


UK Proteostasis Meeting 2026

Two days of discussion & networking around proteostasis research

This meeting is made possible due to sponsorship from:

THE FRANCIS CRICK INSTITUTE

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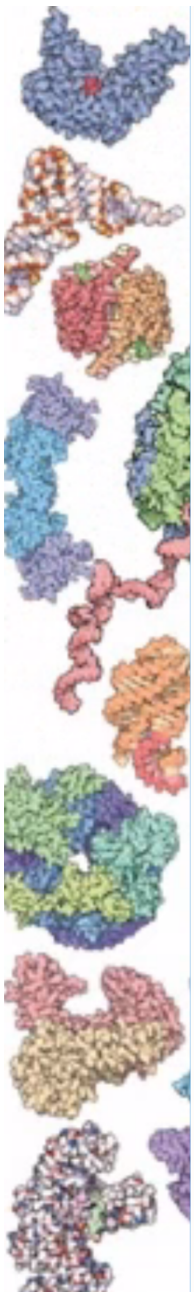

Connecting people | Advancing discovery | Transforming impact

PROTEOSTASIS UK

Bringing the UK proteostasis community together

Proteostasis UK is a national research network that connects scientists to advance our understanding of proteostasis.

By connecting expertise across disciplines and biological scales we aim to accelerate discoveries that can address major societal challenges.

What We Do

- Organise meetings, workshops and networking events.
- Support collaboration through pump-priming grants
- Promote knowledge and expertise sharing
- Support ECR training and career development.
- Share news, updates, and opportunities across the proteostasis community through our monthly newsletter.

Scan to join the network

Free, simple and quick to sign up

UKRI Biotechnology and Biological Sciences Research Council

Find out more at:
https://proteostasisuk.co.uk/

EIRNABio
ENABLING BIOINNOVATIONS

Unlock the secrets of translation with EIRNABio

GLOBAL LEADERS IN THE FIELD OF TRANSLATOMICS

Measure translation directly from sample to biological insight

EIRNABio combines scalable experimental platforms with intuitive analysis tools so researchers can explore translation efficiency, ribosome occupancy, pausing, readthrough and hidden translated regions with confidence.

- **High-throughput Ribo-seq**

Ribo96 enables larger, reproducible studies in a 96-well format.

- **No command line required**

Browser-based EIRNABio Connect makes analysis accessible and shareable.

- **Beyond annotated coding**

Translon Explorer helps uncover uORFs, altORFs and microprotein candidates.

Our Translatomics Services

Ribosome Profiling (Ribo-seq)

Including 96-well format and ultra-low input workflows for precious samples.

Disome Profiling (Disome-seq)

Provides insights into ribosome collisions and ribosome pausing biology.

Polysome Profiling (Polysome-seq)

Quantifies ribosome loading at isoform level across experimental conditions.

tRNA-seq

Assesses tRNA abundance and modifications linked to translation control.

www.eirnabio.com info@eirnabio.com

From High-Throughput Ribo-Seq to Actionable Translational Biology

Ribo96 creates the experimental design space; EIRNABio Connect and Translon Explorer turn scaled datasets into interpretable outputs.

Why Ribo96 helps larger studies

- **Scale:** Profile more conditions, doses, time points and replicates.
- **Automation:** Improve reproducibility and reduce hands-on variability.
- **Low input:** Unlock Ribo-seq for precious samples with RNA in the nanogram range.

Why use EIRNABio-Connect

- Interactive plotting and dynamic visualisation.
- Reproducible workflows and standardised reporting.
- Seamless sharing for collaborative interpretation.

Applications: Turn scaled ribosome profiling into biological decisions

- Drug mechanism of action: Ribosome pausing, TE shifts and pathway-level responses.
- UORF regulation: Condition-specific upstream ORF usage and repression/activation.
- Protein expression optimisation: Codon-optimise constructs and evaluate suppressor tRNA etticacy.
- Disease-specific signatures: Translation-focused phenotypes beyond RNA abundance
- Codon occupancy and readthrough: Codon-level effects, stop-codon readthrough and tRNA-related biology.
- Hidden translation discovery: Expand the translatome and generate new hypotheses.

www.eirnabio.com info@eirnabio.com

SciQuip | Molecular Dimensions

Protecting what matters. Advancing proteostasis together.

As part of the **Calibre Scientific Group**, Molecular Dimensions and SciQuip combine expertise in structural biology, protein crystallisation, cryo-EM and laboratory infrastructure to support researchers at every stage of the proteostasis workflow.

From high-quality reagents and consumables to sample preservation, ULT storage and laboratory equipment, we provide the tools scientists need to accelerate discovery and protect valuable samples.

Stirling VAULT100

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- Largest storage volume per sq. ft. of floor space

*ENERGY STAR Final Test method at -80 °C (112°F) setpoint

Complete solutions for
structural biology & proteostasis

As part of the Calibre Scientific Group, SciQuip and Molecular Dimensions combine expertise, innovation and trusted brands to deliver end-to-end solutions for proteostasis research.

