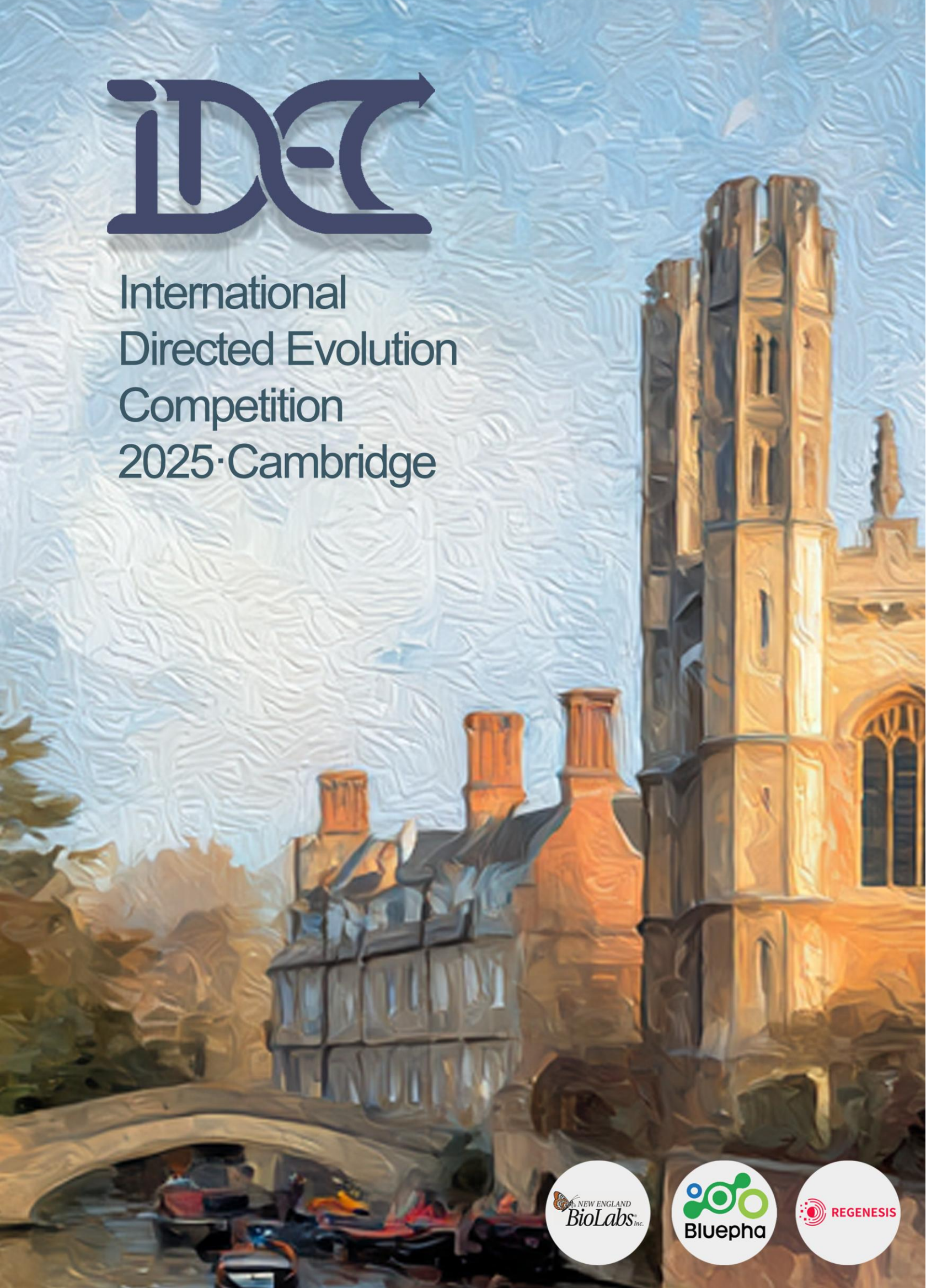




International
Directed Evolution
Competition
2025·Cambridge



IDEC

Instant Photo





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.

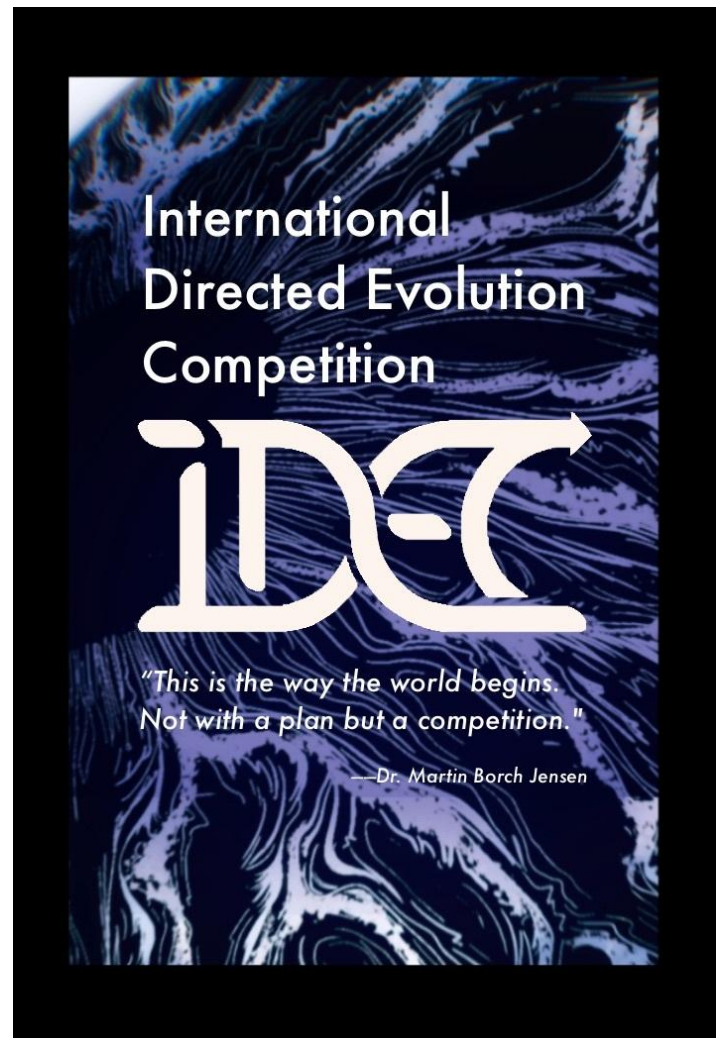
Friendship Stamp: We set two bluetooth thermal printers on site.

