# iDEC

# International Directed Evolution Competition

2026·Cambridge



Instant Photo





# FRIENDSHIP STAMP

This is the Wall of iDEC Friendship!

**Instant photos:** Everyone can have one free snapshot (£5 donation for the second), and you can invite our volunteers to take the photo for you and your friends.

**Friendship Stamp:** We set two bluetooth thermal printers on site.

You can download the APP on your mobile phone, then you can design a stamp pattern or text that represents you, your team, or your project, print it on a sticker, and paste your design, your team's LOGO with your best wish on the handbook of your new friends!



# Contents


1 About iDEC

2 Founding Story

3 Schedule

4 Travel & Venues

6 Registration

10 Abstracts

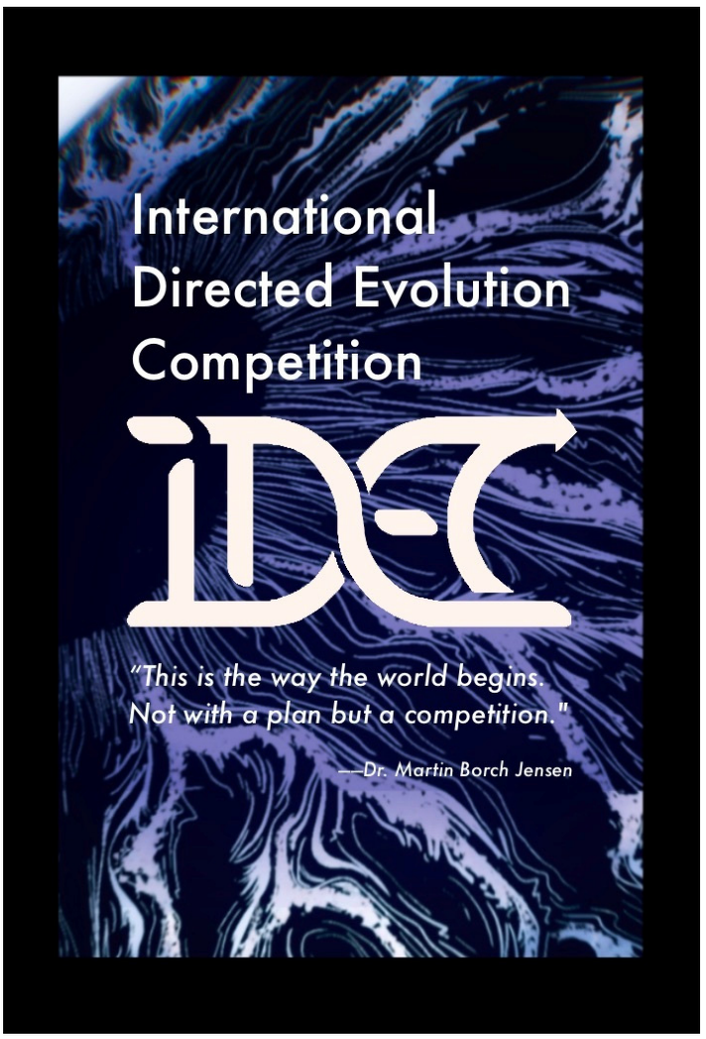
19 Invited Speakers

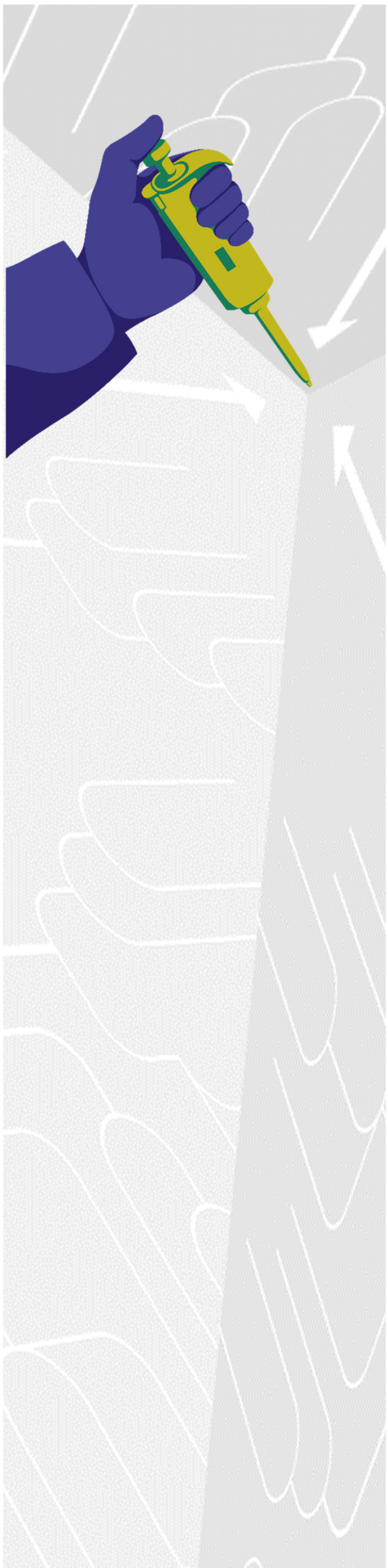
20 Acknowledgment

21 Sponsors & Collaborators

22 Gather Town Guide

23 About Sponsors



# About iDEC

**The International Directed Evolution Competition (iDEC) is a global initiative dedicated to fostering scientific education, technological innovation, and international academic exchange.**

**Directed evolution harnesses the creativity of natural evolution to overcome the limitations of rational design, opening new frontiers in biological engineering and biotechnology.**

**Our mission is to inspire young scientists to explore the power of evolution and transform creative ideas into practical solutions. By connecting students, researchers, and industry partners, iDEC aims to accelerate innovation, encourage collaboration, and bridge scientific discovery with real-world applications.**

**In 2026, the 6th International Directed Evolution Competition returns to Cambridge, bringing together students and mentors from around the world to share discoveries, exchange ideas, and celebrate the boundless potential of directed evolution.**

# The ethos of iDEC

**i**nnovation

**D**iversity

**E**quality

**C**o-construction & Co-operation.




# iDEC Founding Story

2019 marked the 210th anniversary of Darwin's birth and the 160th anniversary of the publication of the masterpiece *On the Origin of Species*.

A discussion about the future of synthetic biology was sparked by Professor Jamie Davies' article, "Real-World Synthetic Biology: Is It Founded on an Engineering Approach, and Should It Be?"

We concur that synthetic biologists should have the freedom to explore diverse methods, and we recognize the growing significance of directed evolution tools in genetic engineering over the next 5 to 10 years. Thus, the idea of fostering the development and talent cultivation of directed evolution through an international event emerged.

In early 2020, the initial concept of hosting the student competition at either the University of Edinburgh or Cambridge University, both of which were Darwin's alma maters, was proposed. We believe that dedicating the first edition of this competition to the memory of Charles Darwin is both fitting and meaningful.

