



PROGRAMME 25TH JUNE 2019

09:15	INTRODUCTION: Tony Kouzarides		
SESSION I			
09:30-10:00	Greg Hannon, Cancer Research UK Cambridge Institute, University of Cambridge		
10:00-10:30	Róisín Owens, Dept of Chemical Engineering and Biotechnology, University of Cambridge		
10-30-11-00	Sara-Jane Dunn Microsoft Research		

CHAIRS

JASON CARROLL



Cancer Research UK Cambridge Institute, University of Cambridge

Coffee

SESSION 2

11:30-12:00	Ed Bullmore, Dept of Psychiatry, University of Cambridge
12:00-12:30	Marcel van Duin, Ferring Pharmaceuticals
12:30-13:00	Salvador Aznar-Benitah, IRB, Barcelona, Spain

JASMIN FISHER



Microsoft Research and Dept of Biochemistry, University of Cambridge

Lunch and poster viewing

PARALLEL TRACKS

	SESSION 3A	SESSION 3B	SESSION 3C	SESSION 3D	
	CNS therapeutics	Oncology	Antimicrobial resistance and the microbiome	Cardiovascular and metabolism	
	<i>Chairs:</i> John Skidmore Maria Spillantini	<i>Chairs:</i> Rebecca Fitzgerald Rab Prinjha	<i>Chairs:</i> Kai Stoeber Andres Floto	<i>Chairs:</i> Sanjay Sinha	
14:30-14:45	Introduction				
14:45–15:00	Zoe Kourtzi	Gillian Griffiths	Leonor Sánchez-Busó	Nick Morrell	
15:00–15:15	George Malliaras	Christian Frezza	Andres Floto	Sanjay Sinha	
15:15–15:30	Jeff Dalley	Justin Bryans	Sven Sewitz	Peter Kirwan	
15:30–15:45	Maria Spillantini	Rebecca Fitzgerald	David Spring	Shamina Rangwala	
15:45–16:00	Michael Jones	Frank McCaughan	Trevor Lawley	Clemence Blouet	
16:00–16:15	Evan Reid				
16.30–17.00	SESSION 4 Start-ups and investment in Cambridge Jonathan Milner (Abcam) and Jason Mellad (Start Codon)				
17:00–18:30	Drinks and networking				

INTRODUCTION

NTRODUCTION

TONY KOUZARIDES



Wellcome Trust—Cancer Research UK Gurdon Institute and Director of the Milner Institute

BIOGRAPHY | Tony Kouzarides PhD, FMedSci, FRS is Professor of Cancer Biology at the University of Cambridge. He is a senior group leader of the Gurdon Institute and founder/ director of the Milner Therapeutics Institute.

Tony did his PhD at the University of Cambridge and postdoctoral work at MRC Laboratory of Molecular Biology and New York University Medical Center. His research group at the Gurdon Institute is focused on epigenetic modifications and their involvement in cancer. He is on the Executive Board of the Cambridge Cancer Centre and founder/director of Cambridge Gravity, a philanthropic vehicle for science at the University of Cambridge. He is the founder of a Spanish cancer charity "Vencer el Cancer" (Conquer Cancer). He is on the Scientific Advisory Board of the Institute of Cancer Research (UK) and of CABIMER (Spain).

Tony is a co-founder and director (1998-2012) of Abcam plc, a co-founder and director (2001-2003) of Chroma Therapeutics, and a co-founder and director (2016-) of STORM Therapeutics.

Tony has been elected member of the European Molecular Biology organization, is a Fellow of the British Academy of Medical Sciences (FMedSci), a Fellow of the Royal Society (FRS), a Fellow of the American Academy of Arts and Sciences and is a Cancer Research UK Gibbs Fellow. He has been awarded the Wellcome Trust medal for research in biochemistry related to medicine (UK), the Tenovus Medal (UK), the Bodossaki Foundation prize in Biology (Greece), the Bijvoet Medal (Holland), the Biochemical Society Award Novartis Medal and Prize.

SESSION I

CHAIR
JASON CARROLL

SESSIOZ

JASON CARROLL



BIOGRAPHY | Jason is an Australian who completed a PhD in Sydney, with Professor Robert Sutherland. He conducted postdoctoral work with Professor Myles Brown at Dana-Farber Cancer Institute and Harvard Medical School, Boston, USA from 2002-2006. He has been running his own group at Cancer Research UK, Cambridge Institute and University of Cambridge since 2007. He is currently a senior group leader at Cancer Research UK, a Director of Research at University of Cambridge, a Fellow at Clare College and the Founder and CSO of Azeria Therapeutics (p34). His lab is interested in understanding mechanisms of hormone-dependent cancer.

GREGORY J. HANNON



Director, CRUK Cambridge Institute, University of Cambridge

TALK TITLE | Insights from a model of breast tumour heterogeneity

ABSTRACT | Single-cell profiling of patient tumours and of mouse models is revealing that many cancers are constituted of communities of genetically and phenotypically distinct clonal lineages. We have created a functional model of breast cancer heterogeneity and used this to study the impact of differential proficiencies of clonal populations during tumour initiation and progression. Our prior studies identified subclones that were proficient at forming circulating tumour cells (CTCs) and linked this to the ability of these cells to perform vascular mimicry. Subsequent work has revealed drivers of this ill-understood phenomenon which are correlated with outcome in a number of tumour types. Intriguingly, only a subset of CTC proficient clones formed secondary metastases. We have investigated drivers of this phenomenon and uncovered a link between the availability of a non-essential amino acid and phenotypic plasticity, which could be important for metastatic progression.

BIOGRAPHY | Greg Hannon FRS FMedSci is a professor of molecular cancer biology and director of the Cancer Research UK Cambridge Research Institute at the University of Cambridge. Professor Hannon is internationally recognized for his contributions to small RNA biology, cancer biology, and mammalian genomics. He has a long history in the discovery of cancer genes, beginning with work at CSHL that led to the identification of CDK inhibitors and their links to cancer. His collaborative innovations have included the development of selective re-sequencing strategies that are now being used within TCGA and the 1000 Genomes project.

RÓISÍN OWENS



University Lecturer,
Dept of Chemical Engineering and
Biotechnology, University of Cambridge

TALK TITLE | 3D conducting polymer electrodes to host and monitor human organs

ABSTRACT | In vitro models of biological systems are essential for our understanding of biological systems. In cases where animal models have failed to translate to useful data for human diseases, physiologically relevant in vitro models are key. Many difficulties exist in interfacing complex, 3D models with technology adapted for monitoring function. Polymeric electroactive materials and devices can bridge the gap between hard inflexible materials used for physical transducers and soft, compliant biological tissues. In this presentation, I will discuss our recent progress in generating 3D electroactive scaffolds capable of hosting and monitoring a physiologically relevant model of the gut to facilitate studies of the microbiome.

BIOGRAPHY | Róisín M. Owens received her BA in Natural Sciences at Trinity College Dublin, and her PhD in Biochemistry and Molecular Biology at Southampton University. She did two postdoctoral fellowships at Cornell University, on Mycobacterium tuberculosis and rhinovirus therapeutics. From 2009-2017 she was a group leader in the Dept of Bioelectronics at Ecole des Mines de St. Etienne. She has been awarded Marie Curie and EMBO fellowships, as well as the European Research Council including starting (2011), proof of concept grant (2014) and consolidator (2016) grants. She is author of 70+ publications and patents and is a 2019 laureate of the Suffrage Science award.

SARA-JANE DUNN



Scientist, Microsoft Research

TALK TITLE | Programming Biology

ABSTRACT | The future of therapeutics will centre on the ability to program biology. This necessitates the development of both theory and tools to understand biological computation, as well as the programming languages, compilers and verification tools that will ultimately be needed to program cells. In this talk, I will introduce work being carried out at Microsoft Research towards these ambitious goals, pushing us towards the era of Living Software.

BIOGRAPHY | Sara-Jane Dunn is a Scientist at Microsoft Research. She studied Mathematics at the University of Oxford, graduating with a MMath in 2007. She remained in Oxford for her doctoral research as part of the Computational Biology group at the Department of Computer Science. In 2012, she joined Microsoft Research as a postdoctoral researcher, before transitioning to a permanent Scientist role in 2014. In 2016, she was invited to become an Affiliate Researcher of the Wellcome Trust-Medical Research Council Stem Cell Institute, University of Cambridge. Her research focuses on uncovering the fundamental principles of biological information-processing, particularly investigating decision-making in development.

SESSION 2

CHAIR
JASMIN FISHER

SESSIOZ >

JASMIN FISHER



Microsoft Research and Dept of Biochemistry, University of Cambridge

BIOGRAPHY | Jasmin Fisher is a Professor of Computational Biology in the Cancer Institute at University College London. Jasmin received her BSc in Biology and MSc in Biophysics from Ben-Gurion University and her PhD in Neuroimmunology from the Weizmann Institute of Science. In 2007 Jasmin joined the Microsoft Research Lab in Cambridge where she was a Principal Researcher until 2019. In 2012 she was also appointed a Reader in the Department of Biochemistry at the University of Cambridge. Fisher's research group develops computational models to study cancer evolution and mechanisms of resistance to identify better personalised treatments for cancer patients. In 2017 Jasmin was named one of the Top Outstanding Female Leaders in the UK Healthcare by BioBeat.

ED BULLMORE



Dept of Psychiatry, University of Cambridge

TALK TITLE | Inflammation and depression

ABSTRACT | There is growing awareness that depression and inflammation are associated with each other. And there is meta-analytic evidence that anti-inflammatory drugs can have mood-boosting effects on secondary endpoints in clinical trials for non-psychiatric disorders. These observations have excited interest in the prospect of developing anti-inflammatory drugs for treatment of major depressive disorders. To support this strategy, we will need clear evidence that inflammation can play a causal role in driving depression; and we will need blood or brain biomarkers of inflammation that we can use to predict which patients with depression are most likely to respond to an anti-inflammatory intervention. I will review recent progress towards these key milestones on the path to anti-depressant drug development targeting immune mechanisms.

BIOGRAPHY | Ed trained in medicine at the University of Oxford and St Bartholomew's Hospital, London; then in psychiatry at the Bethlem Royal & Maudsley Hospital, London. He moved to Cambridge as Professor of Psychiatry in 1999 and is currently Director of the Wolfson Brain Imaging Centre, and Head of the Department of Psychiatry. He is also an Honorary Consultant Psychiatrist and Director of R&D in Cambridgeshire & Peterborough Foundation NHS Trust. From 2005 to 2019, he worked half-time for GlaxoSmithKline, latterly focusing on immunopsychiatry, as described in his recent book "The Inflamed Mind". He has been elected a Fellow of the Royal College of Physicians, the Royal College of Psychiatrists, and the Academy of Medical Sciences.

MARCEL VAN DUIN



VP,Therapeutic Area Head Research Reproductive Medicine and Women's Health, Ferring Pharmaceuticals

TALK TITLE | R&D challenges in Reproductive Medicine & Women's Health

ABSTRACT | Reproductive Medicine & Women's Health comprises a large number of indications that directly or indirectly impact possibilities of men and women to build a family. Even though millions of IVF babies have been born since the inception of this Assisted Reproductive Technology (ART), the etiology of both male and female infertility remains largely unknown. Complications with embryo implantation and placentation appear to be important drivers for obstetrical complications such as spontaneous preterm delivery and preeclampsia. Through both internal research as well as strong external alliances Ferring is committed to driving further applied research to provide new solutions for patients who desire to conceive and deliver healthy babies.

BIOGRAPHY | As Therapeutic Area Head, Dr Marcel van Duin has been since 2014 responsible for overseeing the global research activities covered by the Reproductive Medicine & Women's Health strategy of Ferring Pharmaceuticals. He received his PhD at the Department of Genetics and Cell Biology of the Erasmus University, Rotterdam, The Netherlands. He has 30 years of experience in the pharma industry with positions in Organon, Schering Plough and Merck. During these years he had responsibilities as head of target discovery and pharmacology departments as well as senior therapeutic leadership positions to develop and drive internal and external research projects towards reproductive-biology-based innovation.