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!



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About iDEC

International Directed Evolution Competition (iDEC) is an international initiative focused on creating a scientific community for education, technology sharing, and academic exchange.

Directed evolution, a powerful irrational design approach rooted in rational foundations, will address shortcomings in genetic engineering over the next decade.

Our mission is to inspire young students to harness the creative potential of evolution, arming future bioengineers with the skills to tackle real-world challenges. The synergy of directed evolution technology, youthful creativity, and their innate drive for exploration promises to greatly expand innovation and practical applications, benefiting both the scientific and industrial sectors.

In 2025, the 5th edition of iDEC is being held on-site in Cambridge. We warmly welcome students and mentors from around the world to meet and exchange ideas.

The ethos of iDEC

innovation

Diversity

Equality

Co-construction & Co-operation.



iDEC Founding Story

2019 is 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+1)	Events	
24 th Oct	13:00 – 15:40	Registration (Department of Biochemistry - University of Cambridge)	
		Collect name badges, conference bags	
25 th Oct	8:00 – 8:40	Registration (Gonville & Caius College) Collect name badges, conference bags With Morning Coffee (8:15 – 8:45)	
	8:45 – 9:00	Opening Ceremony	
	9:00 – 9:30	Opening Speech by Prof. Florian Hollfelder	
	9:30 – 10:00	OUC-DE	01
	10:00 – 10:30	McMaster BioDesign	02
	10:30 – 11:00	Coffee Break	
	11:00 – 11:30	OncoStrat_NMU	03
	11:30 – 12:00	Evolution Suisse 2025	04
	12:00 – 13:00	Lunch Break	
	13:00 – 13:30	CPU_CHINA	05
	13:30 – 14:00	Edinburgh	06
	14:00 – 14:30	Coffee Break and hang up posters	
	14:30 – 15:00	LZDX	07
	15:00 – 15:50	Poster Presentations	
	16:30 – 17:30	A special 5th anniversary event	
Time (GMT)		Switch to Winter Time (-1h) at 2:00 AM 26th Oct	
26 th Oct	8:00 – 8:30	Morning Coffee	
	9:00 – 9:30	OUC-Marine Drugs	13
	9:30 – 10:00	PIM-VCA	08
	10:00 – 10:30	SynthImmunol_NMU	09
	10:30 – 11:00	Coffee Break	
	11:00 – 11:30	PIM-NEBS	10
	11:30 – 12:00	LZU-MEDICINE-CHINA	11
	12:00 – 12:30	NEFU_China	12
	12:30 – 13:30	Lunch Break and hang up posters	
	13:20	Group Photo online	
	13:30 – 13:50	Group Photo on-site	
	13:50– 14:40	Poster Presentations	
	14:40 – 15:00	Announce Special Awards and Industry Advisory Group award	
	15:00 – 15:30	Coffee Break	
	15:30 – 16:30	Lecture by Prof. Mark Howarth	
	16:30 – 17:30	Lecture by Prof. Somenath Bakshi	
	17:30 – 18:00	Announce Single Awards and General Awards	
	18:00 – 18:30	Go to the Millworks	
	18:30 – 19:30	Dinner	

Traffic

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. 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.

Cambridge Railway Station to Gonville and Caius College/Møller Institute (partner accommodation)

Cambridge's train station is located south of the city centre. The distance between Cambridge Station and Gonville and Caius College is about 1.3 mile. You can easily reach the College by taxi (12 - 15 min) or bus (20 - 30 min).

From Cambridge railway station to Gonville and Caius College: **Bus 1, Bus 7** depart from the railway station every several minutes, transporting you to the bus station **St Andrew's Street (Bus 1)** or **Emmanuel Street (Bus 7)** for Gonville and Caius College. If you prefer to walk, the journey to the College takes approximately 30 minutes on foot from the railway station.

From Cambridge railway station to Møller Institute: The distance is relatively far. You can take a taxi or **Bus A** (about 40 minutes). For information about Bus A, please visit: <https://www.stagecoachbus.com/routes/east/A/st-ives-trumpington-pr/XEBA000.O>.

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

Airport to Cambridge by Bus

Stansted Airport: National Express coaches offer service from London Stansted to Cambridge.

Heathrow Airport: National Express coaches offer service from London Heathrow to Cambridge.

Please visit the website <https://www.nationalexpress.com/> to find more information.

Note: Please choose the bus station 'City Centre'.