This idea of iDEC received wide support. 8 students and professors form the board of iDEC as charity trustees. Finally, with the support of young directed evolution enthusiasts, volunteers, and sponsors, iDEC was officially started in 2021.

# Schedule

| Date | Timelines | | Poster |
|---|---|---|---|
| | **Time (GMT)** | **Events** | |
| **6th Nov** | 13:00 – 15:40 | Registration (**Department of Biochemistry - University of Cambridge**)<br>Collect name badges, conference bags | |
| **7th Nov** | 8:00 – 8:40 | Registration (**Gonville & Caius College**)<br>Collect name badges, conference bags<br>**With Morning Coffee (8:15 – 8:45)** | |
| | 8:45 – 9:00 | Opening Ceremony | |
| | 9:00 – 9:30 | Opening Speech | |
| | 9:30 – 10:00 | Cambridge | 01 |
| | 10:00 – 10:30 | NEFU-China | 02 |
| | **10:30 – 11:00** | **Coffee Break** | |
| | 11:00 – 11:30 | PIM-NEBS | 03 |
| | 11:30 – 12:00 | SynthImmunol | 04 |
| | **12:00 – 13:00** | **Lunch Break** | |
| | 13:00 – 13:30 | OUC-DE | 05 |
| | 13:30 – 14:00 | McMasterU | 06 |
| | **14:00 – 14:30** | **Coffee Break** | |
| | 14:30 – 15:00 | Evolution Suisse 2026 | 07 |
| | **15:00 – 15:40** | **Poster Presentations** | |
| | **16:00 – 17:30** | **iDEC Ceilidh** | |
| **8th Nov** | 8:00 – 8:30 | **Morning Coffee** | |
| | 9:00 – 9:30 | LZU GANSU | 08 |
| | 9:30 – 10:00 | Edinburgh | 09 |
| | 10:00 – 10:30 | LZU-CHINA | 10 |
| | **10:30 – 11:00** | **Coffee Break** | |
| | 11:00 – 11:30 | VCA-Prudens | 11 |
| | 11:30 – 12:30 | **Lunch Break** | |
| | 12:30 – 13:00 | **Group Photo on-site** | |
| | 13:00 – 13:10 | **Group Photo online** | |
| | **13:10 – 13:40** | **Poster Presentations** | |
| | 13:40 – 14:10 | Earth Trade | |
| | 14:10 – 14:40 | Bluepha | |
| | 14:40 – 15:00 | Panel Talk: Opportunities for Young People in AI- and Evolution-Driven Biomanufacturing | |
| | 15:00 – 15:10 | Announce Industry Advisory Group award | |
| | **15:10 – 15:30** | **Coffee Break** | |
| | 15:30 – 16:30 | Lecture by Prof. Tom Ellis | |
| | 16:30 – 17:30 | Lecture by Prof. Chang Liu | |
| | 17:30 – 18:20 | Announce Single Awards and General Awards | |
| | 18:20 – 18:30 | Walk to MillWorks | |
| | 18:30 – 19:30 | Dinner | |
| **9th Nov** | 9:00 – 10:00 | (Optional) In-person session with iDEC HQ | |
| | 10:00 – 11:00 | (For Challenge Teams) Discussion Meeting on Follow-up Project Cooperation | |

# Travel & Venues

### Important Locations

The iDEC Festival 2026 will take place at several venues across Cambridge. Please check the location for each event carefully.

6 November — Early Registration: Department of Biochemistry, University of Cambridge, Tennis Court Road.

7–8 November — Main Festival: Cavonius Centre, Stephen Hawking Building, Gonville & Caius College, 5 West Road, Cambridge, CB3 9DS.

7 November — Ceilidh: Clare Hall, Herschel Rd, Cambridge CB3 9AL.

8 November — Celebration Dinner: MillWorks, The Watermill, Newnham Road, Cambridge, CB3 9EY.

9 November — iDEC Forum: Bateman Auditorium, Gonville & Caius College, Old Courts, Trinity Street, Cambridge, CB2 1TA.

Accommodation Partner: The Møller Institute, Storey's Way, Cambridge, CB3 0DE, is an official accommodation partner of iDEC 2026, offering discounted rooms for Festival participants.

### Traveling by air:

**Stansted Airport** is the most convenient among London airports, situated just 30 miles away from Cambridge via the M11. **Coaches and trains** are available from Stansted Airport to Cambridge. From **Gatwick and Heathrow airports**, make your way to **King's Cross for a train** to Cambridge. We recommend checking for the most efficient route to Cambridge upon your arrival at the airport.

### Airport to Cambridge by train:

**Stansted Airport:** Inside the Stansted terminal, you will find a railway station where a direct train to Cambridge takes just 35 minutes. Please visit the website to check the train: https://www.stanstedairport.com/getting-to-and-from/by-train/

**Heathrow Airport or Gatwick Airport:** There are no direct train connections from Heathrow airport to Cambridge. You can go to central London stations by **Heathrow Express (to London Paddington) or Gatwick Express (to London Victoria)** first.

From Gatwick Airport, direct Thameslink trains usually run to Cambridge, taking approximately two hours; please check your travel date for engineering works and service changes before booking.

For further transfer options, you can visit the website: https://www.thetrainline.com/ to check the trains.

A frequent train service connects **Cambridge - London**, with trains departing from **Liverpool Street** and **King's Cross stations**. The fastest journey takes just 52 minutes, and during peak hours, there are seven trains per hour.

### Airport to Cambridge by Coach

National Express operates direct coaches between Cambridge and both **Stansted** and **Heathrow airports**. When booking, select Cambridge Parkside (City Centre) as your destination.

For timetables and bookings, visit www.nationalexpress.com.

### Cambridge Railway Station to Festival Venues

**To Department of Biochemistry (6 November — Early Registration):**

- Walking: Approximately 20–25 minutes from Cambridge Railway Station. Follow Station Road and Hills Road, then turn onto Lensfield Road towards Tennis Court Road.
- Taxi: Approximately 5–10 minutes, depending on traffic. Taxis are available outside the railway station.
- Bus: Take a city-centre bus towards Regent Street or Drummer Street, followed by a short walk to Tennis Court Road. Walking directly from the railway station may be more convenient.

**To Stephen Hawking Building (7–8 November):**

- **Bus:** Take the Universal **U2** service towards Eddington and alight at West Road (University Library), a short walk from the venue.
- **Taxi:** Approximately 10–15 minutes.

- **Walking:** Approximately 35–40 minutes.

**To Bateman Auditorium (9 November):**

- **Bus:** Take a city-centre service towards Drummer Street, followed by a short walk to Trinity Street.
- **Taxi:** Approximately 10–15 minutes, subject to city-centre access restrictions.
- **Walking:** Approximately 25–30 minutes.

**To Møller Institute (Accommodation):**

The Møller Institute is approximately 15–20 minutes by taxi from Cambridge Railway Station and 20–25 minutes on foot from the main Festival venue.