SALVADOR AZNAR BENITAH



ICREA Research Professor, Institute for Research in Biomedicine in Barcelona (IRB-Barcelona), Barcelona Institute for Science and Technology (BIST)

TALK TITLE | Epigenetic influence of our (fatty) diet on metastatic-initiating cells

ABSTRACT | We have recently identified cells that are uniquely responsible for the formation of metastasis in different human tumors. These cells have intriguing characteristics: i) they express the fatty acid translocase CD36, and are characterized by a unique lipid metabolic signature; ii) they are exquisitely sensitive to the levels of fat in circulation, and consequently they relate the predisposition of metastasis to the content of dietary fat; and iii) they are highly sensitive to CD36 inhibition, which abolishes their metastatic potential in preclinical models. I will present new data on the characterization of metastatic-initiating cells, emphasizing how dietary lipids exert a striking long-term effect over them, putting forward a novel concept of 'metastatic epigenetic memory' elicited by our diet.

BIOGRAPHY | Salvador Aznar Benitah obtained his Honours BSc in Biochemistry and Molecular Biology at McGill University in 1998. In 2007, after a postdoctoral work in the laboratory of Fiona Watt at the London Research Institute (Cancer Research UK), he established his own lab at the Center for Genomic Regulation (CRG) as a Junior ICREA researcher. In 2014 Salvador was promoted to ICREA Research Professor, one of the most prestigious awards in research in Spain, and moved to the Institute for Biomedical Research (IRB) in Barcelona as a senior researcher. In 2015, he was also appointed as a Foundation Botin Researcher. In 2018, he has been appointed as an EMBO member and has received an Advanced ERC grant.

PARALLEL TRACKS

SESSION 3A
CNS THERAPEUTICS

CO-CHAIRS
JOHN SKIDMORE
MARIA SPILLANTINI

JOHN SKIDMORE



Chief Scientific Officer, The ALBORADA Drug Discovery Institute, University of Cambridge

BIOGRAPHY | John Skidmore is a chemist by training, receiving a BA and DPhil from the University of Oxford. Following a post doc at the University of Liverpool, John joined GSK where he worked as a medicinal chemist and project leader in the pain and neurodegeneration therapeutic areas contributing to the discovery of 4 development candidates. In 2010 John moved to the University of Cambridge, where, funded through the Wellcome Trust's Seeding Drug Discovery scheme, he led a number of protein-protein interaction inhibitor projects in the oncology therapeutic area. In 2015 John moved within the University, to his present position as the CSO of the ALBORADA Cambridge Drug Discovery Institute where he leads a group translating academic research into new treatments for the diseases that cause dementia.

ZOE KOURTZI



Dept of Psychology, University of Cambridge

TALK TITLE | Machine learning tools for modelling prognostic trajectories in dementia

ABSTRACT | Predicting early onset of neurocognitive decline has major implications for timely clinical management and outcomes for dementia patients. Despite advances, we still lack tools for stratifying patients into subgroups for which tailored and effective treatments can be developed. Here, we develop and implement machine learning algorithms for early precision diagnosis from lowcost and non-invasive data. Our algorithms predict reliably the rate of cognitive decline due to AD from cognitive testing data or structural MRI scans that capture the pathology identified by more invasive measurements. Our longer-term aim is to deliver a clinical decision support system that will: a) help clinicians assign the right patient at the right time to the right diagnostic or treatment pathway, b) improve patient wellbeing and reduce healthcare costs, as patients undergo fewer, less invasive, less expensive diagnostic tests, c) guide patient selection for clinical trials to enhance their efficacy and pave the way to drug discovery.

BIOGRAPHY | Zoe Kourtzi is Professor of Experimental Psychology and Computational Cognitive Neuroscience at the Department of Psychology, University of Cambridge. Kourtzi received her PhD from Rutgers University and was a postdoctoral fellow at MIT and Harvard University. She was a Senior Research Scientist at the Max Planck Institute for Biological Cybernetics and then a Chair in Brain Imaging at the University of Birmingham. She moved to the University of Cambridge in 2013 and is the Cambridge University Lead at the Alan Turing Institute.

GEORGE MALLIARAS



Dept of Engineering, University of Cambridge

TALK TITLE | Implantable devices for 'dry' drug delivery in the brain

ABSTRACT | My research is in the area of bioelectronics, specifically the application of organic electronic materials to neural interfacing, aiming to understand how the brain works and to develop new tools for the diagnosis and treatment of neurological disease. Among our achievements are (i) the development of ultra-conformable microelectrode arrays for recording corticograms, recently used in the clinic to record single neuron activity from the surface of the brain of epileptic patients, (ii) the first use of a transistor in recording brain activity, resulting in record-high signal-to-noise ratio, and (iii) the development of an electrophoretic device that prevents/stops seizures in a rodent model of epilepsy through localized drug delivery.

BIOGRAPHY | George Malliaras is the Prince Philip Professor of Technology at the University of Cambridge. He received a PhD from the University of Groningen and did a postdoc at the IBM Almaden Research Center. Before joining Cambridge, he was a faculty member at Ecole des Mines de St. Etienne and at Cornell University, and served as the Director of the Cornell NanoScale Facility. His research has been recognized with awards from the New York Academy of Sciences, the US National Science Foundation, and DuPont. He is a Fellow of the Materials Research Society and of the Royal Society of Chemistry.

JEFFREY W. DALLEY



Dept of Psychology, Dept of Psychiatry, University of Cambridge

TALK TITLE | A preclinical platform for immune target discovery in early life stress and depression

ABSTRACT | Early life stress is a major risk factor for depression in humans. Understanding the aetiological mechanisms involved would dramatically improve the therapeutic options for depression that presently rely on selective reuptake inhibition of monoamine neurotransmitters. There is increasing awareness that early life adversity activates the peripheral and central immune systems putatively to disrupt the normal developmental trajectories of brain regions involved in emotional regulation. The present programme of research uses the experimental approach of repeated early maternal separation (REMS) of rat pups, shown previously to activate the immune systems and cause depression-like behaviours. Using longitudinal MRI, serum cytokine analysis, and sensitive computerised touchscreen tasks, the results of the first phase of this research will be presented.

BIOGRAPHY | Jeff Dalley is a Professor in the Departments of Psychology and Psychiatry at Cambridge University. He is also a Professorial Fellow and Director of Studies in Neuroscience and Psychology at St Catharine's College, and serves as the inaugural Editor-in-Chief of Brain and Neuroscience Advances, and as a member on the steering committee of the Institute for Neuroscience in Cambridge. Educated in New Zealand with a B.Pharm (Hons) degree at Otago University (1983-1986), Jeff Dalley came to the UK in 1989 to undertake a PhD in neuropharmacology at UCL. He subsequently completed postdoctoral positions in the labs of Clare Stanford (1993-1994), David Nutt (1995) and Trevor Robbins (1996-2007) before establishing his own translational neuroscience group in Cambridge.

MARIA GRAZIA SPILLANTINI



Dept of Clinical Neurosciences, University of Cambridge

TALK TITLE | Tackling protein aggregation to treat Parkinson's disease

ABSTRACT | Maria Grazia Spillantini's group works on the molecular neuropathology of diseases characterised by tau and alpha-synuclein aggregation such as forms of Frontotemporal dementia and Parkinson's disease respectively. With her collaborators, she identified alphasynuclein as the main component of the filaments that form the Lewy bodies in Parkinson's disease and dementia with Lewy bodies and described one of the first mutations in the MAPT gene leading to frontotemporal dementia and Parkinsonism linked to chromosome 17. In order to determine the role of tau and alpha-synuclein aggregation in neurodegeneration and to identify mechanism-based therapies for tauopathies and alpha-synucleinopaties her lab uses transgenic mice, primary cultures, human IPSC-derived neurons and glia as well as human brain tissues.

BIOGRAPHY | Maria Grazia Spillantini is Professor of Molecular Neurology in the Clinical School of Cambridge University. She was born in Arezzo, Italy. After receiving a Laurea in Biological Sciences, summa cum Laude, from the University of Florence she joined the MRC Laboratory of Molecular Biology where she obtained a PhD in Molecular Biology from Cambridge University, Peterhouse. In 1996 she moved to the Department of Clinical Neurosciences of Cambridge University where she is now Professor. She became a Fellow of the Academy of Medical Sciences in 2010, a Fellow of the Royal Society in 2013 and Knight Officer of the Star of Italy in 2018. She is Fellow at Clare Hall and life member of Peterhouse.

MICHAEL JONES



CEO, Cell Guidance Systems

TALK TITLE | Delivering treatment of Parkinson's disease

ABSTRACT | Fragility (short half-lives) and toxicity (low cell-specificity) make growth factors (GFs) amongst the most difficult class of proteins to deliver therapeutically. Although systemic delivery has been possible in a few cases (e.g. EPO), these are exceptions and surgical delivery is even more challenging. More commonly, toxicity either severely limits or completely precludes therapeutic delivery. As a consequence, many GFs (and other proteins) have lain clinically dormant. To awaken the clinical potential of GFs, a protein delivery system capable of achieving durable delivery (weeks-months) is required. We have developed a 'plug-and-play' technology which generates pure cocrystals of a target protein contained within a polyhedrin protein excipient. This enables (1) efficient purification, (2) stabilization and (3) sustained-delivery of essentially any protein, including GFs. In collaboration with researchers at Kings College London, we are applying this technology to treatment of Parkinson's disease.

BIOGRAPHY | Michael Jones is the CEO and founder of Cell Guidance Systems. He received his PhD in skin cancer molecular biology from Newcastle University, UK, before pursuing research in genomics and cancer at Cambridge University and Chugai Pharmaceuticals in Japan. During his research career, he published over 30 papers and patents. Michael progressed to roles in corporate development and was the COO of Reprocell (a Japanese stem cell company) before establishing Cell Guidance Systems in 2010. The company has a hybrid model providing products and services which generate revenues supporting therapeutic programmes of research.

EVAN REID



Cambridge Institute for Medical Research, University of Cambridge

TALK TITLE | Understanding cellular mechanisms of axonopathy in hereditary spastic paraplegias

ABSTRACT | My group focuses on understanding molecular mechanisms causing hereditary spastic paraplegias (HSPs). These are genetic conditions in which axons develop selective distal degeneration. We primarily focus on spastin, a protein encoded by the gene most commonly mutated in HSP. Through this work, we have discovered a cellular pathway linking HSP proteins involved in endoplasmic reticulum shaping and endosomal tubule fission to a common feature of lysosome dysfunction. We propose this is the key underlying pathology in many genetic subtypes of HSP. We are now investigating the mechanisms by which lysosome dysfunction could cause axonal degeneration in HSP, with the aim of identifying tractable therapeutic targets, and are attempting to develop a screenable neuronal model system.

BIOGRAPHY | Evan Reid graduated in Medicine from Glasgow University in 1991 and trained in Medical Genetics in Glasgow and Cambridge. In 2001 he completed a PhD in the laboratory of David Rubinsztein. After this he held a Lectureship in Medical Genetics at Cambridge until 2004, before becoming first a Wellcome Trust Advanced Fellow and then, in 2008, a Wellcome Trust Senior Research Fellow in Clinical Science. He has been a Pl at the Cambridge Institute for Medical Research since 2008 and was appointed as a University Lecturer /Honorary NHS Consultant in Medical Genetics, University of Cambridge, in 2014. Since 1995, his research has been focused on the clinical features, genetics and cell biology of the hereditary spastic paraplegias.