MAIN ENTRANCE

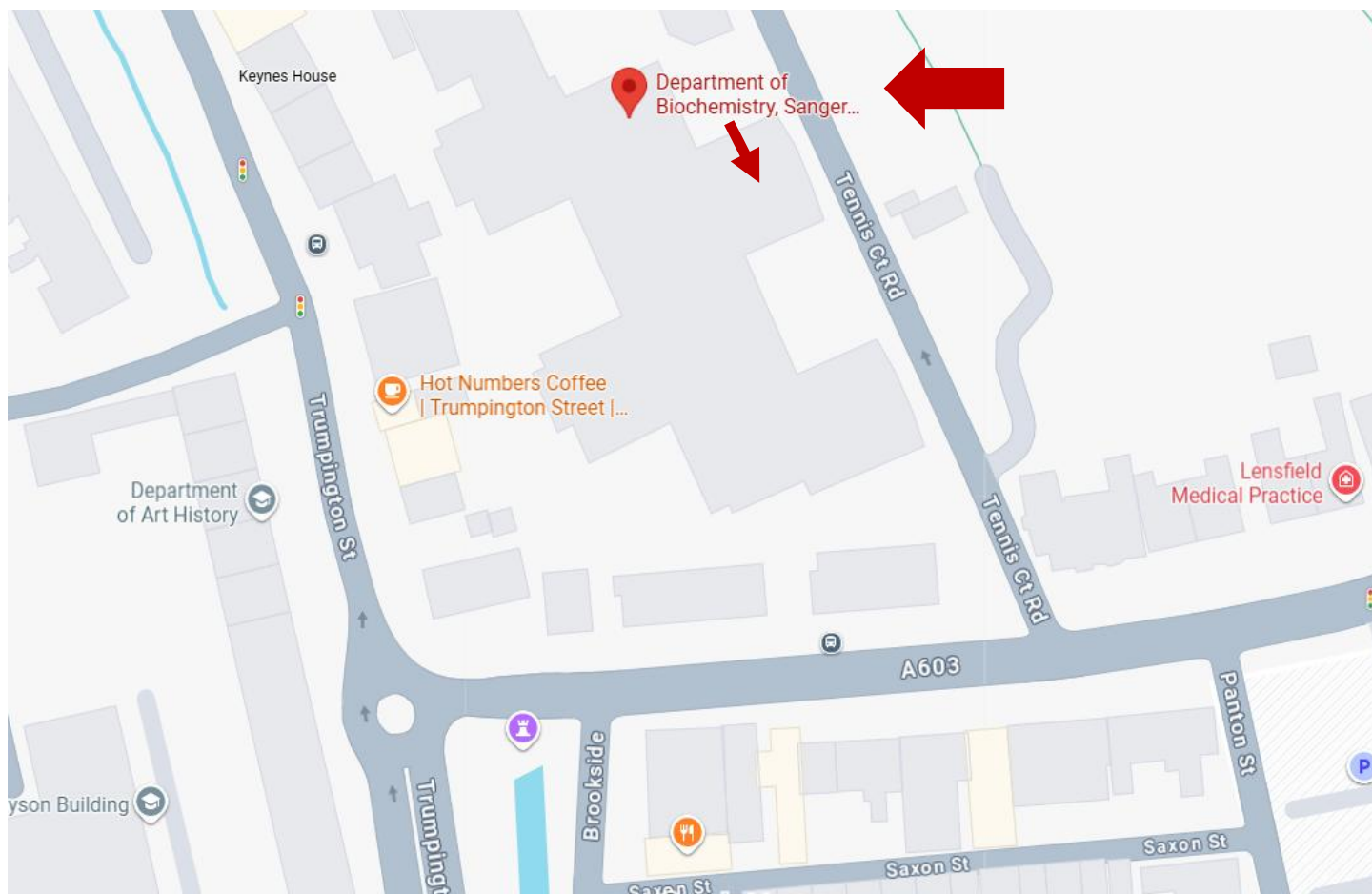
Please use the map on the page 6 to find the **Porter's Lodge at Gate of Humility**, which is the entrance to the Gonville and Caius College. The venue is located in the **Bateman Room** and **Bateman Auditorium**.

Registration

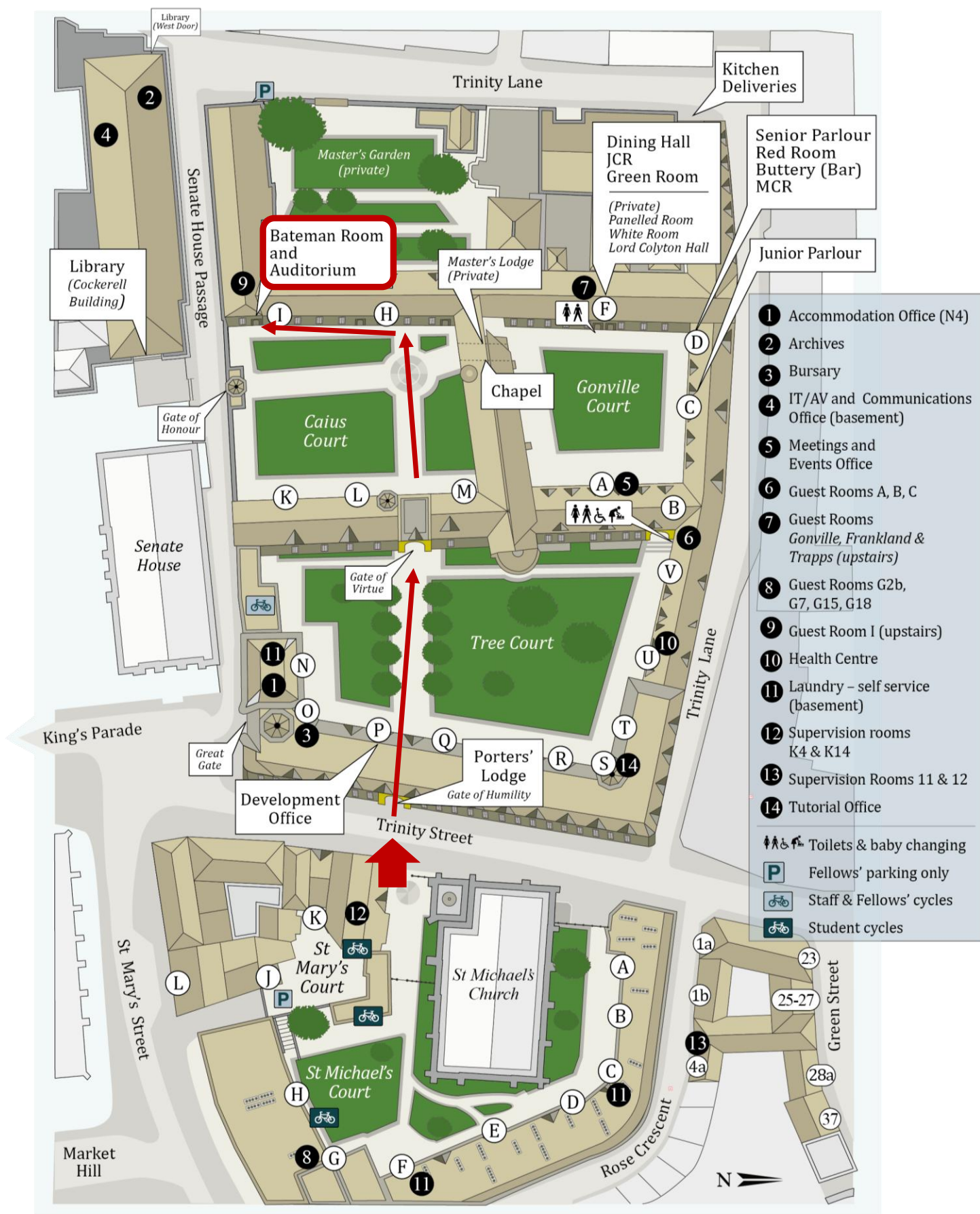
When registering, teams can receive a conference bag, conference brochure, IDEC hat, and name cards. The slides can also be copied to a computer at the venue.