Please visit https://www.google.com/ and search the bus information by entering 'Cambridge Station to your destination'

## Important Railway Travel Notice

Sunday, 8 November 2026: Planned engineering works will affect trains between Stevenage and Cambridge, with replacement buses operating on affected routes. Participants travelling to or from London King's Cross should check the latest information and allow extra time.

For updates, visit https://www.nationalrail.co.uk.

## MAIN ENTRANCE

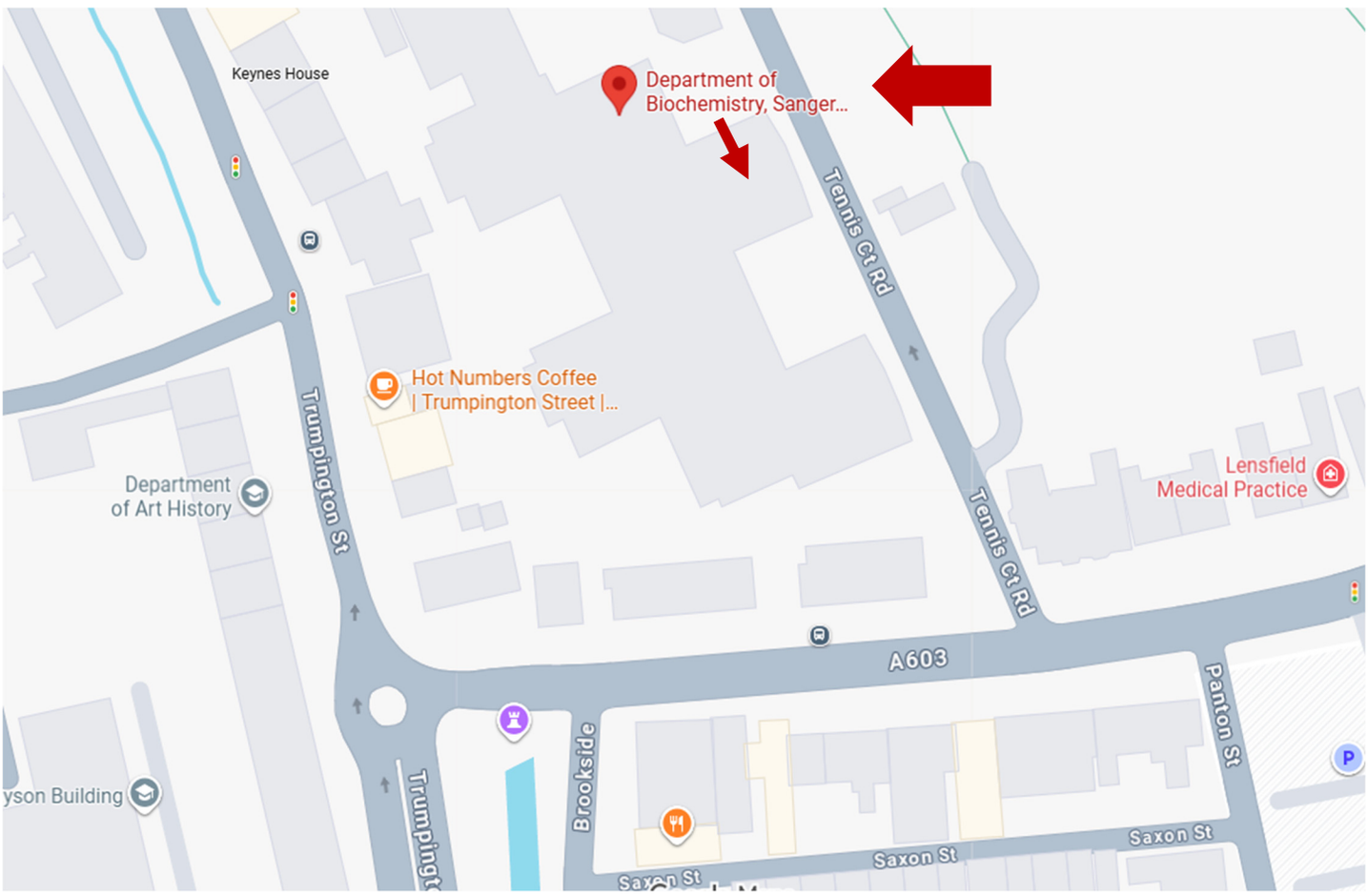
Please use the map on the page 7-8 to find the **Cavonius Centre in Stephen Hawking Building** and **Bateman Auditorium**.

# Registration

When registering, teams can receive a conference bag, conference brochure, iDEC hat, and name cards. The slides can also be copied to a computer at the venue.

**Please note** that **registration in the afternoon of the 6th Nov will be held at the Department of Biochemistry at Cambridge University (Meeting Room A, Sanger Building, 80 Tennis Ct Rd, Cambridge CB2 1GA) 13:00 – 15:40.**