PARALLEL TRACKS

SESSION 3B ONCOLOGY

CO-CHAIRS
RAB PRINJHA
REBECCA FITZGERALD

RAB PRINJHA



VP head of Epigenetics Research Unit, Oncology, GSK

BIOGRAPHY | Rab Prinjha currently leads the merged Epigenetics Research Unit supporting both the ImmunoInflammation and Oncology Therapy Area Unit portfolios. In addition, Rab is also currently interim Head of the Adaptive Immunity Research Unit. Prior to leading the Epigenetics DPU he led the Target Progression department with responsibilities for target selection, validation and epigenetic compound characterisation along with coordinating academic collaborations. He joined Epigenetics from the II-virtual group which was responsible for implementing the externalisation and portfolio diversification strategy of the TA. Previously he led a Target Validation group in the Neurology CEDD focussed on neurodegeneration. In addition to advancing many programs while in Neurology he cloned a novel inhibitor of CNS regeneration called Nogo-A and led this program from gene cloning to Candidate Selection and into clinical trials. Rab cofounded the GSK Biology Council and is a member of the OpenTargets and Milner Therapeutics Consortium Innovation Boards and sits on the MRC PSMB Board. He was a member of the Padlock Board until their acquisition by BMS. He is a Fellow of the Royal Society of Biology and was elected to the Academy of Medical Sciences in 2017. Rab joined GlaxoSmithKline from academia including a post-doc in developmental neuroscience at Guy's Hospital and PhD in molecular biology of the cell cytoskeleton at UCL.

GILLIAN GRIFFITHS



Cambridge Institute for Medical Research, University of Cambridge

TALK TITLE | Cancer assassins: fine-tuning killer cells

ABSTRACT | Our immune system defends our bodies against a multitude of pathogens as well as combatting cancers when they arise. Killer cells in the immune system are specialised to recognize and destroy infected and cancerous cells, which they do with remarkable specificity. My laboratory's research is focused on understanding the molecular mechanisms that control killer cells. We use many different approaches to identify the mechanisms controlling killing including studies of genetic diseases and high-resolution imaging. Our studies have revealed new mechanisms that control killing that are important when harnessing these cells to combat cancers using immunotherapies.

BIOGRAPHY | Gillian obtained her PhD at the MRC Laboratory of Molecular Biology in 1984, with Cesar Milstein. She started her own lab at the Basel Institute for Immunology before moving to University College London, the Dunn School of Pathology, Oxford, and the Cambridge Institute for Medical Research (CIMR) where she was Director 2102-2017. She was elected as a Fellow of the Academy of Medical Sciences in 2005, a member of EMBO in 2006, and a Fellow of the Royal Society in 2013. Her research is focused on understanding the cell biology and molecular mechanisms controlling secretion from cytotoxic cells of the immune system, with inspiration from primary immunodeficiencies, high-resolution imaging and unexpected parallels between biological systems.

CHRISTIAN FREZZA



MRC Cancer Unit, University of Cambridge

TALK TITLE | Mitochondria and cancer: the emerging paradigm of oncometabolism

ABSTRACT | The Frezza laboratory is mainly interested in investigating the emerging connection between cancer and metabolism, with a particular focus on mitochondrial metabolism. By using a combination of biochemistry, metabolomics and systems biology, we investigate the role of altered metabolism in cancer with the aim to understand how metabolic transformation regulates the process of tumorigenesis. Our aim is to exploit these findings to establish novel therapeutic strategies and diagnostic tools for cancer.

BIOGRAPHY | Christian Frezza is Programme leader at the MRC Cancer Unit, Cambridge Cancer Center, at the University of Cambridge, UK. He studied Medicinal Chemistry at the University of Padova, Italy, and gained his MSc in 2002, after a period of research on mitochondrial toxicity induced by photoactivable anticancer drugs. Christian then joined the laboratory of Luca Scorrano in Padova to start a PhD on mitochondrial dynamics and apoptosis. In 2008, he moved to the Beatson Institute of Cancer Research in Glasgow as recipient of an EMBO Long Term Fellowship, where he investigated the role of mitochondrial defects in tumorigenesis. He moved to the MRC Cancer Unit in 2012 as tenure track Group Leader and became a Programme Leader in 2017.

JUSTIN BRYANS



Executive Director, Drug Discovery, LifeArc

TALK TITLE | Genetics – changing the DNA of healthcare

ABSTRACT | The 'omics' revolution is transforming the way we view healthcare. Not only is it providing opportunities to identify novel targets and strengthen target validation, but it is also challenging our current approaches to healthcare. Traditionally, the healthcare system has treated disease as symptoms appear in patients; the 'omics' revolution could provide us with opportunities to asses and manage disease risk and even deflect that risk down benign pathways. This is challenging our traditional research models to develop synergies between those involved in research into drugs, diagnostics, devices and digital health. At LifeArc we are exploring how this new landscape will open up possibilities for new collaborations.

BIOGRAPHY | Justin Bryans is Executive Director, Drug Discovery at LifeArc. He trained at the Universities of York and Oxford and has worked as a medicinal chemist for over 25 years in Biotech and Pharma, including Parke-Davis and Pfizer, delivering a number of clinical candidates. He joined LifeArc in 2005 where he currently leads the drug discovery team collaborating with academics on cutting edge science to deliver proof of concept and develop potential drugs for diseases of high unmet need. Justin teaches on drug discovery at QMUL, UCL and the Wellcome Trust. He also sits on the Drug Discovery Committee for Cancer Research UK and is a Fellow of the Royal Society of Chemistry.

REBECCA FITZGERALD



MRC Cancer Unit, University of Cambridge

TALK TITLE | What is required to shift cancer diagnosis and therapy towards earlier stage disease

ABSTRACT | Early diagnosis of cancer leads to better outcomes. Unfortunately, nearly half of all new cases of cancer in England are diagnosed at the later stages III or IV, when patient prognoses are poor and intense treatments lead to significant comorbidity. Late diagnosis of cancer is a major driver of NHS cancer treatment costs, since advanced cancers are 2.5 times more costly to treat than the early stages of the disease. However, existing early diagnosis strategies are not succeeding and fewer than 10% of asymptomatic cancers are detected through screening programmes. This talk will explore how new technologies hold promise to improve early detection of cancer and how improved risk stratification could enable tailored treatment to be given to those at highest risk early on in their disease course.

BIOGRAPHY | Rebecca is Professor of Cancer Prevention at the University of Cambridge. Her laboratory is based in the University's MRC Cancer Unit and she is a Consultant Gastroenterologist at Cambridge University Hospitals NHS Trust. Rebecca leads a University wide programme in the Early Detection of Cancer. The focus of her own research is to improve methods for early detection of oesophageal cancer through better understanding of the molecular pathogenesis. Rebecca has been awarded several prizes for her work on the Cytosponge™ and associated assays (Westminster medal 2004, NHS Innovation prize 2011, BMJ Gastro team of the year award 2016 and the Jane Wardle Prize in 2018). She was elected a Fellow of the Academy of Medical Sciences in 2013 and is an NIHR Senior Investigator.

FRANK MCCAUGHAN



Dept of Medicine, University of Cambridge

TALK TITLE | Lung cancer chemoprevention — a roadmap

ABSTRACT | My work is on the early molecular drivers of squamous lung cancer (SQC). SQC is a devastating disease, for which there are still no targeted therapies. In the lab we build complex organoid and other preclinical model systems of squamous lung cancer. The overall purpose is to understand the molecular mechanisms that drive the disease and to use this information to devise novel approaches to chemoprevention and intervention. Other interests include developing patient-specific micro physiological systems for respiratory diseases and improving strategies for the early detection of lung cancer.

BIOGRAPHY | I am a clinician scientist specialising in respiratory medicine. I trained at the University of Edinburgh which included a molecular pathology B. Med. Sci. with David Harrison. After postgraduate clinical rotations in Manchester, London and Melbourne, Australia, my PhD was funded by a MRC Clinical Training Fellowship at the MRC Laboratory of Molecular Biology (LMB) with Paul Dear. I was then awarded a Wellcome Trust Intermediate Fellowship in the Department of Biochemistry at Cambridge, mentored by Gerard Evan. Currently, I am a University Lecturer in the Department of Medicine and lead clinician for Lung Cancer at Cambridge University Hospitals.

PARALLEL TRACKS

SESSION 3C ANTIMICROBIAL RESISTANCE AND THE MICROBIOME

CO-CHAIRS
KAI STOEBER
ANDRES FLOTO

KAI STOEBER



VP Global Innovation, Shionogi Europe

BIOGRAPHY | Kai Stoeber is VP, Global Innovation at Shionogi Europe. He received his MSc in Biological Sciences from the University of Bonn and his PhD from the University of Cambridge. In academia he had successful tenures at Cambridge and UCL where his research focused on cell-cycle control of DNA replication and cell division. He identified new drug targets and cancer biomarkers commercially developed by start-up and biopharmaceutical companies. He is an advocate for open innovation and open science, is experienced in establishing and coordinating private-public partnerships, and has led projects designed to accelerate research towards medical advancements by forging close collaborative academia-industry interactions. In his current role he works with senior executives in Osaka, Japan, to define and deliver Shionogi's global external innovation strategy. His focus lies on broadening external networks towards integrated research collaborations across core therapeutic areas with key stakeholders in the innovation ecosystem. He identifies and evaluates horizon technologies and new targets or molecules from external sources, develops technology road maps, and engages in preclinical liaison for drug development programs.

LEONOR SÁNCHEZ-BUSÓ



Wellcome Trust Sanger Institute

TALK TITLE | Impact of antimicrobials and sexual behaviour on the spread of gonorrhoea infections

ABSTRACT | My main research is focused on the phylodynamic and phylogeographic analysis of globally-distributed isolates of Neisseria gonorrhoeae, the sexually transmitted pathogen that causes gonorrhoea. My main interests are to study its genomic epidemiology, antibiotic resistance and mechanisms of variation related to virulence. I am approaching these aims through the study of recombination, phase variation, restriction-modification systems and patterns of methylation. Results from these *in silico* analyses come from the integration of data from different sequencing platforms (Illumina, PacBio), which coupled with phenotypic data provide invaluable information about this pathogen of increasing public health concern.

BIOGRAPHY | I am originally from Valencia, a
Mediterranean coastal city in Spain, where I grew up
and did my undergraduate and postgraduate studies in
Biotechnology. My PhD was focused on the molecular
epidemiology of the opportunistic pathogen Legionella
pneumophila in an endemic area of the Valencian
community. This work introduced me to the analysis
of high-throughput sequencing data, in which I am currently
deeply involved. I joined the Sanger Institute in 2015 as a
Postdoctoral Fellow in the Pathogen Genomics team, led
by Prof. Julian Parkhill, to dive into the genomics of the
sexually-transmitted Neisseria gonorrhoeae. I enrolled
in a Staff Scientist position in the same group in 2017.

ANDRES FLOTO



Dept of Medicine, University of Cambridge

TALK TITLE | Killing bacteria ourselves

ABSTRACT | Andres Floto's research is focused on understanding how immune cells interact with bacteria, how intra-cellular killing and inflammation are regulated and subverted during infection, how population-level whole genome sequencing can be used to reveal the biology of bacterial infection, and how therapeutic enhancement of cell-autonomous immunity may provide novel strategies to treat multi-drug resistant pathogens.

BIOGRAPHY | Andres Floto is Professor of Respiratory Biology at the University of Cambridge, a Wellcome Trust Senior Investigator, and Research Director of the Cambridge Centre for Lung Infection at Papworth Hospital, Cambridge. Clinically, Professor Floto specialises in the treatment of patients with CF, non-CF bronchiectasis, and infections with Nontuberculous Mycobacteria (NTM). He is co-chair of the British Thoracic Society NTM guidelines committee, the joint US CF Foundation (CFF) – European CF Society (ECFS) NTM Guidelines Group and the ECFS working group on NTM.

