeast genomes**
Joseph Schacherer University of Strasbourg

15:20-15:40 **Transformer-based deep learning for next generation mass spectrometry-based phosphoproteomics**
Connie Jimenez Amsterdam University Medical Center

15:40-15:55 Behind the scenes of EMBO press
Jingyi Hou 侯婧逸 EMBO press

15:55-16:10 Panel Discussion

16:10-16:30 Refreshment Break

Chair: Pouya Faridi

16:30-16:50 Virtual reality: how ML/AI-based strategies can inform about the functional roles of surfaceome protein communities
Bernd Wollscheid ETH Zurich

16:50-17:10 Chemoproteomics in drug discovery – opportunities for AI?
Ben Collins Queen's University Belfast

17:10-17:20 Generating large-scale perturbation-induced transcriptome data for drug discovery
Dong Wang 王栋 Chengdu University of Traditional Chinese Medicine

Chair: Liujia Qian

17:20-17:40 Universal telomere sequencing reveals hidden diversity underlying genome instability, aging, and cancer
Jia-Xing Yue 岳家兴 Sun Yat-sen University Cancer Center

17:40-17:50 Ultra-sensitive quantitative proteomic profiling of single or few cells enabled by ZenoTOF 8600 ZT Scan DIA
Cui Liu 刘毳 SCIEX

17:50-18:05 AI and the route to personalised/precision medicine & a 5-minute summary (of the session)
Edouard Nice Monash University

18:05-18:20 Closing & Group Photo

18:30-20:30 Welcome Dinner

9 Oct, 2025 Schedule

Session 3 AI

Chair: Yue Xuan 轩玥

9:00-9:05 Opening
Tiannan Guo 郭天南 Westlake University

9:05-9:25 Quantms ecosystem: data, formats and algorithms to generate AI-ready proteomics datasets
Yasset Perez-Riverol EMBL's European Bioinformatics Institute

Chair: Yuxia Jiao 焦玉霞

9:25-9:45 Machine learning for proteomic perturbation biology
Chris Sander Harvard Medical School

9:45-10:05 Publishing in ***Nature Methods*** and pursuing an editorial career
Arunima Singh Nature Methods

10:05-10:25 Refreshment Break

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Chair: Jun A 阿俊

10:35-10:55 **Reactome 4: pathways reimagined – dynamic visualisation and intelligent chat**
Henning Hermjakob European Bioinformatics Institute, EMBL-EBI

10:55-11:15 **A living benchmark to advance AI in proteomics de novo peptide sequencing**
Wout Bittremieux University of Antwerp

Chair: Chris Sander

11:15-11:30 Panel Discussion

11:40-12:40 Lunch

Chair: Allegretti Yuan Hu

14:00-14:20 **Harnessing AI and proteomics for mental health diagnostics and prognostics: towards scalable care in singapore**
Wilson Goh Wen Bin Nanyang Technological University

14:20-14:40 **Towards a causality-oriented Cell in silico: from prediction to design**
Ge Gao 高歌 Peking University

Chair: Wenguang Shao 邵文广

14:40-15:00 **Behind the scenes at Cell Press**
Allegretti Yuan Hu Cell Systems

15:00-15:20 **On the mathemtaical and algorithmic considerations of AI virtual cell Construction**
Peijie Zhou 周沛劼 Peking University

15:20-15:40 Refreshment Break

15:40-16:00 **A controllable foundation model for general and specialized biomolecular structure prediction**
Siqi Sun 孙思琦 Fudan University

Chair: Rui Sun 孙瑞

16:00-16:20 **AIVC enabled by multimodal and dynamical foundation model**
Han Wen 温翰 Peking University

16:20-16:25 **Every cell counts, every peptide matters: from large scale studies to smallest single cells, recent advancements in mass spectrometry-based proteomics**
Daniel Hornburg Bruker

Chair: Yue Xuan 轩玥

16:25-16:30 **Publishing with GPB, a premium journal in the omics field**
Yuxia Jiao 焦玉霞 Genomics, Proteomics & Bioinformatics

