



Virtual Stakeholder Workshop of the CCQM-PAWG Task group on Protein Structure and Activity Measurements

Protein structure and activity

17-20 February 2025

Agenda

Feb 17th 13:00 to 15:30 UTC+1

Welcome: Robert Wielgosz, BIPM

Background: Max Ryadnov, NPL, UK

Session 1: Progress, Challenges and Opportunities	
	Chair, Max Ryadnov, NPL, UK
Integration of structural biology with drug discovery: quantitative challenges for protein description and characterisation	Phil Kerry, Evotec, DE
Generating living datasets and public benchmarking opportunities for sequence-to-function prediction models	Dana Cortade AlignBio, US
Advanced atomic force microscopy for the characterisation of proteins and protein assemblies	Christian Bippes NanoSurf, CH
Understanding synergistic antimicrobial peptide combinations through computation	Chris Lorenz, King's College London, UK
Challenges in quality control for biological reagents	Yuning Chen, Sino Biological Inc., CN
Chair led Q&A	

Feb 18th 13:00 to 15:30 UTC+1

Welcome Day 2: Amandine Boeuf, LNE, France

Chair Feedback Session 1: Max Ryadnov, NPL, UK

Session 2: Protein structure measurements	
Chair, Amandine Boeuf, LNE, France	
Collagen Type 0 – development of a next generation collagen for medicine	Andrew Mearns-Spragg, Jellagen, UK
Cross-linking probes for structural analysis of Tau and phospho-Tau proteins	Cristian Arsene, PTB, DE
Higher-order structure measurement of biotherapeutics by NMR	John Marino, NIST, US
Mapping protein structure and dynamics using mass spectrometry approaches: a nanobody characterisation example	Luise Luckau NML@LGC, UK
Glycomics and glycoproteomics characterization of protein standards by mass spectrometry	Renee Ruhaak, Elena Dominguez-Vega, Leiden University Medical Center, NL
Chair led Q&A	

Feb 19th 13:00 to 15:30 UTC+1

Welcome Day 3

Chair Feedback Session 2: Amandine Boeuf, LNE, France

Session 3: Protein activity measurements	
Chair, Claudia Swart, PTB, Germany	
Interrogating the binding spectrum of INFEX-702: a novel therapeutic antibody targeting <i>P. aeruginosa</i>	Victoria Savage, Infex Therapeutics, UK
Research on protein immuno-affinity concentration and enzyme catalytic concentration measurement	Liqing Wu, NIM, CN
Structural flexibility of CyaA toxin is crucial from secretion to host cell hijacking	Alex Chenal Institut Pasteur, FR
Single-Cell Proteomics: Analytical Parameters, Metrics, and Applications	Adriana Franco Paes Leme LNBio, BR
Characterization of therapeutic protein structures using native IMS-MS in combination with non-denaturing LC methods	Oscar Hernandez Alba, LSMBO-CNRS, FR
Chair led Q&A	

Feb 20th 13:00 to 15:30 UTC+1

Welcome Day 4

Chair Feedback Session 3: Claudia Swart, PTB, Germany

Session 4: Standardization: now and future	
	Chair, Liqing Wu, China
Protein design for reference materials: structure to activity measurements	James Noble NPL, UK
Training AI with standard VLPs: a novel strategy for rapid virus identification	Andrea Valsesia EC JRC, IT
ProMET: Metrology frameworks for protein structure characterisation and better definition of the measurand	Amandine Boeuf LNE, FR
Correlating bioactivity to SI traceable units - present experience and future aspiration	Tim Rudd, MHRA, UK
Chair led Q&A	

Final remarks and Close: Max Ryadnov