SVEN SEWITZ



Eagle Genomics

TALK TITLE | Emerging challenges and opportunities in microbiome data analytics

ABSTRACT | Before joining Eagle Genomics, Sven worked at the Babraham Institute on the computational analysis of promoter-enhancer interactions in primary human blood cells, and at the MRC-LMB on the investigation of the 3D genome organisation in yeast. He has over eight years of experience in analysing and integrating large biological datasets and in deriving novel computational approaches to progress the state of the art in biological data science.

BIOGRAPHY | Sven trained in molecular biology at Oxford University, and cellular and translational biology at the Department of Chemistry, University of Cambridge. He joined the MRC-LMB to acquire computational and bioinformatics skills, after which he led research projects at the Cambridge Systems Biology Centre and the Babraham Institute. He now leads Biological Innovation at Eagle, focusing on bringing machine learning approaches to metagenomics data.

DAVID SPRING



Dept of Chemistry, University of Cambridge

TALK TITLE | Approaches to antibacterial discovery

ABSTRACT | David Spring is distinguished for his wide-ranging contributions to chemical biology, organic chemistry, and chemistry-driven drug discovery. He has pioneered diversity-oriented synthesis to enable the efficient access to novel molecular scaffolds for exploration in drug discovery, particularly those with an antibacterial activity. In collaboration with the Welch and Salmond groups, he has worked on anti-virulence strategies to treat bacteria, such as modulation of quorum sensing.

BIOGRAPHY | David is currently Professor of Chemistry and Chemical Biology at the University of Cambridge within the Chemistry Department. He received his DPhil (1998) at Oxford University under Sir Jack Baldwin. He then worked as a Wellcome Trust Postdoctoral Fellow at Harvard University with Stuart Schreiber (1999-2001), after which he joined the faculty at the University of Cambridge.

TREVOR LAWLEY



CSO, Microbiotica and Wellcome Trust Sanger Institute

TALKTITLE | Precision metagenomics microbiome analysis in personalised medicine

ABSTRACT | Trevor Lawley's research uses advanced metagenomic sequencing and deep culturing to investigate the microbial communities contained on and within host organisms that are associated with health and a range of diseases and syndromes such as infections, autoimmunity, irritable bowel syndromes and cancer. He has pioneered many aspects of the bacteriotherapy concept where defined mixtures of bacteria are used to cure intestinal diseases linked to pathological imbalances in the intestinal microbiota.

BIOGRAPHY | Trevor is a co-founder and Chief Scientific Officer of Microbiotica. He is also Faculty Group Leader at the Wellcome Trust Sanger Institute (WTSI). Trevor began his research at WTSI in 2007 as a Post-Doctoral Fellow in the Microbial Pathogenesis group, focusing on *C. difficile* epidemiology and pathogenesis. He has worked with a global consortium from over 25 institutes to assemble a comprehensive *C. difficile* culture collection, now housed within the Sanger Institute.

Prior to joining WTSI, Trevor held a Canadian Institutes of Health Research post-doctoral fellowship, working in the Laboratory of Professor Stanley Falkow and Dr Denise Monack at Stanford University, USA. Trevor was recognised by the Peggy Lillis Foundation with their Innovator Award 2015 for his ground-breaking work on developing bacteriotherapy for *C. difficile* infections.

PARALLEL TRACKS

SESSION 3D CARDIOVASCULAR AND METABOLISM

CHAIR SANJAY SINHA

NICK MORRELL



Dept of Medicine, University of Cambridge

TALK TITLE | From genetics to new treatments for pulmonary arterial hypertension

ABSTRACT | Pulmonary arterial hypertension (PAH) is a rare disease that affects typically young women and carries a poor prognosis. Even with existing treatments, 3 year mortality is 40-50%. Thus, there remains a major unmet medical need to develop new treatments that target the underlying pathobiology. Our lab is focused on understanding the genetic contribution to PAH and using that information to design novel therapeutic strategies. Our research has identified a critical pathway that maintains pulmonary vascular integrity, involving circulating bone morphogenetic protein 9 (BMP9), generated in the liver, that engages specific receptors on the lung endothelium. Loss of function mutations in this pathway cause PAH. We have shown that exogenous supplementation of BMP9 reverses PAH in genetic and non-genetic preclinical models of disease. Based on this, we are developing, via a spin-out company, BMP9-based therapies for PAH.

BIOGRAPHY | Nick is the British Heart Foundation Professor of Cardiopulmonary Medicine at the University of Cambridge School of Clinical Medicine. His lab studies the genetic and molecular mechanisms of pulmonary arterial hypertension. In 2015 he co-founded and now serves as CEO of Morphogen-IX, a company developing new treatments for PAH based on insights from human genetics. Nick is the Research Director of the Pulmonary Vascular Diseases Unit at Royal Papworth Hospital and leads national and international collaborations to determine the genetic basis of PAH.

SANJAY SINHA



Wellcome Trust—MRC Cambridge Stem Cell Institute, University of Cambridge

TALK TITLE | 'Disease-in-a-dish' for drug discovery in Marfan syndrome

ABSTRACT | Effective medical treatments for thoracic aortic aneurysms are urgently required. The failure of losartan in clinical trials in patients with Marfan syndrome (MFS), despite success in mouse models, requires novel mechanistic and therapeutic approaches. We have established human models of the aortic disease in MFS using patient-derived human induced pluripotent stem cells (hiPSCs). This talk will describe the pathology displayed in vitro and the identification of new therapeutic approaches. This approach using hiPSCs has enabled us to dissect the molecular mechanisms of aortic disease in Marfans, identify novel targets for treatment (such as p38) and provided an innovative human platform for the testing of new drugs.

BIOGRAPHY | Sanjay is a BHF Senior Research Fellow at the University of Cambridge. He completed medical training in Cambridge, followed by a PhD in Manchester. Dr Sinha then carried out post-doctoral studies in the USA before founding his group within the Wellcome Trust—MRC Cambridge Stem Cell Institute. He has established novel human pluripotent stem cell (PSC)-based systems to aid developmental studies and generate human models of vascular diseases, in particular Marfan syndrome. He is also investigating novel techniques to regenerate the damaged heart. Dr Sinha is a Cardiologist and he combines his research work with clinical duties at Addenbrooke's Hospital, Cambridge.

PETER KIRWAN



Wellcome Trust–MRC Institute of Metabolic Science, University of Cambridge

TALK TITLE | Modelling obesity with human hypothalamic neurons

ABSTRACT | Peter Kirwan works in the lab of Florian Merkle, which focuses on understanding the mechanisms underlying obesity — largely a disease of excess food intake that in turn is regulated by specific neuron populations in the hypothalamus. To study these cells and facilitate the discovery of anti-obesity drugs, we have developed methods to efficiently generate human hypothalamic neurons from human pluripotent stem cells (hPSCs). In addition to their human genetic background which can be edited using CRISPR/Cas9, hPSC-derived hypothalamic neurons can be produced in large numbers, physically manipulated and imaged, and readily exposed to candidate cell types, hormones and drugs.

BIOGRAPHY | Peter is a stem cell and neurobiologist, with a primary interest in applying human pluripotent stem cells (hPSCs) for studying and treating disease. Having completed his undergraduate studies in Human Genetics in Trinity College Dublin, he moved to Cambridge to study developmental biology, where in the lab of Rick Livesey at the Gurdon Institute, he focused on recapitulating human cortical circuits in vitro using hPSCs. He is currently a postdoc in the laboratory of Florian Merkle at Cambridge's Institute of Metabolic Science, where his research focuses on utilising hPSC-derived hypothalamic neurons to study pathways implicated in obesity, as well as identifying novel therapeutics.

SHAMINA RANGWALA



Cardiovascular and Metabolism, Johnson & Innovation, London

TALK TITLE | Novel therapeutics for eating disorders - targeting the GDF15/GFRAL axis and beyond

ABSTRACT | GDF15 is elevated under diverse conditions of injury, such as cardiovascular disease, renal disease and cancer, where it correlates with weight loss. The overexpression or administration of GDF15 to obese mice and non-human primates reduces body weight by decreasing food intake. GDF15 binds with high affinity to GDNF Family Receptor -like (GFRAL) Receptor. Gfral expression is restricted to select hindbrain neurons and deletion in mice abrogates the ability of GDF15 to decrease food intake and body weight. The identification of GFRAL as a novel regulator of body weight has initiated investigations into targeting this pathway for the treatment of diseases such as obesity and anorexia. Further, new therapeutic approaches for body weight loss will be discussed.

BIOGRAPHY | Shamina Rangwala is the scientific lead for Cardiovascular & Metabolism (CVM) Therapeutic Area, Janssen R&D, at the Johnson & Johnson Innovation Center in London, focusing on therapies for cardiometabolic and retinal diseases across the EMEA region.

Shamina received her Ph.D. in Pharmacology at The Ohio State University and completed her post-doctoral fellowship at the University of Pennsylvania in Philadelphia, focusing on PPARs and adipokines on body weight and insulin resistance. Subsequently, Shamina joined the Diabetes and Cardiovascular group at Novartis in Cambridge, MA, and then Novo Nordisk in Copenhagen, Denmark. She then joined the Discovery group in CVM at Janssen where she led multiple discovery teams that successfully identified clinical candidates for obesity and metabolic disease.

CLEMENCE BLOUET



Wellcome—MRC Institute of Metabolic Science, University of Cambridge

TALK TITLE | Targeting central metabolic sensing pathways to promote satiety

ABSTRACT | Human obesity is predominantly a disease of brain pathways regulating appetite. Our aim is to help characterize these pathways to eventually develop safe and efficient therapies promoting satiety. Although protein is known to be the most potent appetite suppressant among all macronutrients, little is known about how the mammalian brain senses protein availability to create neural representations that guide behaviour and modulate metabolism. Data obtained across taxa from flies to humans indicate that evolutionary-conserved homeostatic mechanisms tightly control protein intake, and that this control is prioritized over the control of carbohydrate, fat or energy intake. Targeting protein-sensing mechanisms could therefore represent a novel avenue for the development of anti-obesity drugs. The Blouet lab employs a multi-disciplinary approach coupling calcium imaging to characterize the neurophysiology of metabolic-sensing neurons, discrete manipulations of brain neurocircuits and nutrient sensing pathways using cutting-edge molecular genetics, and refined functional assessments in behaving rodents to characterize how proteins are detected by the brain to maintain energy homeostasis in health and disease.

BIOGRAPHY | Clemence obtained a PhD in nutritional physiology from AgroParisTech in Paris and pursued a postdoc in neuroscience at the Albert Einstein College of Medicine in New York. In 2014, she relocated to the UK on a career development award and she is now on a programme leader track position at the MRC Metabolic Disease Unit.

SESSION 4 START-UPS AND INVESTMENT IN CAMBRIDGE

JASON MELLAD
JONATHAN MILNER

SESSIOZ

JASON MELLAD



CEO, Start Codon

BIOGRAPHY | Jason is a scientist entrepreneur passionate about translating innovative technologies into more effective therapies and better patient outcomes. He recently co-founded Start Codon to identify, fund and support ground-breaking healthcare startups from across the UK and beyond. Based at the Milner Therapeutics Institute, Start Codon provides expert guidance, lab/office space, and invests up to £250k in each company for equity. Previously, Jason was CEO of Cambridge Epigenetix where he developed a proprietary epigenetic biomarker discovery platform for the development of new diagnostic assays and the identification of novel drug targets. As a Marshall Scholar, he obtained his PhD in Medicine from the University of Cambridge and has a BSc in Molecular Biology and Chemistry from Tulane University.

JONATHAN MILNER



Abcam

BIOGRAPHY | Jonathan, co-Founder and currently Deputy Chairman of Abcam plc, is an entrepreneur and investor and is passionate about supporting UK life science and high-tech start-ups. He has provided considerable investment and support to over 40 companies and has assisted three technology companies to IPO on the London AIM Stock exchange.