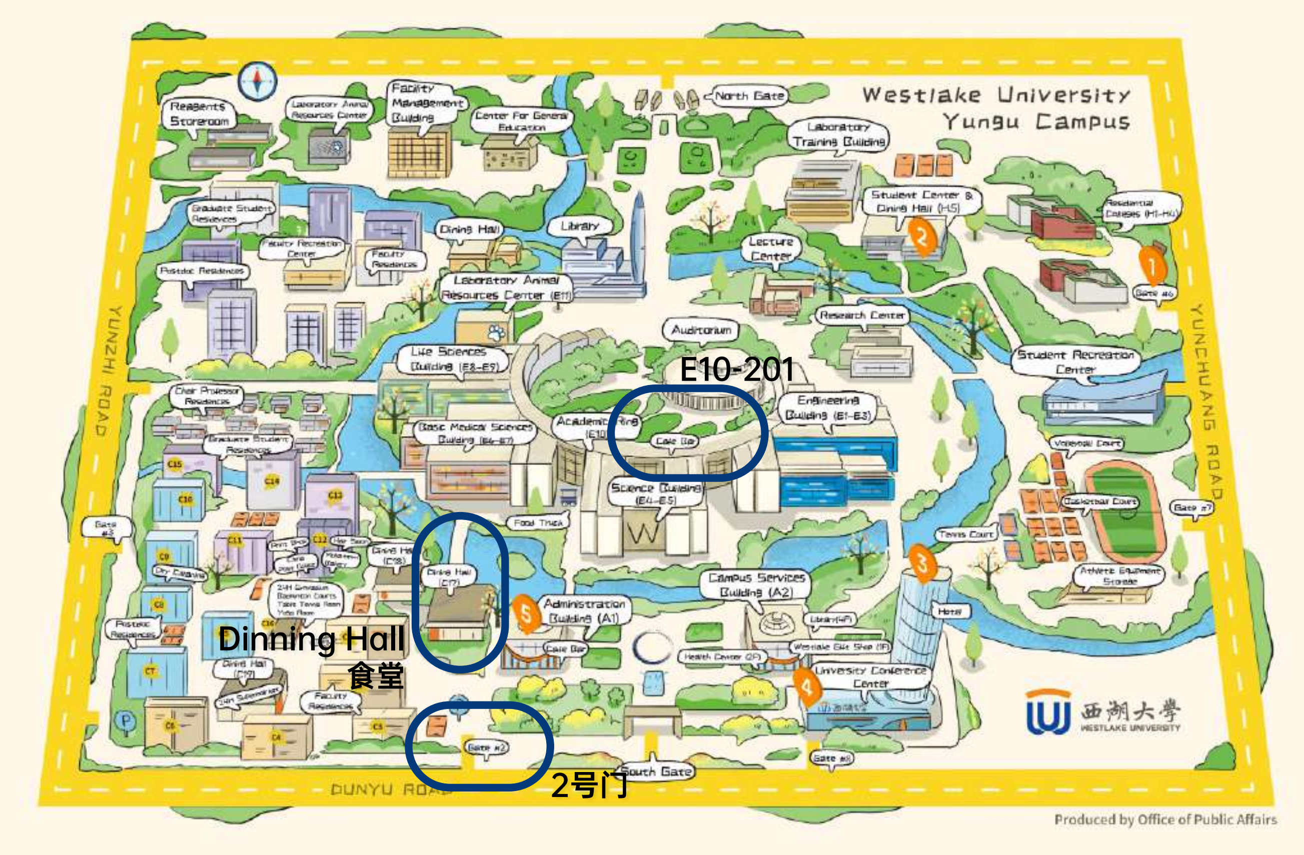
16:30-16:45 Panel Discussion

16:45-17:00 Closing & Group Photo

18:30-20:30 Dinner

Entrance Guide 入校指引

Meeting Location: 2nd Floor, Room 201, Academic Ring E10, Gate #2 entrance, Westlake University (Yungu Campus)
会议地点：西湖大学云谷校区2号门入校 学术环E10 2楼 201会议室



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