Please note that **registration in the afternoon of the 24th Oct 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 25th Oct will be held at the venue (Gonville & Caius College) 8:00 – 8:40. We will have a registration reception at the entrance to the Bateman Auditorium on October 25th.



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, and our on-site judges will also join online teams for poster presentations through Gather Town.

For teams presenting online, we will collect your poster and presentation slides from **October 22nd to October 23rd**. For teams attending the iDEC Festival in person, we will collect your poster file and presentation slides upon your arrival.

As in previous years, about a week before the iDEC Festival, we will send a test link. We request that all online teams test their network connection, screen sharing, and audio transmission in the Gather Town virtual space prior to the competition. The new step for this year is that online teams will need to install Zoom and test launching the Zoom program within Gather Town.

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

All online teams need to test your **internet speed, Zoom’s Function, and try using Gather Town's screen sharing feature.**

We have allocated some **Breakout Rooms** in Gather Town for online teams, providing them with a separate space for communication and rehearsal before their presentations. The **Breakout Rooms** allocations are as follows:

Date		Timelines	Room
25 th to 26 th	Time	Events	A
	No limit	OUC-Marine Drugs (online)	

We would like to kindly require that the participants other than the above-mentioned teams should not enter these rooms to avoid disturbing the preparations of other teams.

Entre Gather Town iDEC 2025: QR code

Pass Word: 2025

Gather Space will open from 25th to 26th Oct. And will briefly open for testing on 20th Oct.



OUC-DE

Semi-rational Design and Machine Learning for Enhancing Tetrasaccharide Production in Alginate

Lyase PyAly (9:30 25th Oct)

Alginate lyases PyAly degrades alginate into alginate oligosaccharides with different degree of polymerization (DP), of which tetrasaccharide (i.e. $D_p = 4$) is the main product. Thus, PyAly has potential in producing tetrasaccharides. Previous work on PyAly has determined the key structural elements function in the specificity for oligo-saccharide products, providing a theoretical basis for modification. Here, we aim to enhance the tetrasaccharide yield of PyAly by combining rational design and machine learning. First, rational design on the substrate binding cleft was carried out and several key residues was selected for site-directed saturation mutagenesis. Next, the oligosaccharide products of mutants were analyzed, and the tetrasaccharide ratio was used for machine learning. The resulting potential mutants directed the following rational design and machine learning until obtaining the target mutants. The combination of rational de-sign and machine learning has been demonstrated efficient for PyAly modification and can be extended to other enzymes.

McMaster BioDesign

Investigation of the Cold-Shock Response Element of *cspA* as a Target for Directed Evolution (10:00 25th Oct)

Recombinant proteins have become one of the most impactful products of the biotechnology revolution. These proteins are typically produced in cell cultures grown at the physiological temperature of the cell line used, with the vast majority at 37°C. However, decreasing this temperature can be exploited to increase production and improve the quality of these proteins. Present approaches to temperature downshifts focus on the benefits resulting from physiological changes to the cells themselves as opposed to the genetic elements regulating the recombinant protein's production. In this study, we report on the *cspA* cold-shock inducible expression system of *Escherichia coli* as a target for directed evolution to increase protein production at reduced temperatures. Using a reporter plasmid containing GFP under the control of the native *cspA* regulatory element, we identified and investigated 3 regions as targets. We used computational prediction of ribosome binding sites to identify potentially beneficial mutations in the upstream box of the 5' untranslated region and a predicted downstream box for error-prone PCR. Additionally, we investigated replacing the native promoter region to determine its viability as a region for directed evolution. Through this work, we provide an outline for using directed evolution as a method for modifying genetic regulation for increasing recombinant protein production at sub-physiological temperatures.





OncoStrat_NMU

Evolutionary Mechanisms and Reversal Strategies of Acquired Resistance to RC48 in Bladder Cancer (11:00 25th Oct)

To elucidate the mechanisms of resistance to Disitamab Vedotin (RC48) in human bladder transitional cell carcinoma (BLCA). Methods: An RC48-resistant cell line (T24-RC48) was established by stepwise dose-escalation from the parental T24 cells. Phenotypic characterisation comprised CCK-8, proliferation kinetics, Transwell migration/invasion assays, and flow cytometry for cell cycle/apoptosis analysis. Mechanisms were explored using transcriptomic and proteomic sequencing. Key findings were validated via qRT-PCR and Western Blot (WB). Angiogenesis assays were performed to investigate the pro-angiogenic ability of T24-RC48. Results: T24-RC48 showed a 10-fold increase in IC₅₀ relative to parental cells, concomitant with enhanced migration, invasion, reduced G2 arrest, and increased resistance to apoptosis. Integrated omics, qRT-PCR and WB identified upregulation of VEGF, PD-L1, RBPJ, and Notch pathway activation. Ivonescimab inhibits the pro-angiogenic activity potentiated by T24-RC48. Conclusion: RC48 resistance involves oxidative stress, angiogenesis, and immune escape. Combining RC48 with ivonescimab may improve outcomes and sustain precision therapy in BLCA.

Evolution Suisse 2025

Directed Evolution Platform for High-Efficiency, Large-Scale Genome Editing using Bridge Recombinases (11:30 25th Oct)

Bridge recombinases are RNA-guided DNA recombinases that catalyse site-specific insertions, inversions, and excisions through a programmable bridge RNA (bRNA) which recognizes both donor and target DNA sequences. Their ability to manipulate large DNA fragments in a targeted manner makes them a powerful genome engineering tool. The applicability is currently limited by low catalytic activity and specificity. Here, we establish a workflow that enables broad computational sampling of the fitness landscape through DML, followed by two evolutionary logics compatible with continuous directed evolution platforms, namely EcORep and PACE, to efficiently converge on local fitness optima. As a proof of principle, we aim to evolve an efficient bridge recombinase for the treatment of α -1 antitrypsin deficiency, enabling replacement of the defective SERPINA1 gene with a healthy copy. Although optimization is ongoing, our results provide evidence that our platform could be used to increase the efficiency of bridge recombinases.