Jonathan gained his doctorate in Molecular Genetics at Leicester University after graduating in Applied Biology at Bath. From 1992–95, he was a post-doctoral researcher at Bath, following which he worked at the University of Cambridge in the lab of Professor Tony Kouzarides researching the molecular basis of breast cancer. He identified the market opportunity for supplying high-quality antibodies to support protein interaction studies, and in 1998, founded Abcam with David Cleevely and Professor Tony Kouzarides.

Jonathan is also a non-executive director of Healx, Shift Bioscience and Syndicate Room. He is also Chairman of Axol Bioscience, Cambridge Allergy and PhoreMost.

In 2015 Jonathan, with Professor Tony Kouzarides, cofounded the Milner Therapeutics Institute at the University of Cambridge. Also in 2015 he co-founded, with Professor Laurence Hurst, the Milner Centre for Evolutionary Studies at the University of Bath.

GLOBAL THERAPEUTIC ALLIANCE



The Milner Therapeutics Institute encompasses both a research institute and a global outreach programme for collaboration.

Research in the **Milner Therapeutics Institute** is funded by:



Our outreach programme is through the Global

Therapeutic Alliance, which aims to build a global research community working together across academia and industry, with Cambridge providing a hub of expertise. The Milner

Therapeutics Consortium is central to this aim (p26), and the Alliance has been expanded with the Affiliated Company (p30) and Affiliated Institutions scheme (p59) to bring complementary expertise and resources to the community, and provide opportunity to extend collaborative links within and beyond Cambridge.



The **Affiliated Venture Partners** programme, operational since October 2017, provides mentoring and potential funding opportunities for the Milner Therapeutics Institute and its Global Therapeutic Alliance, and especially for our in-house company accelerator Start Codon.

MILNER THERAPEUTICS CONSORTIUM

The Milner Therapeutics
Consortium is an academicindustry partnership, active since
June 2015. This is underpinned
by a Consortium agreement,
designed to facilitate speedy
exchange of reagents and fund
collaborative research.



ASTEX PHARMACEUTICALS



Astex is a leader in innovative drug discovery and development, committed to the fight against cancer and diseases of the central nervous system. Astex is developing a proprietary pipeline of novel therapies and has a number of partnered products being developed under collaborations with leading pharmaceutical companies. In October 2013, Astex became a wholly owned subsidiary of Otsuka Pharmaceutical Co. Ltd., Tokyo, Japan. Otsuka Pharmaceutical is a global healthcare company with the corporate philosophy: "Otsuka – people creating new products for better health worldwide." Otsuka researches, develops, manufactures and markets innovative and original products, with a focus on pharmaceutical products for the treatment of diseases and nutraceutical products for the maintenance of everyday health.

For more information about Astex Pharmaceuticals, please visit www.astx.com

For more information about Otsuka Pharmaceutical, please visit www.otsuka.com/en/

ASTRAZENECA



Partnerships and collaborations drive medical innovation today. Our approach to open innovation helps us collaborate with like-minded scientists at the interface of scientific disciplines where true creativity and innovation occurs.

Our scientists in discovery genomics, antibody engineering, antibody technology and screening sciences are already working side by side with scientists from the Medical Research Council and Cancer Research UK.

By being headquartered in Cambridge, we also bring business professionals into the ecosystem. In addition to our science and research collaborations, we support a number of business mentoring initiatives to help UK biotech entrepreneurs advance their business ideas. This includes several programmes run by the University of Cambridge Judge Business School's Entrepreneurship Centre, including Accelerate Cambridge.

AstraZeneca has been supporting the Accelerate Cambridge programme since March 2015. Over 70 AstraZeneca mentors are now involved in the programme and around 75 start-ups have benefitted from their experience so far.

We have over 140 collaborations underway with the University of Cambridge including PhD and PostDoc programmes. We also work with Addenbrooke's Hospital, Royal Papworth Hospital, The Medical Research Council Laboratory of Molecular Biology (LMB), The Cancer Research UK (CRUK) Cambridge Institute, The Wellcome Trust Sanger Institute, Microsoft and members of the technology sector.

FERRING PHARMACEUTICALS



Ferring Pharmaceuticals is a research-driven, specialty biopharmaceutical company committed to helping people around the world build families and live better lives. Ferring Pharmaceuticals have more than 6000 employees operating in 56 countries and have products available in 100 countries worldwide. In 2018 the sales reached EUR 2 Billion.

Ferring is a leader in reproductive medicine and women's health, and in specialty areas within gastroenterology and urology/uro-oncology. We have a fully integrated R&D organization with more than 700 scientists and use around 20% of our annual revenue on R&D. Today, over one third of the company's research and development investments goes towards finding innovative and personalized healthcare solutions to help mothers and babies, from conception to birth. Our R&D mindset is focused on identifying and developing innovations no matter their source. As a global pharmaceutical company, we pursue strategic partnerships that can leverage technologies and capabilities. Our goal is to create long-term mutually beneficial partnerships that advance science and bring innovative medicines to patients around the globe.

GSK



To strengthen and accelerate delivery of our pipeline and the next generation of medicines that we hope will offer significant benefits to patients, we are embedding a new approach to R&D.

This approach focuses on science related to the immune system, the use of human genetics, and use of advanced technologies, and is driven by the multiplier effect of Science x Technology x Culture. We have a broad clinical pipeline including 46 potential new medicines in development for a range of diseases. This includes 16 oncology assets and 33 immunomodulators, reflecting our scientific focus on immunology and human biology. In 2019, we anticipate phase III data read-outs in key areas including HIV, oncology and respiratory.

Our Oncology pipeline is focused on immuno-oncology, cell therapy and cancer epigenetics. Our goal is to achieve a sustainable flow of new treatments based on a diversified portfolio of investigational medicines utilising modalities such as small molecules, antibodies, antibody drug conjugates and cells, either alone or in combination.

Significant investment in a wide range of advanced technologies is central to our new R&D approach. We are developing a core capability in artificial intelligence and machine learning, to enhance our ability to interpret genetics and genomic data. We will also invest in functional genomics, applying techniques such as CRISPR technology, to help discover and validate potential targets.

Partnerships are key to our innovation and include collaborations with the Altius Institute, the UK Biobank, Open Targets consortium and most recently 23andMe.

Current GSK strategy www.gsk.com/media/5349/annual-report-2018.pdf

JOHNSON & JOHNSON INNOVATION

Johnson Johnson

INNOVATION

Johnson & Johnson Innovation seeks to positively impact human health through innovation.

Johnson & Johnson Innovation in EMEA focuses on accelerating all stages of innovation across the region and forming collaborations between entrepreneurs and the Johnson & Johnson Family of Companies. Johnson & Johnson Innovation provides scientists, entrepreneurs and emerging companies with one-stop access to science and technology experts who can facilitate collaborations across the pharmaceutical, medical device and consumer sectors.

In our Pharmaceuticals sector we are divided into six therapeutic areas that run disease and pathway focused portfolios, which are fuelled by world class functions. In our areas of focus*, we drive research from inception/idea through new indications for marketed products until loss of exclusivity.

Under the Johnson & Johnson Innovation umbrella of businesses, we connect with innovators through our Innovation Centre in London, UK, our incubator JLABS @ BE in Belgium, our strategic venture capital arm Johnson & Johnson Innovation — JJDC, Inc. and our Janssen Business Development teams to create customized deals and novel collaborations that speed development of innovations to solve unmet needs in consumers and patients. For more information about Johnson & Johnson Innovation, please visit: www.jnjinnovation.com or follow us on Twitter @ jnjinnovation.com

* Cardiovascular & Metabolism (metabolism, retinal diseases, thrombosis), Immunology (IBD, rheumatology, IL-23 pathway), Infectious Diseases and Vaccines (hepatitis, respiratory infections, bacterial vaccines, viral vaccines), Neuroscience (mood disorders, neurogenerative disorders, glutamatergic pathway diseases), Oncology (hematologic malignancies, solid tumor targeted therapy, prostate cancer, immuno-oncology), Pulmonary Hypertension (Pulmonary Arterial Hypertension, Chronic Thromboembolic Pulmonary Hypertension)

PFIZER



Working together for a healthier world®

At Pfizer, we apply science and our global resources to bring therapies to people that extend and significantly improve their lives. We strive to set the standard for quality, safety and value in the discovery, development and manufacture of health care products. Our global portfolio includes medicines and vaccines as well as many of the world's best-known consumer health care products. Many of those concepts are advanced in collaboration with key leaders across the scientific spectrum via our range of collaborative models (https://www.pfizer.com/science/ collaboration). Every day, Pfizer colleagues work across developed and emerging markets to advance wellness, prevention, treatments and cures that challenge the most feared diseases of our time. Consistent with our responsibility as one of the world's premier innovative biopharmaceutical companies, we collaborate with health care providers, governments and local communities to support and expand access to reliable, affordable health care around the world. For more than 150 years, we have worked to make a difference for all who rely on us. To learn more, please visit us on www.pfizer.com and follow us on Twitter at @Pfizer and @Pfizer_News, LinkedIn, YouTube and like us on Facebook at Facebook.com/Pfizer.

SHIONOGI



Shionogi & Co., Ltd. is a drug discovery-based pharmaceutical company making diligent efforts in the research and development of new drugs that are needed by patients around the world. Shionogi & Co., Ltd. was established in 1878 in Osaka, Japan. The number of employees is approximately 5,000.

The purpose of the Shionogi Group's corporate activities is, as expressed in the opening of its Company Policy, to "supply the best possible medicine to protect the health and wellbeing of the patients we serve." This eternal and unwavering corporate philosophy is a statement of our vision and value to society.

In April 2014 we launched the Shionogi Growth Strategy 2020 (SGS2020). SGS2020 sets our vision to grow as a drug discovery-based pharmaceutical company through clear priorities and focused resourcing, growth led by FIC* and LIC** compounds, and continued improvement of business operations.

In May 2016, we announced the rolling plan for FY2018, with targets of 125B yen of ordinary income and 15% of ROE. We aim to achieve our SGS2020 final-year targets for ordinary income and ROE two years early. As a result, in October 2016, we updated our FY2020 vision and targets accordingly.

^{*} First in Class (FIC): Innovative medicines with particularly high novelty and usability that can change the existing therapeutic paradigm significantly.

^{***}Last in Class (LIC): Unrivaled medicines with clear superiority over others with the same mechanism of action.

AFFILIATED COMPANIES

The Affiliated Company scheme, established in October 2017, now includes 54 organizations which bring diverse expertise and resource to the Milner network.

LIFE SCIENCE TOOLS & SERVICES

DRUG DISCOVERY ASSAYS & CONSUMABLES









































































OBRIZUM®





























* Small and medium-sized enterprises

ABCAM

abcam

As a global life sciences company, Abcam identifies, develops, and distributes high-quality biological reagents and tools that are crucial to research, drug discovery and diagnostics. Working across the industry, the Company supports life scientists to achieve their mission, faster. Abcam partners with life science organisations to co-create novel binders for use in drug discovery, in vitro diagnostics and therapeutics, driven by the Company's proprietary discovery platforms and world-leading antibody expertise. By constantly innovating its binders and assays, Abcam is helping advance the global understanding of biology and causes of disease, which enables new treatments and improved health. The Company's pioneering data-sharing approach gives scientists increased confidence in their results by providing validation, user comments and peer-reviewed citations for its 110,000 products. With twelve sites globally, many of Abcam's 1,100 strong team are co-located in the world's leading life science research hubs, complementing a global network of services and support.

