BRITISH PHARMACOLOGICAL SOCIETY

ELRIG UK

New Modalities in Pharmacology & Drug Discovery

Free and in-person | 4 - 5 July 2022 | The Francis Crick Institute, London

Programme

Day 1 - Monday 4 July 2022

12:00 – 13:00	**Lunch & Poster Viewing**
13:00 – 13:10	**Conference Welcome** Sanj Kumar, European Laboratory Research & Innovation Group (ELRIG UK) Rachel Lambert-Forsyth, British Pharmacological Society
13:10 – 14:00	**New Therapeutic Modalities in Drug Discovery** Steve Rees, AstraZeneca, UK
14:00 – 14:30	**Platinum Partner Session** Bio-Rad
14:30 – 15:00	**Refreshment Break**
15:00 – 15:05	**Session Chair Introduction – Larger Molecules: Beyond Rule of Five** Session Chairs: Andy Powell, GSK, UK Hannah Neale, Sosei Heptares, UK
15:05 – 15:35	**Expanding the functionality of de novo cyclic peptides** Dr Louise Walport, Francis Crick Institute, UK
15:35 – 16:05	**Drug discovery beyond the rule of five – Some insight into design of cell permeable ligands for difficult-to-drug targets** Dr Jan Kihlberg, Uppsala University, Sweden
16:05 – 16:10	**Bronze Partner Session** Kiran Sharma, Integra Biosciences Ltd
16:10 - 16:15	**Bronze Partner Session** Avantor Sciences
16:15 - 16:45	**Accelerating biopharmaceutical drug discovery: Getting to the right molecule smarter & faster** Dr Lucy Holt, GSK, UK
16:45 - 17:00	**Industry Insider Partner Session** WuXi AppTec
17:00 - 17:45	**New modality opportunities for 'Beyond Rule of Five' molecules** Round table discussion
17:45 - 19:00	**Networking**

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Day 2 - Tuesday 5 July 2022

08:00 – 09:00	**Registration**
09:00 - 09:10	**Conference Welcome** Professor Cherry Wainwright, Robert Gordon University in Aberdeen, UK Dr Tim Hammonds, Locki Therapeutics, US
09:10 – 10:00	**Introduction and Perspective on PROTAC degraders** Professor Alessio Cuilli, University of Dundee, UK
10:00 – 10:30	**Platinum Partner Session** Dr Hasse Hedeby, Fida Biosystems
10:30 – 11:00	**Refreshment break**
11:00 – 11:05	**Session Chair Introduction – PROTACS and protein degradation** Session Chairs: Dr Tim Hammond, Locki Therapeutics, USA Dr Catherine Hurd, GSK, UK
11:05 – 11:35	**Studies of a mitotic kinase – from APC/C substrate to new TPD tools** Cynthia Okoye, University of Cambridge, UK
11:35 - 11:40	**Bronze Partner Session** Chris Hirst, Analytik Jena
11:40 - 12:10	**Targeted Protein Degradation – Where next?** Dr Ian Churcher, Amphista Therapeutics, UK
12:10 – 12:15	**Partner Session** AMSBIO
12:15 – 12:45	**Early Drug Discovery Development in AstraZeneca: setting the cascade for PROTAC modalities** Dr Sandra Stefanovic-Barrett, AstraZeneca, UK
12:45 – 13:00	**Industry Insider Partner Session** Miltenyi Biotec
13:00 – 14:00	**Lunch & Poster viewing**

14:00 – 14:05	**Session Chair Introduction – Small Molecule Modalities** Session Chairs: Professor Cherry Wainwright, Robert Gordon University, UK Cassie Messenger, GSK, UK
14:05 – 14:35	**Design and Applications of Bifunctional Small Molecules in Biology** Dr Damien Young, Baylor College of Medicine, UK
14:35 – 14:40	**Bronze Partner Session** Nirmal Perera, LGC – ATCC
14:40 – 15:10	**Programmable Protein Nanoscale Containers** Dr Jonathan Heddle, nCage Therapeutics, Poland
15:10 – 15:20	**Comfort break**
15:20 – 15:50	**Reactive fragments: Expanding the toolbox for small molecule drug discovery** Dr David House, GSK, UK
15:50 – 16:20	**Druggable epitranscriptome in cancer** Maria Berdasco, Josep Carreras Leukaemia Research Institute, Spain
16:20 – 16:30	**Conference Close & Awards**

Speaker biographies and abstracts

Steve Rees, AstraZeneca, UK

Biography:
Steve Rees OBE Steve is Vice-President of Discovery Biology at AstraZeneca with responsibility for reagent generation and assay development, functional genomics, and cell and gene therapy. Previously Steve led the Screening Sciences department with accountability for Compound Management, Hit Discovery and Lead Optimisation biology. Prior to joining AstraZeneca, Steve worked at GlaxoSmithKline for 24 years. He has served as Chair of the European Laboratory Research and Innovation Group and Chair of the European council of the Society of Laboratory Automation and Screening, and is Industry Trustee of the British Pharmacological Society. Steve was awarded an OBE in 2021 for services to science and the COVID19 response.