Time for Lunch

Chef’s choice sandwiches on a combination of farmhouse white, wholemeal or gluten free bread (equivalent of 1½ rounds per person) served with homemade crisps, fruit bowl, Chef’s cake of the day, water, tea and coffee

Safety Tips for Lunch

The lunch will be held in the Bateman Room.

However, due to limited space, we invite teams to collect their food in two separate time slots:

Group A: 12:00 – 12:20

PIM-VCA, PIM-NEBS, OUC-DE, OncoStrat_NMU, McMaster BioDesign

Group B: 12:20 – 12:40

CPU_CHINA, Evolution Suisse 2025, Edinburgh, NEFU_China, LZDX, LZU-MEDICINE-CHINA, SynthImmunoI_NMU

Teams are invited to collect their food in the Bateman Room and bring it back to the Bateman auditorium. Our volunteers will guide everyone to collect your food.

Bon Appétit!

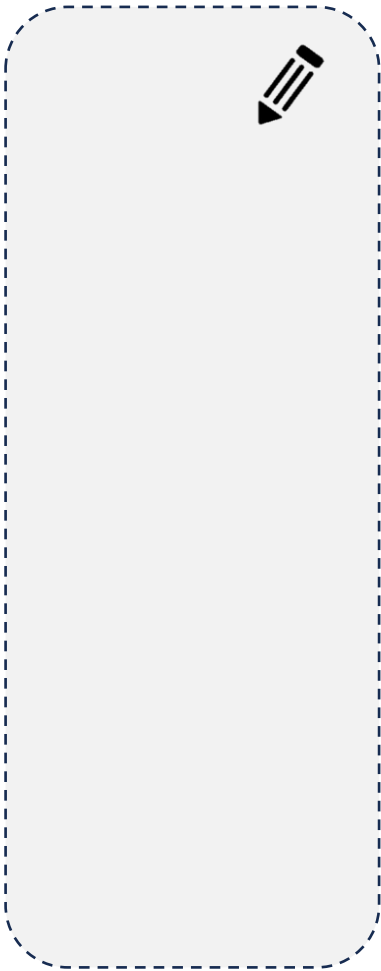
CPU_CHINA

Rational Design of a Peptide Ligase from HRV-3C

Protease

(13:00 25th Oct)

The development of efficient peptide ligases is a cornerstone of protein engineering and biopharmaceutical synthesis. However, existing ligases often suffer from limitations such as low catalytic efficiency, reaction reversibility, or stringent substrate pre-activation requirements. This study aimed to convert the HRV-3C protease, a highly specific cysteine hydrolase, into a novel peptide ligase through rational design. Our primary strategy involved computationally engineering a hydrophobic active-site pocket to suppress the enzyme's intrinsic hydrolytic activity by sterically hindering the access of nucleophilic water molecules. This work underscores a critical challenge in enzyme engineering and suggests that future design strategies must pivot from passively excluding water to actively enhancing the binding affinity and nucleophilicity of the desired acceptor substrate, enabling it to kinetically outcompete the hydrolysis reaction.





Edinburgh

Development of a High-Throughput Assay for Directed Evolution of Polypropylene-Degrading Enzyme HIS1

(13:30 25th Oct)

The UK produced 197.1 thousand metric tonnes of polypropylene (PP) in 2022; only ~1% of this gets recycled. HIS1 (HPPD Inhibitor Sensitive 1), a Fe(II)/2-oxoglutarate-dependent oxygenase demonstrated up to 13.55% degradation of PP, highlighting a potential single-enzyme solution (Tan *et al.*, 2024). We aimed to improve the efficiency of HIS1 through a semi-rational directed evolution approach (Delgado *et al.*, 2019), generating a more hydrophobic interface for improved substrate affinity. We tested an array of possible assays for the detection of PP degradation in the presence of the unmodified HIS1. TBO and Ni-PV assays show robust and reproducible signals; their compatibility with high-throughput workflows was demonstrated through a proof-of-concept positive control test. AFM indicated increases in PP surface roughness after purified HIS1 treatment; other tests provided limited corroborating evidence. Computational analyses indicated seven residues for mutation; library construction was initiated but deferred. By addressing the lack of a high-throughput screen, our research aims to accelerate progress in polymer degradation.

LZDX

Engineered *Lactobacillus* enables real-time monitoring and inhibition of oral plaque biofilms

(14:30 25th Oct)

Dental caries is the most common oral disease, with an incidence rate exceeding 70% in the population. The biofilm of dental plaque, formed by *Streptococcus mutans* (*S.m.*) and other bacteria, minerals, and food debris through co-aggregation adhesion, is the main culprit in the development of caries. It is particularly concerning that due to a lack of oral health education, the public often fails to recognize the early symptoms of caries. Early caries in hidden areas are even harder to detect, exacerbating the problem. To address these issues, our team has designed a biological system capable of locating and eliminating high-risk plaque biofilms. Specifically, we've integrated the signal reception module of the quorum sensing system, Com system, from *S.m.* into probiotics (*Lactobacilli*), creating engineered bacteria. Additionally, we've developed a unique signal amplification system. When the co-aggregated engineered bacteria within the biofilm receive virulence signals from *S.m.*, they trigger the expression of fluorescent proteins and antimicrobial peptides, thereby enabling the localization and elimination of plaque.

Poster Presentations (15:00 - 15:50 GMT+1, 25th, 13:50 – 14:40 GMT, 26th)

TEAMS	NO.	LOCATION
OUC-DE	1	On-site
MCMASTER BIODESIGN	2	On-site
ONCOSTRAT_NMU	3	On-site
EVOLUTION SUISSE 2025	4	On-site
CPU_CHINA	5	On-site
EDINBURGH	6	On-site
LZDX	7	On-site
PIM-VCA	8	On-site
SYNTHIMMUNOL_NMU	9	On-site
PIM-NEBS	10	On-site
LZU-MEDICINE-CHINA	11	On-site
NEFU_CHINA	12	On-site
OUC-MARINE DRUGS	13	Online

Poster Presentations will be held in the **Bateman Room**, a historic but limited-space venue.

For fire safety reasons, the posters will be presented in **two separate sessions, with six posters in each session**.

Each team may send 3–5 members to present their poster to the judges.