Contact: www.abcam.com

ACTIVE MOTIF



Active Motif is the industry leader in developing and delivering innovative tools to enable epigenetics and gene regulation research. We are committed to providing the highest quality products along with superior service & support to the life science, clinical and pharmaceutical/drug discovery communities. Whether you are an expert in the field of epigenetics or a researcher interested in integrating epigenetics research into your studies, our comprehensive portfolio of experts will enable you to tackle your most difficult scientific challenges. We provide:

- Innovative products for chromatin immunoprecipitation and DNA methylation
- Epigenetic services
- Antibodies for ChIP and ChIP-Seq
- Recombinant proteins and substrates
- Multiplex histone PTM quantitation products & services
- Luciferase reporter assays

For more information:

- Products for ChIP www.activemotif.com/chip www.activemotif.com/dna-methylation
- Epigenetic Services www.activemotif.com/services
- Antibodies for ChIP & ChIP-Seq www.activemotif.com/abs
- Recombinant Proteins and Substrates www.activemotif.com/proteins
- Histone PTM multiplex assay www.activemotif.com/luminex
- LightSwitch Luciferase Assay System www.activemotif.com/lightswitch

Contact: www.activemotif.com

AMGEN



Amgen is committed to unlocking the potential of biology for patients suffering from serious illnesses by discovering, developing, manufacturing and delivering innovative human therapeutics. This approach begins by using tools like advanced human genetics to unravel the complexities of disease and understand the fundamentals of human biology.

Amgen focuses on areas of high unmet medical need and leverages its expertise to strive for solutions that improve health outcomes and dramatically improve people's lives. A biotechnology pioneer since 1980, Amgen has grown to be one of the world's leading independent biotechnology companies, has reached millions of patients around the world and is developing a pipeline of medicines with breakaway potential.

Contact: www.amgen.com

APTAMER GROUP



The Aptamer Group is a world leader in the development of aptamers. Aptamers are ssDNA or ssRNA molecules that possess antibody-like affinity with the benefit of chemical synthesis, ease of modification and conjugation. Aptamers bind to a wide range of molecules with high specificity, including proteins, peptides, cells, tissues & excitingly: small molecules. Aptamers can also be raised against toxic or poorly immunogenic targets where antibodies cannot make those suitable replacements in many applications. This is a very exciting concept for the future of therapeutic and diagnostic markets as we now have a means of assessing drug targets, key proteins and nucleic acids known to play a role in disease that were previously thought to be out of reach.

The aptamers we develop are used in a variety of areas of life sciences research including:

- Protein Purification
- Lateral Flow Assay
- ELISA
- Biosensors
- Fluorescence Microscopy
- Flow Cytometry
- Immunoprecipitation

We develop aptamers for use in clinical and non-clinical diagnostics and as candidate molecules for targeted therapeutics. We have also developed a first in-kind biomarker discovery process, which is set to breathe new life into the proteomics market. A recent report has projected that the aptamer market will be worth approximately \$5bn by 2025, so we want to work with companies like yours to establish aptamers as a leading technology.

Contact: www.aptamergroup.co.uk

AZERIA THERAPEUTICS



AI VIVO is a Cambridge-based company providing an intelligent systems pharmacology platform to accelerate drug discovery and development. We uniquely combine systems biology, machine learning and AI to build a disruptive technology that enables unexpected discoveries and orders-of-magnitude gains in scalability, speed and cost. Our team of systems biologists, system pharmacologists and machine learning experts believe that biology, health and disease are all about balances and imbalances. We developed a proprietary discovery pipeline to represent I) balances in a healthy normal condition, and 2) imbalances induced by diseases, treatments and the microbiome.

We then use our optimised Al-driven prediction engine to link these balances and imbalances with mechanisms, indications and chemical space. We use this data to alleviate pathological imbalances and restore stability with unprecedented accuracy by I) identifying novel unexpected modulation strategies (e.g. mechanisms, pathways, targets), and 2) predicting corresponding modulators (e.g. compounds, peptides, metabolites). This disruptive platform speeds up and de-risks the discovery process by concurrently identifying multiple candidates and pre-selecting the best opportunities through experimental validation. We then offer successful validations as IP-protected data packages to be acquired or in-licensed.

Al VIVO is currently engaged in predicting, validating and developing: novel mechanisms and pathways for selected disease areas; drug combination candidates for drug repositioning and life cycle management; microbiome-based solutions and product development. We partner with pharma, biotech, CROs and academics.

Contact: www.aivivo.co



Azeria Therapeutics is the world's first pioneer factor drug discovery company developing breakthrough treatments for hormone resistant breast and prostate cancer patients where there are significant areas of unmet clinical need.

Founded in 2017 by Dr Jason Carroll, a leading expert in pioneer factors in cancer, Azeria is using its proprietary suite of approaches encompassing proteomics, bioinformatics, and genomics to identify biologically meaningful and chemically tractable targets to enable a pipeline of small molecules designed to inhibit pioneer factors.

Pioneer factors dictate where in the genome the transcription factors associate with DNA and what genes are regulated, and in many cases, are essential for transcription factor DNA binding. In its lead programme, Azeria is targeting the essential pioneer factor FOXAI, which has shown to be pivotal in the tumour development and maintenance of Estrogen receptor (ER) positive luminal breast cancer and is also thought to be critical in the development of prostate cancer.

Based in Cambridge, Azeria successfully raised £4 million in a Series A financing in 2018, provided by specialist oncology investment fund, the CRT Pioneer Fund, managed by Sixth Element Capital.

Contact: www.azeriatherapeutics.com

BenevolentAl

Benevolent AI, founded in 2013, creates and applies AI technologies to transform the way medicines are discovered and developed. The company seeks to improve patient's lives by applying technology designed to generate better data decision making and in doing so lower drug development costs, decrease failure rates and increase the speed at which medicines are generated. The company has developed the Benevolent Platform — a discovery platform used by BenevolentAI scientists to find new ways to treat disease and personalise drugs to patients.

Contact: www.benevolent.ai

BIOMAX INFORMATICS



Biomax Informatics AG was founded in 1997 as a spin out of the Max Plank Institute by Professor Dr Hans-Verner Mewes, Dr Klaus Heumann and Dr Dmitrij Frishman. We are headquartered in Munich (Germany) with global offices in London (UK), Vienna (Austria) and Madison Wisconsin (USA). Biomax provides computational solutions that have helped clients manage their knowledge assets and use them to make better decisions, develop innovative products and find new ways to solve complex problems. While Biomax has proven expertise in several life science sectors, Biomax solutions are increasingly applied to new areas by the most innovative organizations in the world.

Our flagship product BioXM is a semantic integration and knowledge management system that can tie EMRs to NGS workflows, pharma ELNs and clinical studies along with IP queries that give useable intelligence to the team. This is just a small example of the diverse data types that we have the capability of working with. The data can be visualized via most commercial visual analytics software.

In addition, our software is successfully used to personalize treatment and improve outcomes at a major centre of excellence for COPD treatment, with validated results. Our latest product is the NeuroXM Brain Science Suite which enables the integration of high-dimensional neuroimaging data with gene expression, electrophysiology and pharmacology to facilitate reproducibility and interoperability in neuroscience.

Contact: www.biomax.com

BLACK BELTTX



Founded in 2013, BioAscent is a leading provider of integrated drug discovery services based at the former Organon / MSD R&D site in Newhouse, Scotland.

Our drug discovery services include de novo assay development, target analysis and bespoke screening strategies, compound screening (including high-throughput and fragment screening), medicinal and synthetic chemistry, computational chemistry, DMPK, compound management and on-demand library access.

Our team of expert scientists has experience of successfully working from assay development through to preclinical and clinical candidates across all biological target classes and major therapeutic indications; and we are working with a number of innovative medium, small and virtual biotech and academic customers to progress their small-molecule drug discovery projects.

As part of its compound management service, BioAscent currently holds and manages over I million compounds for our customers, in both liquid and solid formats. Through the Compound Cloud service, the company provides rapid on-demand access to an IP-free library of ~125,000 lead like compounds in screening-ready format.

Since 2013, the BioAscent team has been responsible for:

- 100 biochemical and biophysical assays for drug discovery projects
- 50 hit validation/characterisation projects
- 30 hit-to-lead campaigns
- 80,000 screening plates delivered to our global customers/partners

Contact: www.bioascent.com

Black Belt TX is a privately-held, immuno-oncology company focused on the discovery and development of novel therapeutics that utilize the body's immune system to fight cancer. Black Belt TX has been created as a spin-off from Tusk Therapeutics which has been acquired by Roche in September 2018. The team has a deep understanding of cancer immunology, a proven track-record and has strong ties with world-renowned scientific advisors. The company is funded by Droia Oncology Ventures, a specialist venture capital firm, investing solely in oncology companies. Black Belt TX is in the preclinical stages and operates from the Stevenage Bioscience Catalyst in Stevenage, UK.

BTG



We are a global healthcare company focused on Interventional Medicine. Our mission is to provide imaginative new ways to treat disease, making a real difference for patients, and a valuable contribution to healthcare. Today we have a growing portfolio of products that advance the treatment of cancer and vascular conditions.

As medicine moves from major surgery to minor procedure, no company endeavours to do more to help doctors in their quest to see more, reach further and treat smarter. We understand their needs and equip them with tools and techniques that would have seemed like science fiction only a generation ago.

BTG Interventional Oncology is committed to transforming the way cancer is treated with our portfolio of minimally-invasive, highly targeted cancer therapies that can be personalised to each patient's needs. Our products are used to treat or provide symptomatic relief for people with cancer and benign tumours. To learn more about BTG Interventional Oncology, please follow @BTGIO on twitter or visit: www.btg-io.com

We invest in clinical evidence that helps demonstrate the value of our treatments to patients, doctors, and healthcare systems. We are always interested to hear from like-minded research organisations regarding collaborating to find elegant new ways to extend our power over disease and transform patient care. We specialise in the local delivery of therapeutics and in interventional procedures for the treatment of cancer, either alone or in combination.

Contact:

Karen Skinner, VP Immuno-Oncology | www.btgplc.com

CAMBRIDGE CANCER GENOMICS



Cambridge Cancer Genomics (CCG.ai) builds the software to enable data-driven precision oncology. Our precision Al platform enables oncologists to provide more effective, personalised cancer treatment for everyone. We ensure that each patient has the right treatment, at the right time, to beat their cancer.

CCG.ai's intelligently designed algorithms analyse and interpret DNA mutations from a cancer patient, providing genomic insights into individual tumours as they change; giving actionable molecular insights into treatment effectiveness; providing personalised treatment and trial recommendations; and powering intelligent trial design and drug development.

CCG.ai are actively seeking partnerships with industry and academic institutions to grow and develop our machine learning and computational biology expertise in Cambridge, whilst maintaining an international presence through partnerships with clinical centres worldwide. As an affiliate of the Milner Therapeutics Institute, we will continue to use our influence to highlight the UK's expertise in commercialisation of the Life Sciences on the global stage.

Contact: www.ccg.ai

CAMBRIDGE EPIGENETIX



Cambridge Epigenetix has provided academics with tools to measure epigenetic modifications in the genome since 2013. We focus on utilising epigenetics to improve human health with early diagnostics and disease monitoring.

The epigenetic modification 5-hydroxymethylcytosine (5hmC) has been shown to mark transcriptionally active genes and regulatory regions (gene enhancers). Unlike the relatively static genome sequence, 5hmC is highly dynamic and changes occur early in disease development. Gene enhancers are a major determinant of cell/tissue-specific transcriptional activity and 5hmC patterns could provide crucial information regarding the cell/tissue of origin.

The link between 5hmC, active genes and tissue-specific enhancers supports the considerable potential for 5hmC to be exploited for detection and monitoring of disease states, from both solid and liquid biopsies.

We are focusing on the development of early diagnostics using our proprietary 5hmC technology (HMCP). This technique is well suited to liquid biopsy or cfDNA analysis as the input required is low (typically 3–5ng cfDNA). We also partner with key opinion leaders working in areas where 5hmC has potential to solve clinical problems.

