

Do you need quick and meaningful information on the structure of your proteins?



Join us to learn about applications on HDX-MS (Hydrogen/deuterium exchange-Mass Spectrometry)

Hydrogen/deuterium exchange (HDX) combined with mass spectrometry (MS) provides a powerful combination of technologies for the analysis of biotherapeutic protein conformation and examination of higher-order structural dynamics and epitope mapping.

In recent years, **HDX-MS** has become an indispensable tool for both structural biology and the biopharmaceutical industry to answer important questions concerning **biotherapeutic structure, stability, and interactions**.

Panelists in this webinar will describe the underlying principles and benefits of HDX-MS analysis, and will demonstrate specific applications of the technology for **rapid and meaningful assessment of protein structure studies**.

[Register](#)

Date: Wednesday, 4th November 2020
Time: 10:00am – 12:00pm AEDT

Presentations include:

- Protein therapeutic analysis by HDX-MS: Allostery, Epitope mapping and small molecule discovery **Professor Ganesh Anand, National University of Singapore**
- An Integrated Workflow for HDX-MS Investigations of Protein Conformation and Dynamics **Caryn Hepburn, Waters Australia**
- Deciphering proteins multifunctionality using a hybrid structural biology approach
Dr Ashish Sethi, University of Melbourne
- Elucidating G-protein coupled receptor (GPCR) structural dynamics
Dr Tracy Josephs, Monash Institute of Pharmaceutical Sciences
- **Followed by a Live Q&A Session**

Presenters:



Professor Ganesh Anand

Professor Ganesh heads the Chemical Biology and Drug Discovery group at the Department of Biological Sciences, National University of Singapore.

His lab investigates allostery, conformational dynamics of intrinsically disordered signaling enzymes and transmembrane receptor signaling. Other projects include protein dynamics in viral maturation and fragment-based drug discovery. The lab uses amide hydrogen/deuterium exchange mass-spectrometry.



Caryn Hepburn

Caryn Hepburn has worked as an applications specialist for the Waters brand for the past ten years. She joined Waters Australia in 2019 and is responsible for providing technical and applications support to scientists working with Waters chromatography and mass spectrometry systems.

Her passion lies with time of flight and tandem quadrupole mass spectrometry, with a primary focus on acquiring high quality data and finding meaning through software-based processing. One of her keen interests is centered around hydrogen/deuterium exchange mass spectrometry system based at the University of Melbourne, Bio21 Mass Spectrometry Proteomics Facility, and its use in characterizing conformation and interactions of complex proteins of therapeutic interest.



Dr Ashish Sethi

Ashish Sethi obtained his PhD in 2017 from the University of Melbourne. Currently he is working as a postdoctoral research fellow for Prof. Paul Gooley (NMR lab) and A/Prof. Isabelle Rouiller (Cryo-EM lab) in the Department of



Biochemistry & Molecular Biology, University of Melbourne.

His major interest lies in understanding the multifunctional human and viral proteins. He is currently working on understanding the interaction between rabies viral Phosphoprotein, which is also a multifunctional protein, and the human STAT-1. He is also looking at the structural & functional differences between human and parasite AAA ATPase enzyme, p97 using a combination of solution NMR, Cryo-EM & HDX-Mass spec.



Dr Tracy Josephs

Dr Josephs is a Victorian Endowment for Science Knowledge (VESKI) Fellow in the Drug Discovery Biology (DDB) Theme at the Monash Institute of Pharmaceutical Sciences (MIPS). Dr Josephs has built extensive biophysical, structural and pharmacological technical expertise, and applied these to unravel atomic and molecular insights into proteins that are critical for human health and fundamental to cellular processes.

Through a long standing collaboration with Dr Daniel Garama from the Hudson Institute of Medical Research, they have used native and hydrogen deuterium exchange (HDX) mass spectrometry to understand the distinct and dynamic conformations that are stabilised by agonists and drugs that bind GPCRs to fill key fundamental knowledge gaps that are critical for developing GPCR-targeting drugs.

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