**Meeting Room A is on the left as you enter the door.**

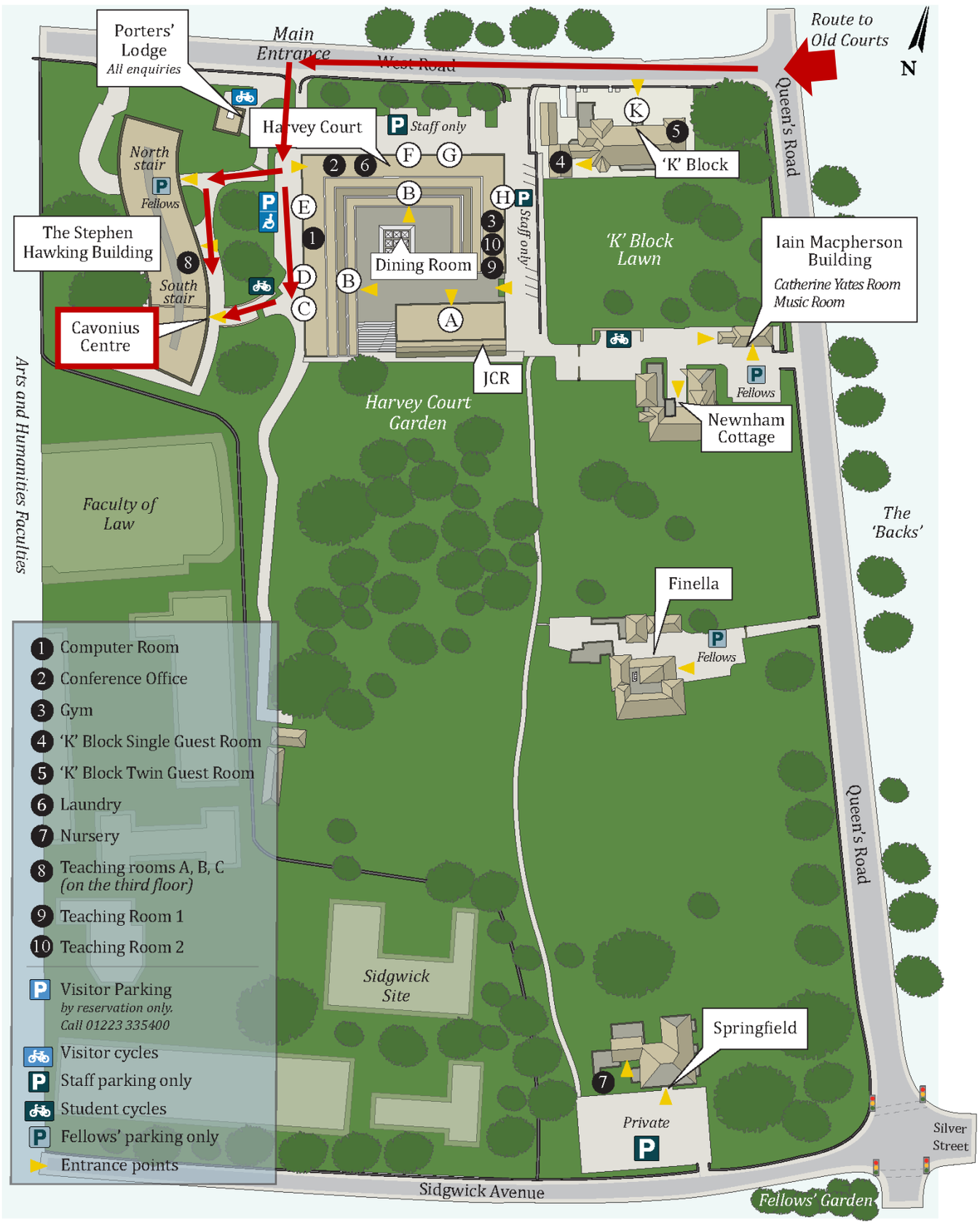



**Registration in the morning of the 7th Nov will be held at the venue (Stephen Hawking Building, Gonville & Caius College) 8:00 – 8:40**. We will have a registration reception at the entrance to the Cavonius Centre in Stephen Hawking Building on 7th Nov.

Gonville & Caius
UNIVERSITY OF CAMBRIDGE

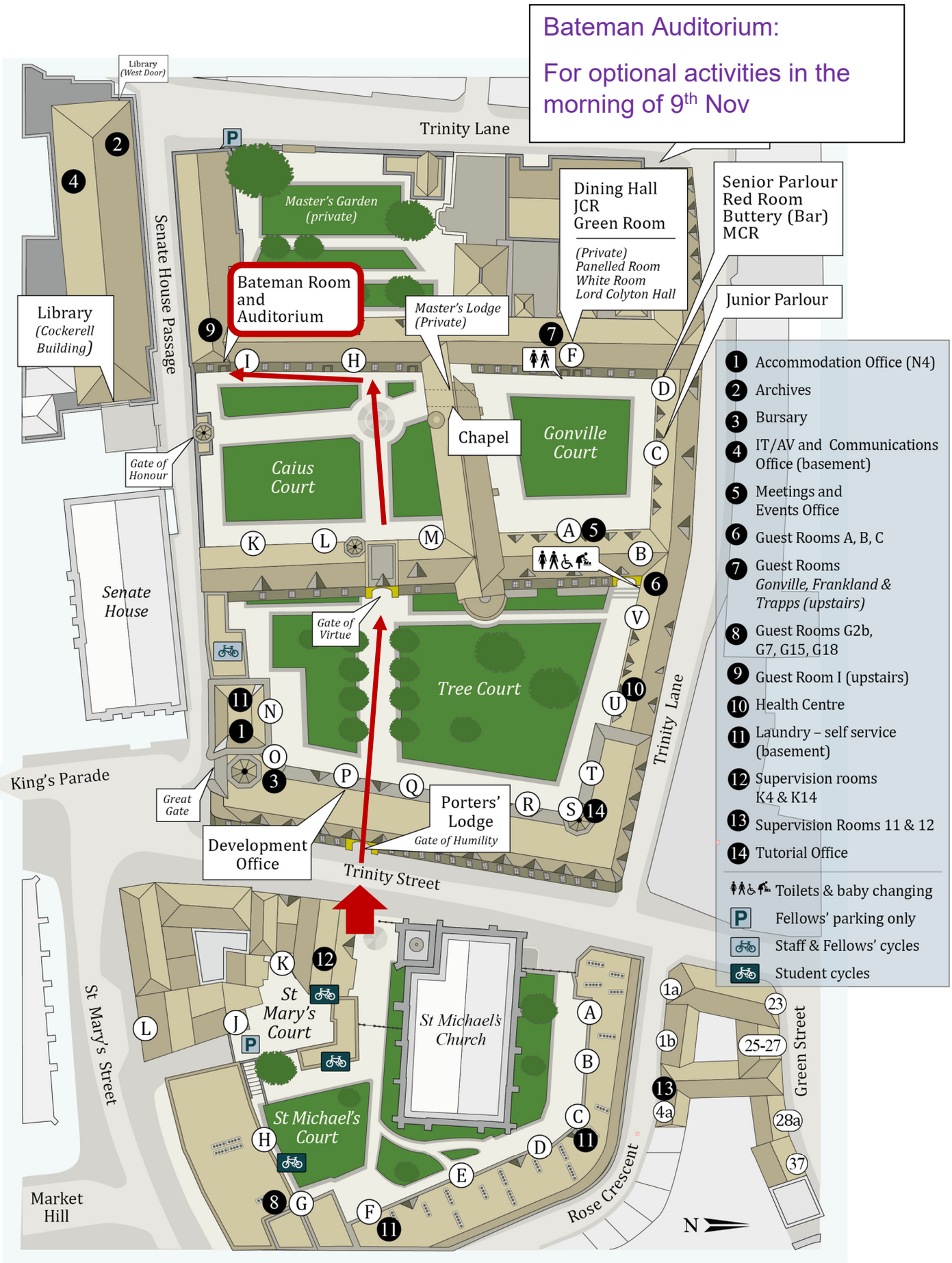
Cavonius Centre in Stephen Hawking Building: For main event from 7th to 8th

# Harvey Court




Design, N Hawksworth, www.wayfinding-consultants.co.uk, 01223 693082

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Design, N Hawksworth, www.wayfinding-consultants.co.uk, 01223 693082

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# Online - Gather Town

To facilitate remote participation, Gather Town Space will remain open this year.

We will integrate Zoom with Gather Town to seamlessly blend online and on-site activities. All posters will be displayed synchronously on Gather Town.

As no teams will be delivering their presentations online this year, Gather Town will primarily serve as a virtual platform for participants who are unable to attend the festival in person. It will allow them to follow the competition presentations, explore team posters, and ask questions remotely.

Based on the situation at the on-site venue, all on-site teams will use Gather Town for their presentations directly, and we will also open the Zoom as a backup.