Professor Rebecca Fitzgerald is an MRC Programme Leader at the MRC Cancer Unit. Her group is working to identify ways to determine individuals with Barrett's Oesophagus at risk of cancer development. Correctly identifying high risk groups would enable optimal care for these individuals whilst reducing the burden on endoscopy units for those at low risk. We have been collaborating with the Fitzgerald group, by providing our HMCP technology to see if 5hmC may be a suitable biomarker.

Contact: www.cambridge-epigenetix.com

CAMENA BIOSCIENCE



Camena Bioscience is a synthetic biology company that developed gSynth™, an enzymatic, rapid and highly accurate DNA, RNA and XNA synthesis technology. For more information on our rapid and accurate synthesis technology, please visit our website www.camenabio.com or contact info@camenabio.com

Contact: www.camenabio.com
Steve Harvey | steve@camenabio.com

CANTABIO PHARMACEUTICALS



Cantabio Pharmaceuticals Inc. is a preclinical stage biotechnology company focusing on the research and development of disease modifying therapeutics candidates for Alzheimer's disease (AD), Parkinson's disease (PD) and other related neurodegenerative diseases. Through its proprietary drug discovery programs Cantabio is targeting the reduction of protein aggregation, oxidative and glyoxal stress, which are believed to be some of the main causes of AD and PD. Cantabio's research strategy integrates a detailed therapeutic focus, target family biophysics, and drug discovery technology and expertise into an innovative drug discovery approach to develop small molecule pharmacological chaperones for clinical trials. These small molecule pharmacological chaperones act to stabilize the native functional form of selected protein targets against misfolding when they lose their function and/or become toxic. In addition, the company is developing therapeutic proteins that can pass through the blood-brain barrier to supplement existing levels of proteins which display loss of function during disease conditions. Cantabio is specifically developing the following therapeutic programs: (1) CB101: small molecule pharmacological chaperones targeting the DJ-I protein for PD; (2) CB201: engineered cell-penetrant DJ-I protein for PD; (3) CB301: small molecule pharmacological chaperones targeting the Tau protein for AD. The company has operations in Silicon Valley (USA), Cambridge (UK) and Budapest (Hungary), where multidisciplinary in-house R&D is carried out in our laboratory facility. Cantabio also has strong academic links with a number of academic institutions including the University of Cambridge and Purdue University, allowing cutting edge academic research support to Cantabio's therapeutic programs.

Contact: www.cantabio.com

CELL GUIDANCE SYSTEMS



Cell Guidance Systems is developing protein PODS™, a protein-stabilization platform technology. Protein instability is a recurring problem in the development of effective protein drugs, diagnostic assay controls, and delivery of effective vaccines. Cell Guidance Systems PODS™ platform technology utilizes a patented technology to produce polyhedron crystals containing constrained target proteins. This production process results in proteins with significantly enhanced stability in storage and greatly extended release profiles. Working in collaboration with world-class research institutes and with other companies, Cell Guidance Systems is developing PODS™ proteins for use as therapeutics in regenerative medicine and as cold chain independent vaccines.

Contact: Ines Ferreira | Michael Jones info@cellgs.com | www.cellgs.com

CELL SIGNALING TECHNOLOGIES



Founded by research scientists in 1999, Cell Signaling Technology (CST) is a private, family-owned company with over 400 employees worldwide. Active in the field of applied systems biology research, particularly as it relates to cancer, CST understands the importance of using antibodies with high levels of specificity and lot-to-lot consistency. That's why we produce all of our antibodies in-house and perform painstaking validations for multiple applications. As part of our services, we are also able to cater for custom formulations, lot reservations, custom conjugations as well as custom antibody production. And the same CST scientists who produce our antibodies also provide technical support for customers, helping them design experiments, troubleshoot, and achieve reliable results.

Contact: Mark Twigden | www.cellsignal.eu

CENSO BIOTECHNOLOGIES



Censo Biotechnologies is a specialist discovery service company supporting the discovery and development of new targeted treatments for neurodegenerative, neuroinflammatory and rare diseases, by using stem cell technology to predict how drugs will behave across a given population. Censo provides access to existing human iPSC lines, and ethically sources human tissue, both healthy and with clinically relevant disease specific mutations, to custom create new clinically relevant human patient iPSC lines for diseases such as Alzheimer's, Parkinson's, ataxias and ALS. Using highly reproducible differentiation protocols to create cell types like microglia, astrocytes, cortical and sensory neurons, we offer both customised and standard phenotypic assays to deliver disease relevant compound characterisation, and studies of genotype-phenotype relationships, providing our clients with an understanding of human therapeutic efficacy and patient population therapeutic response variability.

Contact: www.censobio.com

DEFINIENS

DEFINIENSthe tissue phenomics company

Definiens is a leading Artificial Intelligence (AI)-based biomarker analysis provider for immuno-oncology therapy research and development. Our consulting services use the Tissue Phenomics® methodology, which is closely integrated with histochemistry assay development, image analysis and bioinformatics. This novel approach reveals insights within the tissue tumor microenvironment — becoming the basis for immune profiling, biomarker discovery, and patient stratification.

Our expert team of pathologists and data scientists is equipped with the latest deep learning and machine learning technology to make sense of big data. We combine complex tissue images and multi-omics data to yield robust results, which enables our clients to make better, more confident decisions.

Definiens was founded by Nobel Laureate Dr Gerd Binnig and is a member of the AstraZeneca group and a trusted global partner for researchers in biotechnology. Additional clients include renowned biopharmaceuticals and prestigious academics, who have collectively published over 1,000 scientific papers using Definiens' products and services.

Please visit www.definiens.com and follow us on social media for the latest developments.

Contact: Aziz Mustafa | amustafa@definiens.com www.definiens.com

DEFINIGEN

DefiniGEN.

DefiniGEN has world-leading expertise in the area of iPSC production and metabolic disease modelling. The company has a unique platform technology for generating phenotypically validated human cell disease models for a range of rare metabolic and liver diseases, to optimize preclinical drug discovery. DefiniGEN's proprietary OptiDIFF platform generates terminally differentiated human cells of endodermal lineage from iPSCs. We provide iPSC-derived hepatocytes, pancreatic cells, and intestinal organoids from healthy and diseased donors which closely resemble human primary cells. Off-the shelf products include:

- Alpha-I antitrypsin deficiency
- Glycogen storage disease type Ia
- Familial hypercholesterolemia
- MODY3 Diabetes
- Neonatal Diabetes

The application of these technologies in drug discovery provides pharmaceutical companies with more predictive *in vitro* human cell products enabling safer and more effective treatments. This technology platform can be combined with our cutting edge CRISPR gene-editing service to produce a wide range of bespoke validated disease model cell products enabling pharmaceutical companies to effectively reprofile and reposition their drug libraries.

To find out more about our products and services, please visit: www.definigen.com

Contact: Richard Willock | +44 7972 486 427 richard.willock@definigen.com

DIAGENODE



Diagenode is a leading global provider of complete solutions for epigenetics research, biological sample preparation, and diagnostics assays based in Liege, Belgium and NJ, USA. The company has developed a comprehensive approach to gain new insights into epigenetics studies. The company offers innovative Bioruptor® shearing and IP-Star® automation instruments, reagent kits, and high quality antibodies to streamline DNA methylation, ChIP, and ChIP-seq workflows. The company's latest innovations include a unique, full automation system, the industry's most validated antibodies, the Megaruptor shearing system for long fragment generation in sequencing, and epigenetics assay services.

At Diagenode, our goal is to build products with pride and the highest level of performance. Our team of epigenetics experts develop products by getting feedback from our customers as well as the scientific and medical communities around us. We strive to develop superior and easy-to-use products to bring epigenetics research and diagnostics to new frontiers.

Contact: www.diagenode.com

DOMAINEX



Domainex is a fully integrated drug discovery CRO with a reputation for speed and innovation. Built on an exceptional track record of drug candidate delivery, it has a world-class discovery team with the unrivalled track record of an average of one candidate drug delivered every year.

Domainex offers the following services:

- Medicinal chemistry incorporating intellectual design and efficient synthetic chemistry under the mantra 'every compound counts'
- Stand-alone computer-aided drug design and bioanalytical chemistry services
- Protein cloning, expression, purification and characterisation using E coli and baculovirus-infected insect cell systems
- Combinatorial Domain Hunting, Domainex's proprietary technology which enables the rapid identification of stable and soluble domains of proteins
- A highly differentiated and efficient approach to hit discovery, encompassing: LeadBuilder, Domainex's proprietary virtual screening platform; and Fragment-Builder, Domainex's integrated FBDD platform
- Assay development and compound screening covering biochemical, biophysical and cell-based systems to support all stages of drug discovery
- X-ray crystallography services incorporating dedicated beamline time at the Diamond Light Source beamline

Domainex's discovery platform technologies enable rapid progression of drug discovery projects, from drug target through to Candidate Drug; even for challenging drug targets. In addition, Domainex's successes with academic drug discovery collaborations showcase our approaches to these programmes.

Contact: www.domainex.co.uk

EAGLE GENOMICS



Eagle Genomics' award-winning AI augmented knowledge discovery platform is revolutionising how scientists conduct life sciences research and is bridging the gap between data and new insights in a rapid, systematic and traceable way. It puts data science at the fingertips of biologists to drastically reduce time and cost of research, enabling customers to achieve radical productivity improvements and true data driven discovery. Eagle Genomics are thought leaders in life sciences smart data management and analysis. Over the last decade, we have collaborated with a range of blue chip clients in the healthcare, personal care and agritech sectors, enabling them to deliver game changing products and technologies into their respective markets. At Eagle Genomics, we innovate at the intersection of biology, data science and bioinformatics. We combine our knowledge in these fields with best in class enterprise software skills to achieve an audacious goal — to develop the enterprise information architecture for the genomics era. We are also proud of our strong links to research and development in the critical emerging markets of human genomics and microbiomics. We are headquartered in the epicentre of genomic research at the Wellcome Campus in Cambridge, with locations in London's Knowledge Quarter, the New York Genome Centre and Station F in Paris.

Contact: www.eaglegenomics.com

ELPIS BIOMED



Elpis BioMed offers command line access to life, combining synthetic biology with stem cell technology, which makes the consistent and efficient reprogramming of cells possible for the first time.

The Company's proprietary technology allows unique control over the execution of a cell's genetic code and enables highly controlled reprogramming of cells, providing a source of pure, mature, and consistent cell products at industrial-scale quantities.

The technology is widely applicable and can be used for research, drug discovery and toxicology, and has been validated for use in cell therapy. Elpis's IP can also be applied to biomanufacturing (it is already used in the field of cultured meat), can be easily adopted for bioproduction, and is suitable for advanced synthetic biology applications, such as the control of synthetic circuits for carbon capture.

The Company has a strong founding team with experience in cell therapy, drug discovery, and stem cell biology. The team of scientific advisors consists of world-leading stem cell, synthetic, and computational biologists from Cambridge and Stanford.

Contact: www.elpisbiomed.com | info@elpisbiomed.com

ENPLAS FUROPE

Enplas

At Cambridge Enplas Life Science Lab (C.E.L.L), which is part of Enplas Europe Limited, we are working on innovative research in the life science market. Enplas decided to take a step forward in the life science market 17 years ago to answer the needs for microfluidic chips. With the creation of CELL, we are looking to apply this expertise to bring new innovations to the biotechnology market. CELL as a lab is working on biotechnology applications such as organ on a chip, single cell and droplet microfluidics for the life science industry (pharmaceutical, cosmetic, food testing, environment).

In addition, we are seeking new innovations where we can provide financial investment, management expertise, engineering support and global quality supply support. In a nutshell, Enplas can transform your ideas into a mass production chip using our expertise and global facilities.