Abstract:
Across the drug discovery community recent years have seen the development of a series of new therapeutic modalities to treat and maybe cure disease. This includes new small molecule modalities including PROTACs, molecular glues and small molecules targeting RNA, the many nucleotide therapeutics from short antisense oligonucleotides and siRNA to mRNA medicines, many novel protein, peptide and antibody therapeutics and cell and gene therapies. These new technologies are enabling the research scientist to progress highly validated targets that have proven intractable to traditional small molecule discovery towards the clinic, while facilitating the creation of medicines for many novel targets being identified through target discovery initiatives. Through this innovation we are approaching the situation where the concept of an intractable target can be consigned to the past offering huge opportunity for the treatment of disease.

Dr Louise Walport, Francis Crick Institute, UK

Biography:
Louise Walport obtained her doctorate under the supervision of Professor Chris Schofield and Professor Christina Redfield focussing on mechanistic studies of histone demethylases. Following further postdoctoral work in Oxford, she was awarded a Marie Skłodowska-Curie Global Fellowship to work in the group of Hiroaki Suga at the University of Tokyo, where her interest in cyclic peptides arose. Since 2018, she is a lecturer in the Chemistry Department at Imperial College London and a group leader at the Francis Crick Institute. Her group is particularly interested in developing new approaches to understand the regulation of enzyme-catalysed post-translational modifications using cyclic peptide-based tools.

Abstract:
mRNA-display based cyclic peptide discovery platforms provide powerful routes to rapidly identify tight binding hits to almost any target of choice. Genetic code reprogramming strategies permit wider chemical space to be covered through incorporation of non-canonical amino acids. In this talk I will describe recent work from my group expanding the functionality that can be encoded in cyclic peptide libraries. I will describe our recent efforts to develop a novel mRNA display strategy, photocrosslinking-RaPID (XL-RaPID), and exploit its ability to accelerate the discovery of cyclic peptides that photocrosslink to a target of interest. As a proof of concept, we generated a benzophenone-containing library and applied XL-RaPID screening against a model target, the second bromodomain of BRD3. Our crosslinking screening resulted in two optimal candidates that selectively labelled the target protein in cell lysate. Overall, our work introduces direct photocrosslinking screening as a versatile technique for identifying covalent peptide ligands from mRNA display libraries incorporating reactive warheads.

Dr Jan Kihlberg, Uppsala University, Sweden

Biography:
Professor Jan Kihlberg holds a chair in Organic Chemistry at Uppsala University, Sweden since 2013. His key research interest is to understand what properties convey cell permeability, aqueous solubility and target binding to drugs in the beyond rule of 5 space and to translate this knowledge into guidelines for design. His group has a particular interest in the structure-property relationships of macrocycles and proteolysis targeting chimeras (PROTACs). It is also involved in synthesis of macrocycles originating from natural products as ligands for difficult-to-drug targets. He has published 172 peer reviewed articles, 18 research reviews and four book chapters. Before moving to Uppsala Professor Kihlberg spent ten years at AstraZeneca R&D in Gothenburg, seven of which as Director of Medicinal Chemistry. He obtained his PhD in organic chemistry at Lund University in 1988.

Abstract:
We have found that cell permeable and orally absorbed drugs that modulate difficult-to-drug targets are often found in the chemical space beyond the rule of 5 (bRo5). Macrocycles were enriched among these drugs, most likely because they provide superior binding to targets that have large and/or featureless binding sites. We are investigating structure-property relationships for bRo5 compounds to facilitate their design.

We have studied the conformations of macrocycles and other oral drugs in the bRo5 space using NMR spectroscopy and analysis of crystal structures and found that they often behave as molecular chameleons. In a nonpolar, membrane-like environment they populate less polar and more compact conformational ensembles than in a polar environment such as water. As a

result of their fine-tuned flexibility molecular chameleons combine aqueous solubility, cell permeability and target binding; properties that otherwise would have been mutually exclusive for compounds in the bRo5 space.