Molecular Dimensions

Accelerating discovery in structural biology

High-quality reagents and consumables for protein crystallisation, purification, production, and cryo-EM

- Premium protein crystallisation screens and optimisation reagents
- Wide range of solutions to support protein production and purification
- Cryo-EM grids, plunge freezing consumables and accessories
- Expertise and support to accelerate your structural biology research

SciQuip

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- 2D Sample storage solutions
- Scientific consumables
- Service, validation and technical support

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Visit our stand

Meet our specialists to discuss:

- Protein crystallography
- Sample preservation
- Sustainable lab equipment
- Structural biology workflows
- Cold storage solutions

Molecular Dimensions

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UK PROTEOSTASIS MEETING 2026

Bioluminescent tools for protein stability, degradation & target engagement

20–21 July 2026 · The Francis Crick Institute, London

ABOUT PROMEGA

Founded in 1978 and headquartered in Madison, Wisconsin, Promega develops reagents, assays and automation for the life sciences. The portfolio spans protein analysis and expression, protein degradation, cell-based and biochemical assays, drug discovery, genomics and nucleic acid analysis, and genetic identity underpinned by the bioluminescent detection chemistries Promega is known for.

FOR PROTEOSTASIS RESEARCH

HiBiT

Antibody-free quantification of endogenous protein levels and degradation kinetics. A standard readout for targeted protein degradation, PROTAC and protein-stability studies.

NanoBRET® Target Engagement

Live-cell measurement of compound–target binding and occupancy, from biochemical characterisation through to cellular potency.

TarSeer™ BRETSA™ EARLY ACCESS

Tracer- and antibody-free target engagement in live cells, measuring ligand-induced changes in protein thermal stability. Suited to challenging targets across hit validation and lead optimisation.

NanoLuc® luminescent chemistry

The bright, stable luciferase behind these tools, including the thermostable StabiLuc™ used in BRETSA.

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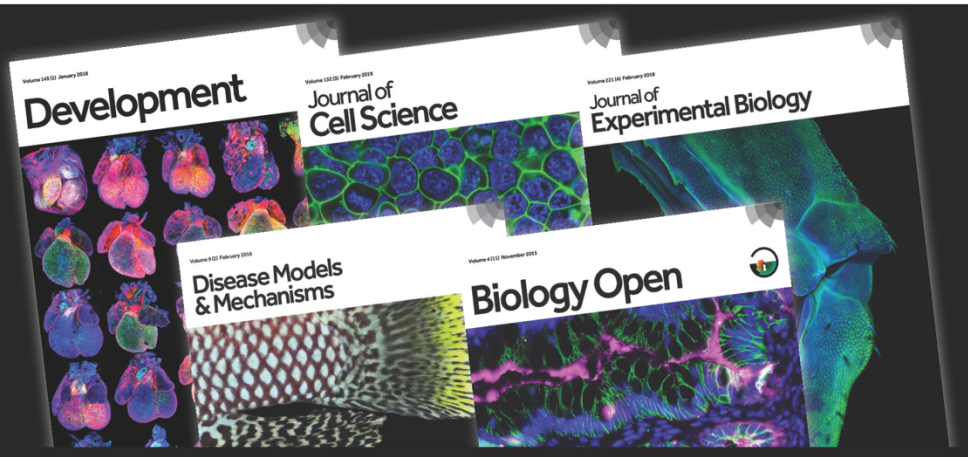

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Schedule

Day 1: Monday July 20th

09:30 - 10:30 am – Arrival/coffee/registration

10:30 - 10:45 am – Welcome and important information (*John Labbadia*)

Keynote Talk (*Session chair, Maruf Ali*)

10:45 - 11:20 : Laurence Pearl (Institute of Cancer Research / University of Sussex)

"Protein kinase regulation by the HSP90 molecular chaperone system"

11:20 – 12:00: PI Flash talks 1 (*Session chair, David Balchin*)

Adam Grieve, Adan Pinto-Fernandez, Adrian Rousseau, Alex van Vliet, Andrew Wood, Arjuna Ratnayaka, Della David, Eugenia Clerico, Heidi Olzscha, Heike Laman, Ioannis Smyrnias, Janet Kumita, Jasmeen Oberoi, John Christianson

12:00 – 12:40: Flash talks for posters 1-30 (*Session chair, David Balchin*)

12:40 - 14:10: Lunch and posters 1 (*Poster numbers 1-30*)

Research Talks 1 (*Session chair, Maruf Ali*)

14:10 – 14:25: Daniel Maddison (University of Cambridge)

“BiP mediated disaggregation of amyloid-beta throughout the secretory pathway”

14:25 – 14:40: Claudia De Miguel (MRC LMB)

“Termination of the Integrated Stress Response”

14:40 – 14:55: Max Thompson (Babraham Institute)

“Clearance of age-associated aggregates by late-life DAF-2 inhibition”

14:55 – 15:10: Francesca van Tartwijk (British Antarctic Survey / University of Cambridge)

