AGRICULTURAL UNIVERSITY OF ATHENS

**AGRICULTURAL UNIVERSITY OF ATHENS**
**DEPARTMENT OF BIOTECHNOLOGY**

*REGULAR SEMINAR SERIES*

## 1. Seminar Title

**HDX-MS: From Artificial Membranes to the Conformational Dynamics of Membrane Proteins in Their Native Environment**

## 2. Presenter Information

Full Name: Argyris Politis

Affiliation: BSRC Fleming, University of Manchester

Email Address: politis@fleming.gr

## 3. Date (Athens Timezone) & Location

***Date:*** *Friday 27/11/26*

***Time:*** *14.30-15.30 EEST / EET*

***Timezone:*** *Athens, Greece (EET / EEST)*

***Location:*** *Hassiotes Building, room B, Department of Biotechnology, AUA*

***Type:*** *Onsite/Hybrid*

**Join**: **Microsoft Teams Meeting**

**Link:** https://teams.microsoft.com/meet/3589306089217806?p=rMJIN3S6oigJetNrQf

Meeting ID: 358 930 608 921 780 6

Passcode*: uo2eX6Ti*

## 4. Abstract

In this talk, I will present our journey towards interrogating the structural dynamics and function of membrane proteins within their native lipid environment. We develop and apply the emerging hydrogen–deuterium exchange mass spectrometry (HDX-MS) to investigate the conformational dynamics of membrane proteins and their interactions with the surrounding lipid environment. We have recently established approaches to probe lipid-mediated conformational dynamics in membrane transporters, opening new opportunities to understand how the membrane environment modulates protein function. Building on this work, our current research focuses on elucidating how membrane composition and pharmacologically relevant ligands shape the conformational landscapes of membrane proteins and their complexes, including transporters and G-protein-coupled receptors (GPCRs), important for human health and disease. Moreover, we are developing computational tools and software to visualise, analyse and interpret HDX-MS data, including novel strategies to resolve and characterise co-populated conformational states of membrane proteins. Together, these advances aim to establish HDX-MS as a powerful approach for investigating the structural mechanisms of membrane proteins in physiologically relevant environments.