Predicting the conformations and properties of molecular chameleons is difficult, making their design challenging. However, machine learning shows great promise for differentiation between compounds that have high or low cell permeability. Computational conformational analysis provides accurate information on the conformations of fairly rigid macrocycles, whereas flexible ones still remain challenging.

Dr Lucy Holt, GSK, UK

Biography:
I have 15 years of experience in drug discovery at GSK, and before that 6 years at a Biotechnology company, Domantis (which span out from MRC-LMB where I completed my PhD work). Having worked across different aspects of Biopharmaceutical Drug discovery, I recently led a multidisciplinary matrix team to embed new technology and methodology to transform and accelerate GSK's Biopharm Drug Discovery process. Now I head the Antibody Protein Science team within Biopharm Discovery. We have accountability for antibody production and initial characterisation throughout the discovery process.

Abstract:
This presentation discusses the need for identification of exquisite specificities in therapeutic antibody discovery. It demonstrates GSK's use of automation to keep the discovery funnel wider for longer. This includes the ability to express and purify panels of antibodies in a high-throughput, automated manner, enabling parallel screening for biological function and developability, accelerating the drug discovery process. I will put this and other recent evolution in large molecule drug discovery in context and discuss areas showing exciting potential for the future.

Professor Alessio Cuilli, University of Dundee, UK

Biography:
Alessio Ciulli holds the Personal Chair of Chemical Structural Biology at the School of Life Sciences, University of Dundee. He is also the Director of the newly announced Dundee's Centre for Targeted Protein Degradation (CeTPD). Dr Ciulli's laboratory has made important contributions to selective chemical intervention on protein-protein interactions targets and to the development of proteolysis-targeting chimeric molecules (PROTACs) as a viable strategy for targeted protein degradation. Amongst his most significant discoveries are the fragment-based design of ligands for the E3 ligase von Hippel-Lindau (VHL), and their use to design one of the first VHL-based PROTACs: the BET degrader MZ1. Dr Ciulli's Lab later illuminated fundamental insights into PROTACs' mechanism of action, solving the first crystal structure of a PROTAC ternary complex. Dr.

Ciulli is the scientific founder of Amphista therapeutics, a company that develops new protein degradation platforms. Before joining Dundee, Dr Ciulli was a group leader at the University of Cambridge, where he previously earned his PhD degree and carried out postdoctoral research. Amongst his honours are the EFMC Prize for Young Medicinal Chemist in Academia, the ICBS young chemical biologist award, the RSC Capps Green Zomaya Award in medicinal computational chemistry, and election as Fellow of the Royal Society of Chemistry.

Abstract:
Bivalent degrader molecules (also known as PROTACs) recruit proteins to E3 ligases for targeted protein degradation. Formation of a ternary complex between the PROTAC, the E3 and the target leads to the tagging of the target protein by ubiquitination, and subsequent proteasomal degradation.

Over the past 8 years, PROTACs have witnessed significant development and exponential rise in interest and adoption across academia and the biopharma industry, mostly enabled by the discoveries of high-quality, drug-like small-molecule ligands for the E3 ligases cereblon (CRBN) and von Hippel-Lindau (VHL). They are today firmly established both as chemical tools to study biology and as next-generation medicine, with a first wave of PROTAC molecules advancing in clinical trials against cancer and other diseases. Degrading rather than inhibiting a target protein offers a novel modality of chemical intervention, and advantages such as more efficacious drug response at lower doses, and enhanced target selectivity, with potentially reduced side effects and disease resistance.

This lecture will offer an introduction and a perspective on this rapidly evolving field. It will outline some of the key discoveries from our laboratory that helped to elucidate their mechanism of action and to provide a rational basis for their design and optimisation. I will also highlight current trends and future direction we and others in the field are taking in the design and development of the next generation of targeted protein degradation systems, including recent expansion beyond bivalency, tackling of challenging targets, and the development of novel PROTAC-inducible technologies to degrade any target protein e.g. BromoTag.

Cynthia Okoye, University of Cambridge, UK

Biography:
Cynthia is a final year PhD student and Gates Cambridge scholar in the Department of Pharmacology at the University of Cambridge. She is based in the labs of Dr Catherine Lindon and Professor Laura Itzhaki and her project aims to harness the anaphase-promoting complex for targeted protein degradation. Before her PhD, she obtained her bachelor's degree in Chemistry

at Williams College, Massachusetts where she studied the effect of clinical and synthetic missense mutations in beta-lactamase.