“Organelle morphology reflects proteostatic stress in the Antarctic spiny plunderfish Harpagifer antarcticus”

15:10 – 15:50: PI Flash Talks 2 (*Session chair, David Balchin*)

Jose Luis Rosa, Maria Jimenez-Sanchez, Melody Clark, Adam Benham, Rahul Samant, Viktor Korolchuk, Yvonne Nyathi, Cara Eldridge, Katarzyna Ciazynska, Frederica Theodoulou, Chrisostomos Prodromou, Yu Ye, Catherine Lindon, Colin Hammond

15:50 - 16:20: Coffee break

Research Talks 2 (*Session chair, Ivana Bjedov*)

16:20 – 16:35: Virginia De Cesare (MRC PPU / University of Dundee)

“E2s that behave differently: UBE2Q1 non-canonical ubiquitylation machinery”

16:35 – 16:50: Abid Javed (Francis Crick Institute)

“Dissecting the Trigger factor-nascent chain engagement on the ribosome using cryo-EM”

16:50 – 17:05: Sam Taylor (University College London)

“An ER-to-cytosolic stress response promotes proteostasis and reproductive health”

17:05 - 17:50: Proteostasis UK Networking Session (*Session chair, Della David*)

“Proteostasis UK Network: Bringing the UK Proteostasis Community Together”

17:50 - 18:30: Flash talks for posters 31-60 (*Session chair, David Balchin*)

18:30 - 20:00: Dinner and posters 2 (*Poster numbers 31-60*)

20:00 - 21:00: Drinks

Day 2: Tuesday July 21st

08:30 - 9:30 am: Arrival and coffee

Keynote talk (*Session chair, Maria Jimenez-Sanchez*)

09:30 - 10:05: Sylvie Urbe (University of Liverpool)

“Mechanisms of Mitophagy: How Ubiquitylation and Mitochondrial Import Govern Quality Control Pathways”

Research Talks 3 (*Session chair, Maria Jimenez-Sanchez*)

10:05 – 10:20: Nerea Blanes Ruiz (King’s College London)

“p62 modules astrocytic handling of pathological tau under inflammatory conditions”

10:20 – 10:35: Yassin Ben Khoud (Imperial College London)

“Structure of ER chaperone complex GRP170-ATP-BiP suggests a new model for substrate engagement”

10:35 – 10:50: Wen Kin Lim (Babraham Institute)

“Impact of RNA oxidation on ribosome dysfunction and proteostasis with age”

10:50 – 11:05: Tamara Sijacki (The Francis Crick Institute)

“Investigating the in-situ architecture of bacterial degradation complexes”

11:05 – 11:30: Coffee break

11:30 - 11:45: Proteostasis UK ECR talk (*Session chair, Maruf Ali*)

Jasmeen Oberoi (University of Sussex)

“The Proteostasis UK ECR Network”

11:45 - 12:25: Flash Talks for posters 61-90 (*Session chair, David Balchin*)

12:25 - 14:00: Lunch and posters 3 (*Poster numbers 61-90*)

14:00 - 14:45: Proteostasis UK industry panel session (*Session chair, Colin Adrain*)

“An Industry Perspective on Proteostasis Research: Building Successful Academia–Industry Partnerships”

14:45 – 15:15 – Coffee break

Research Talks 4 (*Session chair, Ivana Bjedov*)

15:15 – 15:30: Julie Maupin (University of Florida)

“Archaeal post-translational systems and proteostasis networks”

15:30 – 15:45: Nicholas Marzano (University of Oxford)

“Escaping the HSP70 trap: how HSP90 restores protein folding”

15:45 – 16:00: Marian Peteri (University of Dundee)

“Genome-wide CRISPR inhibition screen reveals UPR-mediated suppression of ER-phagy”

16:00 – 16:15: Girish Ram Mali (University of Oxford)

“Ciliophagy promotes motile cilia recycling under stress”

16:15 – 16:30: Renren Chen (MRC LMB)

“Pathological TDP-43 filaments accumulate at synapses and cause synaptic dysfunction”

16:30 – 16:45: Tom McGirr (Queen’s University Belfast)

“4EHP-mediated translational repression maintains cell survival following ionizing radiation”

16:45 - 17:00: Closing remarks and prizes (*John Labbadia*)

17:00 – 18:00: Extended networking

Travel and accommodation

We strongly recommend booking early. When planning your journey, please allow additional time for travel, particularly during peak hours.

The Francis Crick Institute, 1 Midland Road, London NW1 1AT, UK, is centrally located next to King's Cross St Pancras, one of London's main transport hubs with easy access by train, tube and bus.

Getting there: Check the Francis Crick Institute website for travelling information https://www.crick.ac.uk/about-us/visit-us and plan your route with the Transport for London journey planner.

Accommodation: Many hotels are located just a few minutes' walk from King's Cross and St Pancras stations, including hotel chains such as Premier Inn, Holiday Inn or Travelodge, alongside independent hotels and guesthouses.