# Entre Gather Town iDEC 2026: QR code

# Password: 2026

## Gather Space will open from 7th to 8th Nov.

# Cambridge

## Directed Evolution of Novel Intrinsically Disordered Proteins (IDP) to Improve the Solubility of Recombinant Proteins (9:30 7th Nov)

Protein aggregation limits recombinant protein production, motivating the development of short solubility-enhancing and protective peptides. We combined computational library design with experimental selection to explore variants derived from intrinsically disordered NEXT and SSB tags and the CAHS1 protective protein. NEXT and SSB libraries were evaluated using carbenicillin selection linked to aggregation-prone β-lactamase while CAHS1 variants underwent freeze-thaw selection. Sequencing of variants revealed changes in variant composition across all three libraries, supported by Monte Carlo-calibrated chi-squared tests. Property based clustering associated NEXT and SSB enrichment with greater predicted charge and hydrophilicity. There is also an enrichment of CAHS1 variants with a stronger amphiphilic helical character. These findings identify candidate property trends and sequences for further investigation. Further work is required to characterise reproducibility of findings and quantify protein solubility. This workflow provides a foundation for subsequent evolution and validation of IDP-derived solubility enhancers and protective peptides.

# NEFU-China

## Efficient Dual-Pathway Valorization of Lignin-Derived VA via Biosensor-Assisted Directed Evolution (10:00 7th Nov)

Lignin is an abundant renewable source of aromatic carbon, yet its structural heterogeneity severely limits biological valorization. A three-step biological funneling strategy was established to converge diverse lignin-derived aromatics into vanillic acid (VA), providing a unified starting point for downstream engineering. Building on previous experimental evidence from our laboratory supporting 4-HB (4-HB)-to-chorismate (CHA) conversion, the pathway was extended upstream by investigating VA-to-4-HB conversion, with the low catalytic activity of the demethoxylation enzyme (ODM) identified as a key bottleneck. By integrating error-prone PCR with a PobR-based 4-HB-responsive transcriptional biosensor, variant 1-20-7 was identified. Its measured activity was 29.28-fold that of the wild type (WT) upon rescreening. Meanwhile, a VA-to-Pyruvate (Pyr) pathway was constructed toward fully green bioconversion. Finally, a low-cost, modular microfluidic platform was developed to support future high-throughput screening. Together, molecular evolution, pathway engineering, and hardware-assisted screening provide a framework for the valorization of lignin-derived carbon.

# PIM-NEBS

## Beyond Geometric Preorganization: A Bottleneck-Guided Pre-Reaction-State Framework for PET Hydrolase Engineering (11:00 7th Nov)

Enzyme engineering can identify PET hydrolase variants with improved activity, yet the catalytic bottleneck relieved by a beneficial mutation often remains unclear. Here we compare two experimentally validated FAST-PETase substitutions discovered through distinct design routes. Graph-learning-guided Y87Q preserves the global fold while remodeling the second-shell environment and increasing the population of geometric pre-reaction states (PRSs). Molecular dynamics and distortion/interaction analysis associate this redistribution with a reduced structural cost of reaching the transition-state region. By contrast, the active-site substitution S187Y enhances PET-film hydrolysis in two enzyme scaffolds despite weak correspondence between docking score and activity, and quantum-chemical analysis indicates enhanced transition-state interactions. These results motivate a two-level framework separating PRS quantity, the accessibility of attack-compatible configurations, from PRS quality, their conditional chemical productivity. This bottleneck-guided framework links conformational sampling with chemical reactivity and provides a mechanistic basis for iterative PET hydrolase engineering.

# SynthImmunol

## STAR-Trap macrophages selectively capture IL-6/sIL-6Rα complexes to attenuate IL-6 trans-signaling (11:30 7th Nov)

IL-6 trans-signaling is mediated by recruitment of widely expressed gp130 by the IL-6/sIL-6Rα complex, expanding IL-6 responsiveness and promoting chronic inflammation. Selective inhibition therefore represents an important strategy for anti-inflammatory intervention. We targeted the composite gp130-binding surface formed by IL-6 and sIL-6Rα. RFdiffusion and ProteinMPNN generated 27 de novo candidate proteins, which were fused to the FcRγ intracellular domain and screened through B cell surface display and flow cytometry to identify a lead sequence. We coupled dCas9-Activation-Induced Cytidine Deaminase*Δ-mediated hypermutation with gp130-caspase9 functional selection, linking B cell somatic hypermutation to survival-based selection and enriching variants with complex-selective binding and gp130-competitive activity, termed STAR6. Surface expression of the evolved protein in macrophages extended competitive blockade to cell-mediated complex capture and clearance. This study harnesses B cell somatic hypermutation for functional evolution of de novo-designed proteins and translates selective recognition of a cytokine-receptor complex into cellular clearance, providing a strategy for selectively modulating IL-6 trans-signaling.

# Time for Lunch

**Chef's Selection of fresh meat, fish and vegetarian wraps, baguettes and sandwiches.**

**Served with tea and freshly brewed coffee, orange juice and mineral water, vegetable crisps and fresh whole fruit with a sweet of the day**

# Safety Tips for Lunch

**Due to the large number of attendees, we kindly ask everyone to queue in an orderly manner when collecting food. Once you have collected your meal, you can return to the conference venue promptly or enjoy your meal in the outdoor areas, weather permitting.**

**Bon Appétit!**

# OUC-DE

## Semi Rational Engineering of MddH for Enhanced $H_2S$ Methylation Toward Whole Cell Cascaded Biosynthesis of DMS (13:00 7th Nov)

Hydrogen sulfide ($H_2S$) is a toxic inorganic-sulfur pollutant. Bioconversion of waste-gas-derived $H_2S$ into dimethyl sulfide (DMS) offers a promising route for sulfur resource recycling. However, wild-type SAM-dependent methyltransferase MddH exhibits low substrate affinity and substrate inhibition. In this study, homologous alignment and molecular docking were performed to build the MddH-SAM-$H_2S$ ternary complex model. Key residues E63, E91 and T108 were selected to construct site-directed mutants (E63Q, E91Q, T108I) and combinatorial variants. Whole-cell biocatalysis combined with headspace gas chromatography was applied to characterize catalytic performance and quantify MeSH and DMS production. E91Q significantly increased DMS production by 5.1%, whereas E63Q blocked the second methylation step. This work establishes an optimized biocatalytic module for DMS production. It should be noted that the current work focuses on in vitro characterization using crude cell lysates; reliable quantitative whole-cell assays will be pursued in future work.



# McMasterU

## Temperature-controlled cell lysis of modified oleaginous *Saccharomyces cerevisiae* using RNA thermosensors (13:30 7th Nov)

Our project aimed to engineer *Saccharomyces cerevisiae* to overexpress lipids coupled with lysis driven by temperature control. Through computational modeling, a pool of a variety of RNAts narrowed down to the three most optimal. These sequences successfully yielded melting temperatures between 36-44°C. Lipid accumulation was further validated through Nile Red fluorescence readings comparing wild-type BY4741 yeast strain and BY4741 PXA1 yeast strain, which showed higher levels of lipids in the knock out strain than wild type. PXA1 is a gene that brings lipids to the peroxisomal membrane for their degradation; by deleting it, more lipids built up. The other strategy to overexpress lipid synthesis genes such as ACC1** and DGA1 were not able to be validated experimentally due to optimization constraints. Thus, while the theory of the project was verified through modeling data and literature, more troubleshooting for in vitro experiments should be conducted in the future.