Abstract:
Aurora kinases are major regulators of the cell cycle, undergoing ubiquitin-mediated destruction at the end of each mitosis under control of the anaphase-promoting complex (APC/C) ubiquitin ligase.
Research in the Lindon lab aims to understand how ubiquitin-mediated proteolysis of Aurora A (AURKA) regulates its activity, both in the context of its cognate APC/C-driven degradative pathway and through use of targeted protein degradation (TPD) tools such as PROTACs.
Detailed study of AURKA degradation has elucidated substrate-specific elements, or degrons, required for targeting by the APC/C. An ongoing collaboration between Lindon and Itzhaki labs seeks to exploit the knowledge of degrons from AURKA and from other APC/C substrates to design new TPD tools, so-called 'protein degraders', designed by functionalizing stable protein scaffolds with grafted peptide ligands. I will present results showing unexpected behaviour of different degron combinations that calls into question existing assumptions about APC/C-substrate interactions and holds promise for efforts to create protein degraders that harness the ubiquitination activity of the APC/C.

Dr Ian Churcher, Amphista Therapeutics, UK

Biography:
Ian joined Amphista Therapeutics as Chief Scientific Officer in 2020 where he leads a portfolio of projects focused on the development of next generation approaches to targeted protein degradation. Ian was one of the pioneers of the application of targeted protein degradation to drug discovery as Head of the Protein Degradation Discovery Performance Unit at GSK from 2012 including an extensive collaboration with Prof Craig Crews (Yale). Ian built a team which demonstrated the viability of the VHL-recruiting PROTAC strategy and advanced a portfolio of projects from early proof of degradation through to clinic-enabling studies. During a career in pharma at Merck & GSK, Ian led a range of discovery projects across many therapy areas from target validation through to lead optimisation and clinical entry as well as a number of applications of novel technology to drug discovery. More recently, Ian was SVP Drug Discovery at artificial intelligence biotech BenevolentAI where his team applied novel AI methods to tackling a series of drug discovery challenges across a portfolio of target identification and chemical optimisation projects.Ian holds an MA and D.Phil. in Chemistry from the University of Oxford where he was also Visiting Professor in the Department of Chemistry.

Abstract:
Targeted protein degradation (TPD) approaches have quickly become a new modality in the drug discoverer's armoury promising transformation

therapeutic options due to the unique, catalytic mode of action, delivering efficacy by removing disease-causing proteins. Many first generation agents have now progressed to clinical studies generating encouraging early data. This success has shown the huge potential of the field but has been based on the use of a limited number of degrading mechanisms, utilizing a small set of ubiquitin E3 ligases, most notably cereblon & VHL. This talk will reflect on the areas where current TPD approaches are highly effective but also highlight where limitations are beginning to emerge and there is a need for next generation protein degrading approaches using new biological mechanisms and chemical warheads. Areas where further advances are needed include achieving degradation in a specific tissue or across a much wider range of tissues/tumor types; designing degraders with reduced susceptibility to emergence of tumor resistance and identifying new degrader chemistries which allow favourable in vivo profiles including oral dosing and the ability to penetrate the CNS. Amphista's research into new TPD mechanisms has the potential to address each of these areas of opportunity and data to exemplify this will be shared.

Dr Sandra Stefanovic-Barrett, AstraZeneca, UK

Biography:
Sandra obtain bachelors degree in Molecular Biology at University of Belgrade and moved to UK to do PhD in Institute for Animal Health, Pirbright laboratories. During the PhD she worked on cellular changes induced by ASFV (African Swine Fever Virus). Her first postdoc was in NIH, Bethesda,USA in laboratory of Dr Ramanujan Hegde during which time she published the discovery of novel pathway for membrane protein insertion. Next two postdoctoral positions were back in UK, in Babraham and University of Cambridge respectively. Her work at University of Cambridge, CIMR focused on degron induced proteasome degradation at the cytosolic face of endoplasmic reticulum. She has joined Cellular Assay Development group in AstraZeneca in April, 2019.