- **Session 1 (Posters 1–6):**
 **15:00–15:50 (GMT+1), October 25th**
 - Please hang your posters between 14:00–14:30.
 - Posters should be removed at 15:50 after the session.
 - Poster boards will be set up during the afternoon tea break on the 25th.
- **Session 2 (Posters 7–12):**
 **13:50–14:40 (GMT), October 26th**
 - Please hang your posters between 13:20–13:30 on October 26.
 - Posters should be removed at 15:20 after the session.

Special event for the 5th anniversary of iDEC

- Cambridge River Punting Tour

This year marks the **5th edition of iDEC**, a significant milestone in our journey.

To celebrate the 5th anniversary of iDEC, we have prepared a special activity for all participants

— a **Cambridge punting tour (16:15 – 17:05 25th Oct)**.

In collaboration with Granta Moorings, we will provide 7 traditional punts for all participants.

Each boat will be guided by a University of Cambridge student, offering an **approximately 50-minute journey** along the river to enjoy the city’s beautiful historic scenery.

For everyone’s safety and comfort, participants will be divided into 7 groups, with one boat per group.

During the trip, please remain seated, avoid standing, switching seats, or rough play on the boat.

The boarding point is at Millworks, one of the most picturesque mooring spots in Cambridge, where we will also have our dinner on the 26th. It is about a 15-minute walk from the conference venue.

Please follow our volunteers closely and be cautious when crossing the roads.

If you feel unwell or are unable to join this activity, please inform one of our volunteers.

Boat	Teams	Volunteer
Boat 1	PIM-NEBS	1
Boat 2	PIM-VCA	0
	OncoStrat_NMU	
Boat 3	McMaster BioDesign	1
Boat 4	CPU_CHINA	0
	Edinburgh	
Boat 5	Evolution Suisse	0
	LZDX	
Boat 6	NEFU_China	0
	OUC-DE	
Boat 7	LZU-MEDICINE-CHINA	4
	SynthImmunol_NMU	



OUC-Marine Drugs (online)

Semi-rational Directed Evolution of a Deepsea-derived P450S18 for Phenazines Construction

(9:00 26th Oct)

Deep sea-derived microbes are great sources for novel enzymes due to their extreme living environment, such as high pressure, high salinity, etc. CYP152 family P450s have the ability to directly use H₂O₂ instead of complex redox partners, which have high biocatalytic values in biofuels and fine chemical synthesis. Therefore, in this project, we mined a CYP152 family P450S18 from a deep sea-derived bacteria and improved its catalytic ability toward 1,2-phenylenediamine (OPD, 1). In vitro assays showed that P450S18 can directly transform OPD (1) to 2,3-diaminophenazine (2) through C–N bond construction, in the presence of H₂O₂. We then performed protein structure prediction and molecular docking of OPD with P450S18, and selected eight binding-related residues for further study. Alanine scanning and crude enzyme activity screening indicated F295A, P246A, F176A, F292A, F82A, and Q88A can effectively increase the catalytic activity. Finally, we purified the mutants and accurately measured their *in vitro* catalytic efficiency toward OPD (1). All of the mutants exhibited 1.5~3.5-fold increased activity with F292A as the optimal mutant. Our study provides foundation for further engineering of P450S18 to obtain phenazine derivatives.

PIM-VCA

Accelerating adaptive laboratory evolution via engineering of mutagenesis system for synthetic biology applications

(9:30 26th Oct)

Synthetic biology focuses on engineering microorganisms for applications in industrial production and disease treatment. However, commonly used model strains often lack adaptability to specific environmental or application contexts. Adaptive laboratory evolution offers a broad-spectrum strategy that exposes strains to simulated environmental pressures to gradually enhance their tolerance, but its widespread usage is limited by low efficiency. We present MP6-UTT, a genetic tool for stress-directed evolution that enables highly efficient, broad-spectrum mutagenesis within bacterial cells, significantly accelerating the evolutionary process. Using MP6-UTT, we enhanced *E. coli* BL21 (DE3)'s ability to utilize xylose and tolerate high salinity in seawater. We also improved the survival efficiency of *E. coli* Nissle 1917 under simulated intestinal conditions with tagatose as an additional carbon source, aiding probiotic colonization. Our platform offers a versatile and powerful approach for rapid microbial adaptation, facilitating the real-world translation of synthetic biology projects.



SynthImmunoI_NMU

Engineering IL-2R agonists responsive to lactate-rich tumor microenvironments (10:00 26th Oct)

Adoptive cell therapy (ACT) for solid tumors, particularly pancreatic cancer, is limited by the immunosuppressive tumor microenvironment (TME), where low pH accelerates cytokine degradation and hinders receptor oligomerization. The efficacy of cellular therapeutics is further reduced by the IL-2 receptor (IL-2R) expression profile, as low-dose IL-2 preferentially activates regulatory T cells (Treg), whereas high-dose administration induces systemic toxicity and vascular leak syndrome. Here, we applied de novo design to generate an acid-responsive IL-2R agonist that selectively engages IL-2R $\beta\gamma$ while sparing IL-2R α . Using RFdiffusion, we created 100 IL-2R $\beta\gamma$ agonists and identified high-affinity candidates through AlphaFold3 and HDOCK screening. To confer pH sensitivity, we incorporated the GALA peptide, which folds into an amphipathic α -helix at low pH to promote receptor oligomerization. The optimized agonist, B51G35R-G, exhibited high-affinity binding to IL-2R $\beta\gamma$ but weak IL-2R α interaction, enabling cytokine-independent activation, enhanced degranulation and improved tumor cytotoxicity of effector cells.

PIM-NEBS

Protein Pre-Binding State (PBS) Framework Enables Mechanistic Insights and Engineering of Robust Biocatalysts for Plastic Depolymerization (11:00 26th Oct)

Biotechnological recycling offers a sustainable solution to plastic pollution, with polyethylene terephthalate (PET) posing the most urgent challenge. Rapid PET depolymerization requires robust biocatalysts. We introduce a protein pre-binding state (PBS) framework that captures transition-state-like conformations crucial for catalysis, enabling efficient identification of reactive geometries without exhaustive QM/MM sampling. Guided by PBS, we engineered leaf and branch compost cutinase (LCC), achieving three rounds of improvement. The resulting variant, LCC-ICCG-R2, depolymerized more than 90% of pretreated post-consumer PET at 75 °C within 4 h, yielding over 92% terminal products. Extending PBS beyond PET, we designed a bio-based pyrrolidone-containing polyester (PBTDP) that undergoes efficient enzymatic depolymerization under mild conditions. These applications establish PBS as a versatile platform bridging mechanistic understanding with practical advances in sustainable polymer recycling and computational enzyme design.