# Evolution Suisse 2026

## MutaT7-Driven Continuous Evolution of Engineered *Qt*Encapsulin via Co-Encapsulated dCas9–sgRNA (14:30 7th Nov)

The delivery of a protein and its associated RNA to the same intracellular compartment at a defined stoichiometry remains one of the main challenges for ribonucleoprotein-based therapeutics, such as CRISPR-Cas9 treatments for genetic and neurodegenerative disorders. Protein nanocages offer a potential single-vehicle solution. However, most of them, including the encapsulin of *Quasibacillus thermotolerans* (*Qt*Enc), natively bind only protein cargo. Here, we engineered *Qt*Enc, using catalytically dead Cas9 (dCas9) and single guide RNA (sgRNA) as a model ribonucleoprotein, for dual protein-RNA encapsulation in a continuous evolution system based on the Deaminase-T7 RNA polymerase fusion protein (MutaT7). Although external engineering with His-tag led to aggregation, the mutagenesis plasmid was successfully cloned and a stop-codon reversion assay confirmed MutaT7 mutagenic activity. These results establish a foundation for future work on continuous evolution in cages.

# Poster Presentations (15:00 - 15:40 GMT, 7th, 13:10 – 13:40 GMT, 8th)

| TEAMS | NO. | LOCATION |
|---|---|---|
| CAMBRIDGE | 1 | On-site |
| NEFU-CHINA | 2 | On-site |
| PIM-NEBS | 3 | On-site |
| SYNTHIMMUNOL | 4 | On-site |
| OUC-DE | 5 | On-site |
| MCMASTERU | 6 | On-site |
| EVOLUTION SUISSE 2026 | 7 | On-site |
| LZU GANSU | 8 | On-site |
| EDINBURGH | 9 | On-site |
| LZU-CHINA | 10 | On-site |
| VCA-PRUDENS | 11 | On-site |

**Poster Presentations**

**During the poster presentation session, team members will present their projects directly to judges and attendees at their posters.**

**On-site judges will visit each team's poster and spend approximately 5–10 minutes evaluating its quality. Therefore, each team is required to have at least one member present at their poster throughout the session to introduce their project and answer questions from judges and other attendees.**

# Special Activity 2026

**Scottish Ceilidh — Celebrating 200 Years of Young Minds Exploring Evolution**

This year marks the **200th anniversary of Charles Darwin joining the Plinian Society at the University of Edinburgh (1826–2026)**, a student scientific society where he began sharing his early discoveries and exploring the natural world.

To celebrate this historic milestone and honour **iDEC's own origins in Edinburgh**, we have prepared a special Scottish cultural experience for all participants — **a traditional Scottish Ceilidh (16:00–17:30, 7th November)**.

A *Ceilidh* (pronounced "kay-lee") is a lively Scottish social gathering featuring traditional folk music and group dancing. Accompanied by live musicians, an experienced *caller* will guide everyone through the dances, step by step.

**No previous dancing experience is required!**

The dances are designed to be inclusive, enjoyable, and a wonderful opportunity to meet fellow participants from around the world.

**Venue: Clare Hall, Cambridge.**

For everyone's safety and enjoyment, please follow the caller's instructions, be mindful of other dancers, and avoid pushing or rough movements.

If you feel unwell or prefer not to dance, you are very welcome to enjoy the music and atmosphere as a spectator.

**Let's celebrate two centuries of scientific curiosity, youthful creativity, and the spirit of evolution — together!**



# LZU GANSU

## Engineered *Lactococcus lactis* Achieves Dental Plaque Biofilm Reporting and Clearance

### (9:00 8th Nov)

The initiating factors of oral chronic infectious diseases such as dental caries and periodontal disease lie in the colonization of pathogenic biofilms and microecological imbalance, whereas conventional diagnostic methods have insufficient sensitivity at the occult early plaque stage, and conventional interventions lack targeting specificity. In this study, food-grade safe probiotic *Lactococcus lactis* was used as the chassis to construct an engineered live biotherapeutic system that simultaneously possesses biofilm-targeted anchoring, sensitive sensing and amplification of pathogenic signals, instrument-free naked-eye direct readout, and stringent biocontainment characteristics, providing a safe and feasible novel synthetic biology strategy for non-invasive, point-of-care immediate warning and in situ microecological regulation of early caries in the oral cavity.

# Edinburgh

## Directed Evolution of the Multifunctional Cellulase CxnA

### (9:30 8th Nov)

Commercial biofuel conversion remains economically unviable, and enzyme production accounts for ~30% of production costs. By producing increased endoglucanase, exoglucanase activities, and Cex β-glucosidase activity in *Escherichia coli*, production costs would dramatically decrease. Error-prone polymerase chain reaction mutated the CxnA construct, enabling directed evolution towards improved enzymatic activity. CxnA is a fusion enzyme made of domains CenA (endoglucanase) and Cex (exoglucanase). In silico analyses investigated potential mutations affecting enzyme stability and cellobiose binding, while experimental screening assessed enzyme activities. Congo red screening identified candidate mutants retaining endoglucanase activity, while X-gluc screening revealed baseline β-glucosidase activity in wild-type CxnA. No mutants exhibited activity comparable to the positive control. A 4-methylumbelliferyl-β-D-cellobioside assay quantified exoglucanase activity. Although limited library sizes and experimental constraints prevented definitive identification of improved variants, there was successful establishment of a CxnA directed evolution pipeline as a proof of concept for iterative cycles.

# LZU-CHINA

## The engineered *Escherichia coli* Nissle 1917 targets the inhibition of intestinal pathogenic *Salmonella* by responding to quorum sensing signals and tetrathionate inflammatory signals (10:00 8th Nov)

In modern surgical intensive care and perioperative clinical management, surgical trauma, systemic stress, and extensive exposure to prophylactic broad-spectrum antibiotics can significantly disrupt the homeostasis of the patient's intestinal indigenous microbiota. This disruption leads to a severe decline in colonization resistance mediated by strict anaerobes, subsequently triggering explosive proliferation and mucosal invasion of opportunistic pathogens, particularly intestinal pathogenic *Salmonella*. Such events markedly increase the risk of enteric sepsis and multiple organ dysfunction syndrome. However, traditional fecal microbiological culture methods exhibit significant delays, and blind empirical antibiotic interventions can exacerbate intestinal dysbiosis and promote antibiotic resistance mutations. There is an urgent clinical need for intelligent live biopharmaceuticals capable of real-time pathological monitoring in situ within the intestinal lumen, non-invasive bedside rapid diagnostics, targeted bactericidal activity, and stringent biosafety containment capabilities. This study employs the probiotic *Escherichia coli* Nissle 1917 (EcN1917), known for its excellent mucosal colonization ability and clinical safety record, as a cellular chassis to design and construct an intelligent diagnostic and therapeutic live engineering system based on a tetracistronic plasmid cooperative regulatory framework.