Abstract:
The continued search for novel modalities to enable so far intractable targets has been a priority for the current, progressive pharmaceutical portfolio.
In recent years, extensive work on PROTACs in academic and industrial research has highlighted the importance of the targeted degradation approach. Directly degrading these disease-inducing proteins is an exciting approach that opens up the target space, because identification of a binder rather than inhibitor and its conversion into a PROTAC is potentially sufficient to reduce target level and thereby activity. As a result of this mode of action, PROTAC cascades focus on target binding, ternary complex formation and target degradation in cells. We therefore had to re-think, re-design and re-optimised our profiling platforms, from target validation, through novel chemistry approaches, to new ways to address safety.

In this presentation, I will address some of the challenges we have faced, the changes we implemented and the way we optimised the workflow in Early drug discovery, enabling us to better understand and work with PROTACs.

Dr Damien Young, Baylor College of Medicine, USA

Biography:
Damian W. Young PhD is Associate Director for the Center for Drug Discovery at Baylor College of Medicine and Associate Professor in the Departments of Pharmacology and Chemical Biology and Pathology and Immunology. His research is focused on applying modern synthetic organic chemistry to constructing collections of biologically active small molecules for drug discovery. He has applied concepts related to generating molecular diversity within small molecules for modulating a variety of disease-associated protein targets. His lab was among the first to apply the principles of diversity generation to fragment-based drug discovery (FBDD) and DNA-Encoded Library (DEL) platforms.

Dr Young received a BS in Chemistry from Howard University and then worked as a process chemist at Trimeris Inc. on the HIV drug enfuvirtide. He received a PhD in synthetic organic chemistry under the direction of Professor Daniel Comins at North Carolina State University and subsequently pursued postdoctoral studies in the lab of Professor Stuart Schreiber at Harvard University and the Broad Institute of MIT and Harvard. Prior to joining Baylor, he was Group Leader within the Chemical Biology Program at the Broad Institute of MIT and Harvard and a Project Leader for the Harvard/Broad Centers of Excellence in Methodology and Library Development (CMLD).

Abstracts:
Fragment-Based Drug Discovery (FBDD) is now a rigorously validated platform for therapeutic discovery. FBDD generally involves the identification of low molecular weight (<300) ligands to disease targets and is followed by their structure-guided optimization to potent lead compounds. However, the assembly of a fragment collection that yields high-quality hits toward a wide swath of biological targets is challenging. Moreover, once hits are determined, the process of fragment optimization can be laborious and time-consuming. To address these issues, we put an upfront investment into the synthesis of a novel fragment collection using a guiding approach called Systematic Chemical Diversity (SCD). An SCD-derived fragment collection contains sufficient chemical diversity to provide hits to disparate targets with high selectivity. Moreover, because the diversity is implemented in a systematic way, structure-activity relationships (SAR) can be discerned leading to rapid synthetic optimization.

Dr Jonathan Heddle, nCage Therapeutics, Poland

Biography:
Jonathan Heddle studied Pharmaceutical Science at The University of Nottingham, UK before moving to The University of Leicester to work on the antibacterial target DNA gyrase and its inhibitors. He then moved to Japan as a Japan Society for Promotion of Science Special Research Fellow where he first studied structural biology before setting up his own laboratory increasingly researching bionanoscience first at Tokyo Institute of Technology and then at RIKEN. He recently moved back to Europe to head a lab at the Malopolska Centre of Biotechnology, Jagiellonian University, Poland where he leads the Bionanoscience and Biochemistry Laboratory. He is interested with combining molecular biology, structural biology and biophysics with diverse areas of science (chemistry, mathematics, physics) with the ultimate aim of building intelligent nanomachines which will have multiple applications, notably in human health.

Abstract:
The scientific and technological progress of humanity is characterised by increasing control over matter at ever smaller length scales. Compared to nature however our abilities are still crude. Nature builds useful nanoscale protein structures molecule-by-molecule. The resulting nanomachines include those that copy DNA to those that harvest energy from light. The ability to design functional, artificial, sophisticated protein structures is highly desirable for many fields ranging from materials to medicine. One of the most useful class of structures are programmable protein containers – stable, hollow and able to display molecules of choice on their exteriors (useful for vaccines and cell-targeting) and able to carry macromolecular “cargoes” of choice in their lumens (useful for protective drug delivery). Here I will give an overview of protein cages and our recent progress in developing them as examples of programmable biological matter whereby their structural changes (e.g. opening and closing of cages to release cargo) can be controlled by external triggers of our choice.