LZU-MEDICINE-CHINA

Metabolically Engineered Probiotics for the Treatment of Perioperative Digestive Disorders (11:30 26th Oct)

To address gastrointestinal diseases caused by dysbiosis of the gut microbiota during the perioperative period (often due to chemical, mechanical, and antibiotic stimuli from surgical preparation), we have engineered the probiotic *Lactobacillus casei*. This strain can colonize the intestinal environment and express downstream genes upon induction by bile salts (which are present only in the intestines).

Firstly, we recombined the OLE1 gene from yeast cells into the engineered probiotic. OLE1 is an unsaturated fatty acid synthase that enables the probiotic to convert short-chain fatty acids (SCFAs) into oleic acid. Studies have shown that oleic acid can enhance the activity of gut probiotics and inhibit the growth of pathogenic microorganisms. Additionally, we incorporated the human defensin DEFB4A sequence into another plasmid. DEFB4A is an oligomeric protein that can be expressed in prokaryotes and has the function of enhancing the intestinal mucosal barrier. Our engineered probiotic can be used as a food additive or capsule to improve and reshape the gut microbiota, enhancing the intestinal epithelial barrier function to treat gastrointestinal diseases during the perioperative period.

NEFU_China

Modular Enhancement of Melatonin Pathway by Evolutionary Optimization of Tryptophan Biosynthesis and AtCOMT Catalytic Function (12:00 26th Oct)

Melatonin (MT), a ubiquitous circadian rhythm regulator, faces increasing global demand. However, its production through conventional methods is hindered by high cost, complexity, and low yield. These limitations pose significant challenges for both basic research and large-scale applications. In this study, the catalytic efficiency of *Arabidopsis thaliana* caffeic acid O-methyltransferase (AtCOMT) in MT biosynthesis was enhanced through systematic optimization of L-tryptophan (L-Trp) synthesis and utilization, combined with enzyme engineering through directed evolution. This study enhanced melatonin precursor tryptophan production to 3.99g/L via upstream genes knockout, overexpression, whole-genome mutagenesis, and tnaC-biosensor screening, achieving a 1609.9-fold increase over the wild-type BW25113. We developed a growth-coupled high-throughput screening system using a synthetic methyl cycle to select AtCOMT mutants. The best variant exhibited 84% higher catalytic efficiency than the highest literature value, demonstrating the power of integrating directed evolution, biosensors, and computational design for melatonin biosynthesis.

Time for Lunch

Chef’s choice sandwiches on a combination of farmhouse white, wholemeal or gluten free bread (equivalent of 1½ rounds per person) served with homemade crisps, fruit bowl, Chef’s cake of the day, water, tea and coffee

Safety Tips for Lunch

The lunch will be held in the Bateman Room.

However, due to limited space, we invite teams to collect their food in two separate time slots:

Group A: 12:30 – 12:50

PIM-VCA, PIM-NEBS, OUC-DE, OncoStrat_NMU, McMaster BioDesign

Group B: 12:50 – 13:10

CPU_CHINA, Evolution Suisse 2025, Edinburgh, NEFU_China, LZDX, LZU-MEDICINE-CHINA, SynthImmunoI_NMU

Teams are invited to collect their food in the Bateman Room and bring it back to the Bateman auditorium. Our volunteers will guide everyone to collect your food.

Bon Appétit!

Group Photo

Group photos are divided into online and on-site.

The online photo session time is 13:20 GMT 26th Oct.

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 13:30 GMT 26th Oct.

The location for the on-site group photo is outside the **Gate of Honour** (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 Professor Florian Hollfelder of the University of Cambridge, deliver the opening talk for iDEC Festival 2025!



iDEC Festival 2025

Opening Ceremony Lectures

Registration QR code
25th Oct 9:00-9:30 GMT+1



How Do We Find New Functional Proteins in Sequence Space?

Dr. Florian Hollfelder

Professor in Chemical and Synthetic Biology
Cambridge University
Holder of an ERC Advanced Grant, Director of Studies and Graduate Mentor at Trinity Hall

iDEC HQ is honored to invite two senior scientists, Prof. Mark Howarth and Prof. Somenath Bakshi 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:



iDEC Festival 2025

Awards Ceremony Lectures

Registration QR code
26th Oct 15:30-17:30 GMT



Bacterial superglues to empower biologics discovery, cell therapy and disease prevention

Dr. Mark Howarth

Sheild Professor of Pharmacology, Cambridge University
Founder of SpyBiotech



**Physiology as a Design Constraint
Harnessing Single-Cell Insights to Shape the Future of Antimicrobial Therapy**

Dr. Somenath Bakshi

Associate Professor
Department of Engineering, Cambridge University

Acknowledgment

iDEC 2025 could not be successfully organized without the help of our sponsors, collaborators, iDEC HQ members and participants.

We thank **Bluepha** and **New England Biolabs** for their generous support.

iDEC 2025 Invited Speakers:

Dr. Shuailong Zhang from Beijing Institute of Technology & OptoSeeker

Dr. Karla Milcic from Havard University & RevivBio

Dr. Christian Diercks from Scripps Research

Dr. Florian Hollfelder from Cambridge University

Dr. Mark Howarth from Cambridge University

Dr. Somenath Bakshi from Cambridge University

iDEC 2025 Judge List:

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

Dr. Fabian Rehm 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. Rongzhen Tian from the MRC Laboratory of Molecular Biology (LMB), UK

Dr. Martin Spinck from the MRC Laboratory of Molecular Biology (LMB), UK

Anne-Cathrin Prowald from the MRC Laboratory of Molecular Biology (LMB), UK

Dr. Yan Liao from the Australian institute for Microbiology & Infection, University of Technology Sydney, AU

Dr. Shiyuan Li from Cathay Fortune Capital Investment, CN

Dr. Yeqing Zong from the Bluepha, CN

iDEC Executive Committee Members:

Prof. Tom Ellis, Shan Jiang, Dr. Nadanai Laohakunakorn, Prof. Chang Liu, Dr. Ella Watkins-Dulaney, Dr. Joanna Sadler

iDEC 2025 Organizers:

Dr. Trevor Y. H. Ho, Chong Teng, Yinan Ren, Katherine Martin, Kening Chen, Tong Lyu, Huandi Xu, Dr. Stefan Bassler, Dr. Svenja Vinke, Levin Joe Klages, Irina Rais, Swaranjeet Singh, Dr. Yang Liu, Dr. Nikos Nikolopoulos, Zachary Liang, Yuancheng Din, Petar Zhotev

iDEC 2025 Sponsor Representatives:

Qiang Geng from Bluepha, Erin Varney and Dr. Emma Mitchell from New England Biolabs.

iDEC 2025 Teams:

OUC-Marine Drugs, PIM-VCA, PIM-NEBS, OUC-DE, OncoStrat_NMU, McMaster BioDesign, CPU_CHINA, Evolution Suisse, Edinburgh, NEFU_China, LZDX, LZU-MEDICINE-CHINA, SynthImmunol_NMU

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 2025 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 Regenesys, the Møller Institute (Cambridge University).

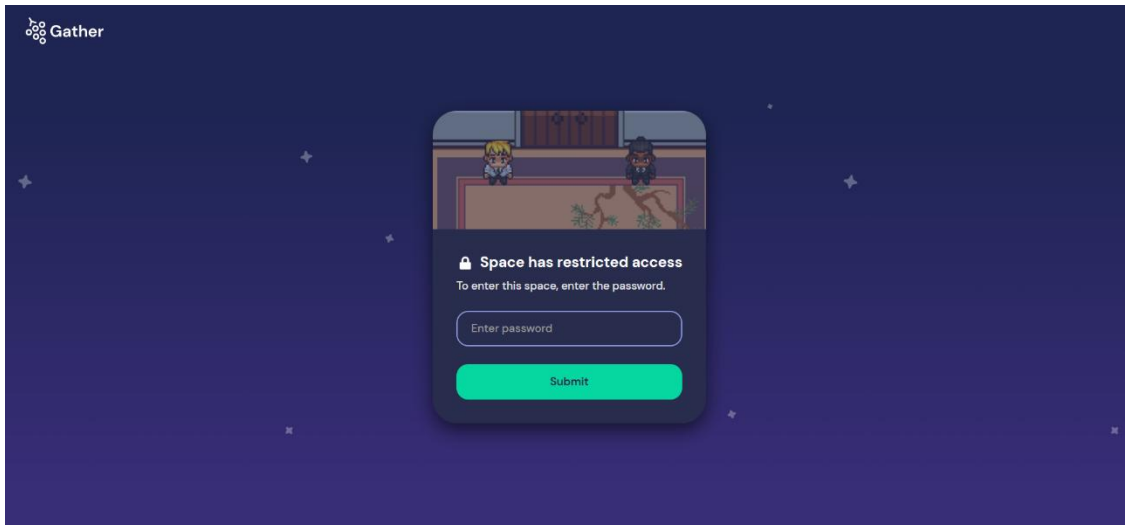


Gather Town Guide

2D virtue 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 2025** space by the link we send. **The password is '2025'.**



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.

iDEC HQ have built breakout rooms for the iDEC teams. The iDEC team can prepare presentations without interruption in a separate virtual room.

In the poster display area, we will hang 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.

Bluepha is a biomanufacturing and material innovation company providing breakthrough products based on synthetic biotechnology. Founded in October 2016, Bluepha has been actively committed to the design, development, manufacture, and marketing of new bio-based molecules and materials, including:

- Bio-polymers PHAs which are biodegradable in any environment without leaving harmful footprints
- Materials for regenerative medicine
- Novel functional ingredients for personal care and medical beauty
- New food additives
- Probiotic products, etc.

The glory of Bluepha is inseparable from the core team coming from top research institutes such as Tsinghua University, Peking University, Chinese Academy of Sciences and the Fortune Global 500. A dream team of experts and consultants is composed of leaders in the field of SynBio industry, education, and research.

In 2022, the first product pipeline of Bluepha with a super-factory of marine degradable material PHA: Bluepha™ was officially started construction in Binhai, Yancheng, Jiangsu, with annual production capacity of 25,000 tons. The performance of Bluepha™ has been verified by several enterprise customers from Fortune Global 500, and has obtained orders and intentional orders from many enterprises. At present, Bluepha has signed strategic cooperation agreements with a few partners worldwide to expand the global market with unlimited potential of Bluepha™.

In addition, Bluepha has reserved dozens of R&D pipelines for new products. The application scenarios cover the fields of health & medical care, agricultural environmental protection, beauty & cosmetic and innovative food. Each product pipeline corresponds to a direct market size of more than \$1 billion.

Since establishment, the Bluepha has built an interdisciplinary team composed of senior scientists and engineers in different fields such as robotics, software development, mechatronics, big data, and synthetic biology. An automated and datamated infrastructure "Synbio OS" was set up. It is expected that in the next 3 years, the R&D cycle of a single Bluepha product pipeline will be shortened by 70% on the existing basis.



Putting science first.

Post-Doctoral Fellowships at New England Biolabs®

Established “By Scientists for Scientists” in 1974, New England Biolabs has always put science first. You may know us for providing the largest selection of DNA and RNA enzymes for molecular biology, but our diverse product portfolio is deeply rooted in our strong commitment to basic research and discovery. Scientists in the Research Department at New England Biolabs conduct research in the areas of:

- Bacteriology and Virology
- Biochemistry and Enzymology
- Genomics and Transcriptomics
- RNA Research
- Technology Development for Life Science Research

A critical part of our Research program is our strong commitment to hiring and training postdoctoral scientists. The Postdoctoral Fellowship program at NEB provides an opportunity for recent PhD graduates to perform research in a modern industrial setting with the freedom to explore interesting scientific questions. Postdoctoral fellows conduct basic research, publish in high quality journals and present at scientific conferences. Our unique culture at NEB emphasizes intellectual curiosity, innovation, and collaboration.

Looking for your next career destination? Check out our current postdoc opportunities on our career page here:



www.neb.com/about-neb/careers

Photo credit: © Robert Benson Photography





International Directed Evolution Competition 2025

This is the way the life begins.
Not with a plan but a competition.