# VCA-Prudens

## From Curiosity to Catalyst: How an AI Agent Enabled a High School Team to Evolve a Better ISCro4 Recombinase (11:00 8th Nov)

Directed evolution has created transformative genome-editing tools, yet its practice demands interdisciplinary expertise — in mutagenesis design, high-throughput screening, and data analysis — that places it out of reach for most student laboratories. Here we show that an AI scientific agent can lower this barrier: as a high school research team, we used Biomni as an on-demand mentor to complete a full directed-evolution campaign on ISCro4, an RNA-guided recombinase that mediates the targeted integration of large DNA fragments. Biomni assisted target selection, troubleshooting of plasmid construction, redesign of the activity assay, DMS-guided mutation selection, and primer design. Screening the resulting variants in *Escherichia coli* identified an ISCro4 variant, A225S, with recombination activity improved over the parent variant. Our work provides a more active ISCro4 variant for large-fragment genome editing and, more broadly, demonstrates that AI agents can enable inexperienced teams to plan, execute, and troubleshoot technically demanding protein-engineering projects.

## Time for Lunch

**Chef's Selection of fresh meat, fish and vegetarian wraps, baguettes and sandwiches.**

**Served with tea and freshly brewed coffee, orange juice and mineral water, vegetable crisps**

**and fresh whole fruit with a sweet of the day**

## Safety Tips for Lunch

**Due to the large number of attendees, we kindly ask everyone to queue in an orderly manner when collecting food. Once you have collected your meal, you can return to the conference venue promptly or enjoy your meal in the outdoor areas, weather permitting.**

**Bon Appétit!**

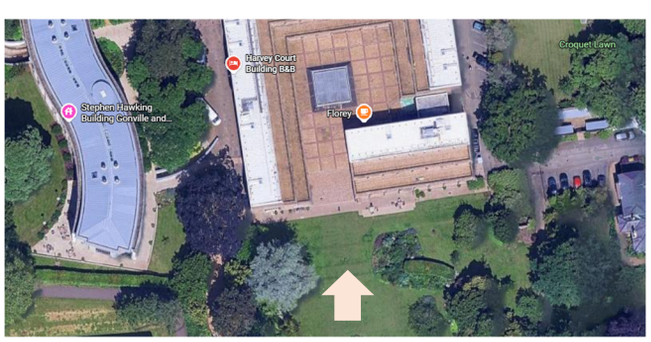
# Group Photo

Group photos are divided into online and on-site.

**The online photo session time is 13:00 GMT 8th Nov.**

The location for the online group photo is the lawn outside the Gather Town venue. Please **choose your favorite look for your avatar**, and choose a location on the lawn where everyone can see you and your name.




**The on-site photo session time is 12:30 GMT 8th Nov.**

The location for the on-site group photo is outside the **Cavonius Centre** (above).

Our volunteers will guide everyone to the photo location after lunch.

Cambridge rains a lot in winter. If it rains, the group photo will be taken indoors.

# Invited Speakers

We are honored to have Dr. Yang Liu from the MRC Laboratory of Molecular Biology deliver the opening talk for iDEC Festival 2026!




iDEC HQ is honored to invite two senior scientists, Prof. Tom Ellis and Prof. Chang Liu in the field of synthetic biology and directed evolution to bring invited lectures to our participants.

The topics of the two invited lectures jointly outline the core themes that contributed to the creation of iDEC:



# Acknowledgment

iDEC 2026 could not be successfully organized without the help of our sponsors, collaborators, iDEC HQ members and participants.

We thank **Bluepha**, **New England Biolabs, Earth Trade, and IDT** for their generous support.

**iDEC 2026 Invited Speakers:**

Dr. Edoardo Gianni from MRC Laboratory of Molecular Biology (LMB), UK

Dr. Vojislav Gligorovski from New York University, US

Dr. Yang Liu from MRC Laboratory of Molecular Biology (LMB), UK

Dr. Tom Ellis from Imperial College London, UK

Dr. Chang Liu from EIT Oxford, UK

**iDEC 2026 Judge List:**

Dr. Yangqi Gu from the MRC Laboratory of Molecular Biology (LMB), UK

Dr. Fankang Meng from the Imperial College London, UK

Dr. Ganesh Agam from the MRC Laboratory of Molecular Biology (LMB), UK

Dr. Oksana Sintsova from the MRC Laboratory of Molecular Biology (LMB), UK

Dr. Yan Liao from the University of Nottingham, UK

Dr. Vojislav Gligorovski from New York University, US

Dr. Sasa Svikovic from AstraZeneca, SE

Dr. Shiyuan Li from Cathay Fortune Capital Investment, CN

Yanci Qiu from the Bluepha, CN

**iDEC Executive Committee Members:**

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**iDEC 2026 Sponsor Representatives:**

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**iDEC 2026 Teams:**

Cambridge, NEFU-China, PIM-NEBS, SynthImmunol, OUC-DE, McMasterU, Evolution Suisse 2026, LZU GANSU, Edinburgh, LZU-CHINA, VCA-Prudens

# Sponsors & Collaborators

iDEC is generously supported by our sponsors and collaborators to carry out public welfare education and young talents in scientific and technological innovation.

This year, our sponsor Bluepha provided iDEC with strong financial and industry-related support again.




At the same time, iDEC 2026 has received strong support from more iDEC sponsors.

We are grateful for the generous support from the industry:







For more information about iDEC sponsors, please read our sponsor pages.

We also maintain collaboration with the non-profit organization Regenesis, the Møller Institute (Cambridge University), Clare Hall (Cambridge University) and the dynamic dance band Flying Cat.



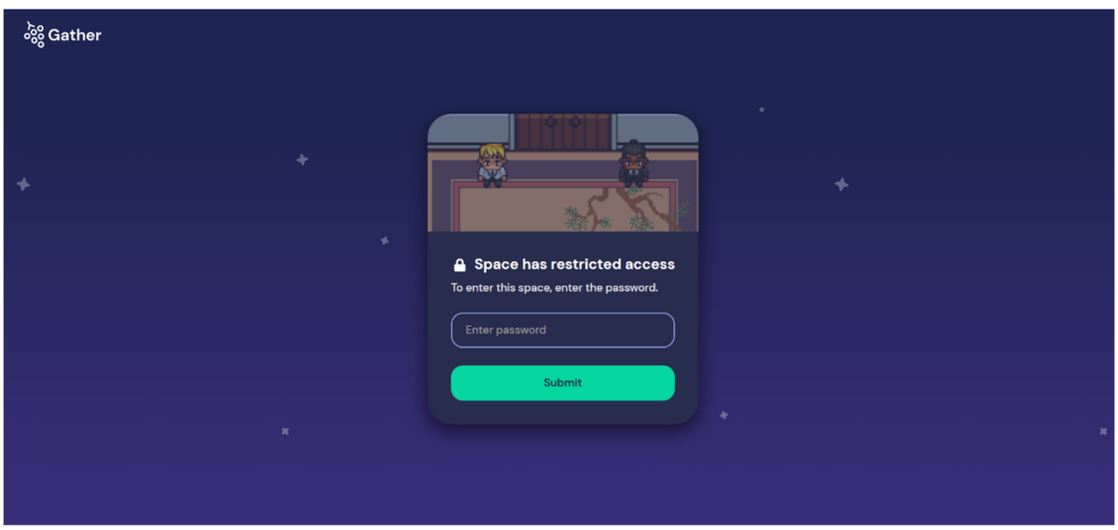



# Gather Town Guide

2D virtual platform Gather Town is used for the online iDEC Festival.