Dr David House, GSK, UK

Biography:
Dr David House, Head of Chemical Biology & Crick-GSK LinkLabs, GSK StevenageDavid completed his PhD in stereoselective synthesis with Dr Stuart Warren in Cambridge and then moved to Geneva to work with Professor Peter Kündig on the synthesis and applications of organochromium complexes. After returning to the UK for a second postdoc with Professor Tim Donohoe, where he developed ‘ammonia-free’ Birch reductions, David joined GSK as a medicinal chemist.During his 20-year career at GSK, David has worked across the full breadth of the discovery organisation. In the Respiratory and Inflammation therapy areas, David led integrated project teams working from target identification through to clinical candidate selection. His areas of expertise

include design of small molecule modulators of nuclear receptors, ion channels and kinases, and his current research interests focus on development of reactive chemical probes for biological target identification and validation. In 2015, David moved into an external facing role, working to establish the Crick-GSK 'LinkLabs': a pre-competitive research collaboration with the Francis Crick Institute which is focussed on developing new methodology in chemical biology and applying this to early-stage biomedical research. With the collaboration reaching a point of maturity, the joint team was able to successfully apply for an EPSRC Prosperity Partnership to co-fund a large 5-year research programme in Systems Chemical Biology which will run to 2026.Alongside the Crick-GSK collaboration, David heads up GSK's Chemical Biology department in Stevenage. His department collaborates closely with others in discovery to accelerate early-stage target insights from genetics through assessment of small molecule target tractability, molecular pharmacology and mode of action.David is a Fellow of the Royal Society of Chemistry, GSK Senior Fellow and adjunct Professor at Imperial College, department of Chemistry.

Abstract:
Reactive fragment libraries are emerging as a powerful entry point for chemical probe discovery, and with a resurgence of interest in covalent drug discovery, screening these libraries can offer an expedient route to small molecule lead identification. This talk will highlight some of the applications of reactive fragments as well describing some of the approaches GSK is taking to building new capabilities through its strategic partnership with the Francis Crick Institute.

Maria Berdasco, Josep Carreras Leukaemia Research Institute, Spain

Biography:
Dr. Berdasco is a molecular biologist with over 15 years of experience in the field of Clinical Epigenetics, firstly as principal researcher at the CNIO (Madrid) and IDIBELL (Barcelona) and recently as Head of the Epigenetic Therapies (EPITARGET) Research Group at Josep Carreras Leukaemia Research Institute. She has participated in international research consortia of European projects, covering funding schemes from the Cooperation Scheme in H2020 (ITN, RISE, COST) as well as she is principal investigator of various other privately funded endeavours and National Programs. To improve the group's research lines in translational research some actions are promoted, including clinical-basic interactions, technological transfer, or agreements with private companies. An aspect of interest for the translational value of the research is her education and professional activities in Bioethics and management of human samples for biomedical research (MsC in Bioethics and Law-UNESCO). In 2019, she has been designated by the Spanish Ministry of Science and Technology as member of the Advisory Committee for Human Tissue and Cell donation and use, a

management structure from the Sub-directorate general for Research on Cellular Therapy at the Instituto de Salud Carlos III.

Abstract:
For the last two decades, epigenetic dysregulation has been recognized as a key factor contributing to human disorders with a few successful small-molecule compounds targeting the enzymes with epigenetic activity in clinical practice. Following the epigenetic model, a new question emerges: can a similar scenario be envisioned for the targeting of biochemical modifications of RNA? The field of epitranscriptomics is boosted by the technical efforts of the last decade to characterize and quantify RNA modifications (especially mRNA) which have led to an increased knowledge of post-transcriptional RNA marks in normal cell fate and development. Interestingly, a number of studies have revealed that deregulated epitranscriptomes are also associated with human pathologies, such as cancer. Although we are still far from obtaining a complete map of RNA modifications, it is clear that RNA does not merely act as an effector molecule but it has an active role in the regulation of gene expression, and consequently, offers a reversible tunable mechanism to be targeted by small- molecule intervention. Preclinical evidences of the benefits of RNA-modifying therapy are found in a few experimental models supporting that the development of innovative therapeutic intervention of RNA modifications will be an exciting reality.

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1. Pre-registration for the meeting is essential. Please register at bps.ac.uk and enter our EventForce registration system.
2. To ensure we minimize the risk of spreading COVID, please ensure that you have had at least two vaccinations against the COVID virus and that you are not presenting with any of the symptoms.
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    b. Use of sexualised or other inappropriate images or unwelcome sexualised content, inappropriate physical contact, unwelcome sexual attention or stalking.
    c. Sustained interruption of speakers or those asking questions.
    d. Unwanted photography or filming.
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