All team members will receive a link to join Gather Town before the opening ceremony. Here is a simple guide on how to use Gather Town.

Every participant must sign in before entering the **iDEC 2026** space by the link we send. **The password is '2026'**.




In the Gather virtual environment, you can set your own image and move freely. When the virtual character is close to others, you can hear each other's voices.

You can also find tables and chairs placed on the carpet in the virtual venue. The carpet area is a private space where only virtual characters who enter the carpet region can talk.

In the poster display area, we will display the posters of each team and marked them with number. During the poster presentation, the judges will visit the poster from time to time and listen to the introduction of the poster content by the team.

The carpet area in front of the poster is a soundproof space, and only people who enter the area can talk to each other.

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Build one platform. Create one hundred products Reach five billion people

## Evolve it in the lab. Scale it in our plant

Founded in 2016, Bluepha designs novel biomolecules and low-carbon production pathways through AI-powered synthetic biology, serving advanced materials, modern agriculture, food, healthcare, and other industries.

Bluepha runs the whole chain in one company: an AI-powered, high-throughput strain engineering platform in Shanghai, pilot-scale process development, and a fermentation base in Yancheng, Jiangsu with 100,000 tons of annual capacity, covering fermentation, extraction and formulation.

Drawing on a decade of proprietary data spanning R&D, pilot-scale testing, and production, Bluepha developed Synbio MARS™, a Multi-Agentic & Robotic System powered by LLMs. The system significantly improves R&D efficiency and capability, shortening product commercialization timelines by approximately 70% compared with industry averages.

From lab to mega-factory, Bluepha has crossed synthetic biology's "Valley of Death." The next step: scaling into global markets.



High-Throughput Fermentation Platform



Total Laboratory Automation

## Industrial strength, in numbers

- 100,000 tons of annual fermentation capacity at our Yancheng, Jiangsu base, covering the full chain from fermentation to extraction to formulation.
- 30× the throughput in our AI-powered strain platform: from 100 to 3,000 strains built, and from 300 to 10,000+ samples tested, per month.
- 3 years → under 6 months: the strain iteration cycle.

## Awards and Honours

- MIT Technology Review's 50 Smartest Companies
- Forbes China's Top 50 Most Innovative Companies
- Raised over RMB 1.5 billion in total, including Series B4
- 120+ invention patents and a team of 200+
- Biotech Unicorn

## Core Products

- **Advanced Materials**
  PHA bio-based materials in mass production · food-contact certified in China, the US, the EU and Japan

- **Agriculture**
  T6P, PHA and peptide-based biopesticides · field trials in 25 provinces

- **Food & Healthcare**
  Gut microplastic remediation · “microplastic-free” paper coatings · injectable anti-wrinkle fillers

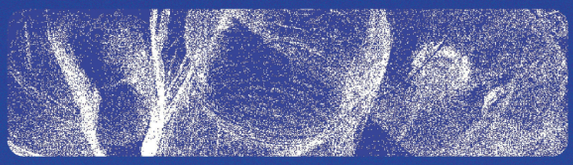
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## We Are Hiring



### Management Trainee

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Management Trainees will complete systematic rotations across R&D, production, sales, and middle- and back-office functions, building a comprehensive understanding of the full value chain of synthetic biology industrialization.



### AI Applications Researcher

Class of 2027. Bachelor’s degree or above in computer science, AI, machine learning, computational biology, or related fields.

**Requirements:**

- Strong foundation in deep learning and machine learning
- Familiarity with PyTorch, TensorFlow, or similar frameworks
- Hands-on experience in model training and tuning
- Strong engineering skills in Python and scientific computing tools

You will build AI models that learn from high-throughput screening data and full-process fermentation data, from the lab to the plant.



### R&D Scientist

Class of 2027. Master’s degree or above in synthetic biology, microbiology, molecular biology, or related fields.
You will design, build and screen strain variants on our AI-powered, high-throughput platform, then follow them through bioreactor arrays (0.5 to 200 liters) toward plant-scale fermentation.

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- Meaningful impact.

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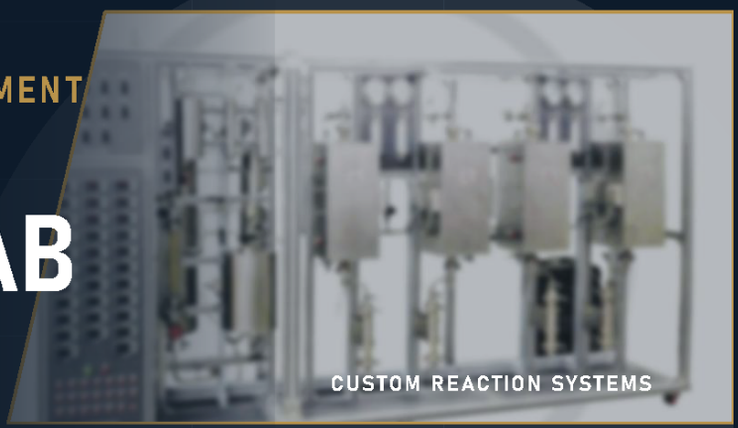
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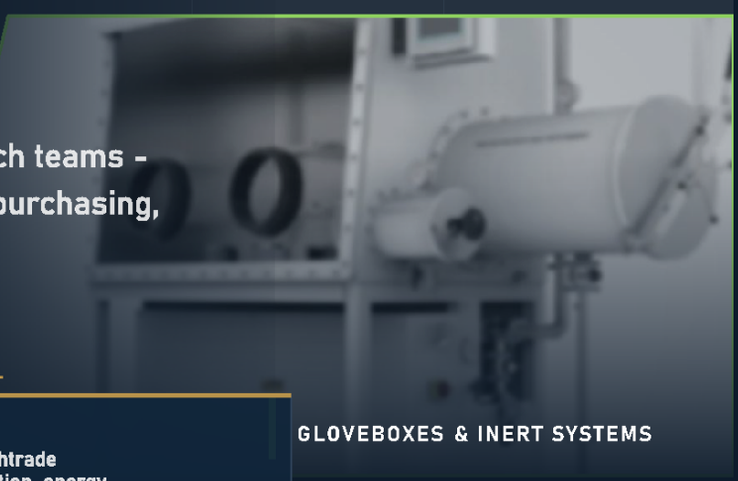
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