Contact: www.enplas.com
Camille Hetez | c-hetez@enplas.com
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EUROFINS DISCOVERY



Eurofins Discovery supports Drug Discovery through the combined expertise of Cerep, DiscoverX, Panlabs, Villapharma, and Selcia Drug Discovery. We offer a broad portfolio including medicinal and synthetic chemistry, *in vitro* pharmacology products and services, cell-based phenotypic assays, ADME-Tox, in vivo drug safety and efficacy, custom proteins, and assay development services.

Eurofins Discovery also offers DiscoveryOne, an integrated drug discovery platform providing project management, expertise and resource, to support your project from target identification and validation, through hit identification, lead optimization and on-time delivery of robust preclinical candidates. The highly industry experienced DiscoveryOne team has a 100% track record of delivering preclinical candidates for our customers, with a number entering the clinic most recently. Eurofins Discovery has been a trusted life science partner for BigPharma, Biotechs, Academic groups and Not-for-profit organisations. Through DiscoveryOne our customers can simplify the outsourcing of contracts to a single provider.

Trust our DiscoveryOne team to be your hand-in-hand partner and provide innovative solutions for your drug discovery endeavours.

Contact: www.eurofinsdiscoveryservices.com

FLUID ANALYTICS



Fluidic Analytics - Understand the Machinery of Life

Proteins are the building blocks of life. They form the structure of cells, regulate cellular activity and carry out the biochemical processes that underpin function in every living organism. Just as DNA tells what could happen over lifetimes, proteins and their behaviour tell us what is happening now.

Fluidic Analytics envisions a world where information about proteins and their behaviour transforms our understanding of how the biological world operates, and helps all of us make better decisions about how we diagnose diseases, develop treatments and maintain our personal well-being.

By building the world's best tools, software and services for protein characterisation and making them universally accessible in the lab, in the clinic or at home, we are making this vision a reality not just for a small group of expert users, but for everyone who can benefit.

Our products are based on a fundamentally new technology platform developed at the University of Cambridge. This platform enables the rapid characterisation of proteins based on the physical properties that determine their function. And because proteins are characterised in solution and in their natural state — without the need for surfaces, matrices or ionisation — this platform gives our customers' access to unique quantitative insights into protein behaviour that are not accessible using other approaches. Interested in a better understanding of how the biological world functions? We can help.

Contact: www.fluidic.com

GE LIFE SCIENCES



GE Healthcare Life Sciences focus on the development of tools, technologies and services enabling:

Cell & Gene Therapy, Bioprocessing, End to end Manufacturing, Bio manufacturing platform development (for mAbs, vaccines, viral vectors and much more), Analytics, Protein research, Genomics, Cellular Analysis, Molecular Biology, Research Hardware from early stage development all the way to large biopharma production.

Contact: www.gehealthcare.com

GENEDATA



Genedata transforms life science data into intelligence with a portfolio of advanced software solutions and scientific consulting. With award-winning, user-friendly platforms and deep domain expertise, Genedata enables dramatic increases in productivity and quality of research, development, and production.

The Genedata portfolio of advanced software solutions is built on open, enterprise-level client-server architecture, which can be deployed to a variety of infrastructures, including on-premises or cloud-based installations. Genedata solutions deliver a high degree of built-in business logic, integration, performance, and scalability to researchers, scientists, and managers. Genedata also offers a range of services and support, from installation and customization to global roll-out support, training, data analysis, application consulting and IT consulting services, all tailored to clients' specific needs. Highly skilled professionals bring extensive domain knowledge and experience to your organization.

Today, the world's leading pharmaceutical, agrochemical, and biotechnology companies, as well as some of the most innovative life science research institutions rely on Genedata. Genedata recently released its latest version of Genedata Profiler[®], the enterprise solution of choice for efficient and effective omic-based translational and exploratory clinical research that enables global research organizations to achieve their vision of precision medicine. Breaking down data silos and allowing controlled access to every research team member, the platform provides self-service data analytics that generate valuable scientific insights at scale, while enabling compliance with increasingly complex data privacy laws and regulatory requirements.

Contact: www.genedata.com

GENESTACK



Genestack brings together bioinformatics and software development expertise to provide solutions for data and metadata management, as well as analysis pipelines and a range of interactive visual analytics tools.

Our portfolio of products and services includes a combination of off-the-shelf modules, customisation, and new apps prototyping. We draw on decades of industry and academic experience to provide customers with tailored data management solutions and scientific consultancy.

We work with clients in the pharmaceutical, consumer goods, biotechnology and healthcare industries to help them get the most out of their data and maximise the return on investment into data production. We aim to make the lives of people who do bioinformatics simpler. Our goal is to help our users leverage high-throughput multi-omics data and fast-track drug discovery, precision medicine and bioinformatics research in the post-genomic era.

Currently we are releasing Omics Data Manager (ODM), a data management system for multi-omics, biological and healthcare data. ODM is a software product that enables its users to create a FAIR data catalogue, by solving common pain points in data management such as data silos, lack of metadata standards, and unclear data relationships. ODM is the result of a fruitful collaboration with a top pharmaceutical company.

Contact: www.genestack.com

HEALX



Healx is a leading tech company focused on accelerating treatment discovery for rare diseases. To achieve this goal, Healx have developed the most comprehensive AI-based drug discovery platform for rare diseases: Healnet, which uses the latest AI, ML, NLP and data mining techniques to discover monotherapy and combination therapies.

Healnet integrates AI with deep pharmacology to allow highly-parallel rare disease drug discovery to take place at a large scale. This process significantly reduces the time, cost and risks associated with drug discovery. Using Healnet, Healx have shown that it's possible to translate drugs into the clinic 80% faster and about 90% cheaper than conventional drug discovery methods. There are 7,000 known rare diseases that affect 350 million people worldwide and 95% of these diseases still do not have an approved treatment. Healx believe that every rare disease patient deserves a treatment and have made it their mission to translate 100 rare disease treatments towards the clinic by 2025.

Healx was founded in 2014 by Dr Tim Guilliams, a biochemical engineer and founder of the Cambridge Rare Disease Network (CRDN), and Dr David Brown, the inventor of Viagra and former Global Head of Drug Discovery at Roche.

Contact: www.healx.io

INTELLEGENS



Intellegens creates solutions that encapsulate our unique deep learning algorithm Alchemite, capable of training artificial intelligence models from very sparse or noisy data. Since spinning out from the University of Cambridge, we have been partnering in multiple domains, including drug discovery, healthcare and infrastructure, bringing our generic technique to bear on high-value commercial problems.

We are seeking partners who are working with large, incomplete datasets or experimental data, where our ground-breaking machine learning approach will be able to add most value.

Contact: Tom@intellegens.ai | www.intellegens.co.uk

LABKEY



ONE Solution for ALL your research data management requirements.

LabKey is a small privately-owned life sciences-dedicated custom informatics solution provider, with over 15-years' experience solving research data challenges around the world, and has recently opened its European office, near London, UK.

Described as a 'TOOLKIT, the core platform, LabKey Server offers modular data management tools and resources, which are applied to address individual or multiple research data challenges, that scientists need to overcome, every day.

Built with world-class software engineering, LabKey Server is open source, enterprise-quality and can be hosted on premises, or cloud-hosted.

Contact: www.labkey.com Jason Leadley | jason@labkey.com

LINGUAMATICS



Linguamatics, an IQVIA company, delivers market-leading NLP-based AI solutions for high-value knowledge discovery and decision support from text. We empower our customers to speed up drug development and improve patient outcomes by breaking down data silos, boosting innovation, enhancing quality, and reducing risk and complexity. Our award-winning NLP platform is proven across multiple real world use cases. Linguamatics has been trusted for over 15 years to deliver actionable insights that address your most pressing bench-to-bedside challenges with quantifiable ROI.

Our customers include 18 of the top 20 global pharmaceutical companies; the US Food and Drug Administration (FDA); and leading cancer institutes, hospitals, and academic research centers. Linguamatics NLP has been deployed by organizations in pharmaceuticals, biotechnology, healthcare, chemicals and agrochemicals, government, and academia. The company operates globally, with headquarters in Cambridge, UK, and a U.S. office near Boston, MA.

Contact: www.linguamatics.com

Ymedannex

MedAnnex is a privately-owned, preclinical-stage biopharmaceutical company, established in 2009 by Professor Chris Wood, founder of Bioenvision Inc. (NASDAQ: BIV) and NuCana plc (NASDAQ: NCNA). MedAnnex has recently been granted funding via both Innovate UK and Scottish Enterprise, and also received Corporate LiveWire's Healthcare & Life Sciences Award for Innovation in Autoimmune Disease Treatment. MedAnnex's monoclonal antibody approach has shown significant activity and therapeutic potential in experimental models of rheumatoid arthritis, multiple sclerosis and systemic lupus erythematosus (SLE). By modulating the undesirable over-expression of annexin-AI associated with pathways of chronic inflammation, MedAnnex is developing a novel agent for the treatment of complex autoimmune conditions and also exploring other T-cell mediated pathologies. MedAnnex is a member of the Scottish Life Sciences Association and has its headquarters in Edinburgh, Scotland.

METRION BIOSCIENCES



Metrion Biosciences is a UK-based Contract Research Organization (CRO) focussed on delivering a range of high quality ion channel drug discovery services. We provide highly skilled electrophysiology screening services to support client medicinal chemistry optimisation programmes, CiPA compliant cardiac safety profiling assays, neuroscience assays and translational assays. Working closely with our collaborators Assay. Works, AMRI and Concept Life Sciences, we also offer an expert fully integrated ion channel drug discovery service. Metrion offers flexible business models according to the scope of each programme, with both fee-for-service and collaborative options available. Please contact us to discuss your next ion channel project or to request a quotation.

Contact: www.metrionbiosciences.com

MICROBIOTICA



The microbiome represents a paradigm shift that affects every aspect of biomedicine: our gut bacteria control health and disease, and can themselves be a novel type of medicine. Since its foundation in late 2016, Microbiotica has shown itself to be a global leader in this exciting new sector based on its unique platform which brings precision medicine to the microbiome. In June 2018 it signed a strategic alliance with Genentech in IBD worth \$534m, the largest microbiome deal at the time. In the same month, the company signed a collaboration with University of Adelaide to access Ulcerative Colitis clinical samples. These deals demonstrate the remarkable speed with which Microbiotica is building its position in the microbiome field while simultaneously advancing its pipeline.

Microbiotica's platform, based on ground-breaking science developed at the Sanger Institute, enables unprecedented precision in identifying bacteria linked to health or disease. Key elements are a unique capability to isolate all bacteria from any individual, and the leading collection of bacterial genomes which is being expanded to comprise the definitive global collection. Together with Al, these capabilities enable identification of therapeutic bacteria and progression as oral therapies. The company has built an expert team of 35 scientists and is driving programs in C. difficile, Ulcerative Colitis and Immuno-oncology (bacterial co-therapy).

Contact:

info@microbiotica.com | www.microbiotica.com

MODIQUEST RESEARCH



For over 10 years ModiQuest® Research has specialized in the generation of monoclonal antibodies against difficult targets for R&D, diagnostic and therapeutic applications. Using our proprietary ModiVacc™ (hyper-immune stimulatory cell immunization), ModiFuse™ (electrofusion-based hybridoma generation), ModiSelect™ (antigen-specific B-cell selection) and ModiPhage™ (phage display) technologies, we can generate monoclonal antibodies from multiple species against virtually any target. Besides lead antibody generation, we also provide antibody engineering (ModiTune™), such as affinity maturation and humanization, and production (ModiXpress™) in transient and stable mammalian cell systems. All services are offered on a fee-for-service basis.

Contact: www.modiquestresearch.com

NEMESIS BIOSCIENCE



We are a biopharmaceutical company developing Symbiotics® — DNA therapeutics administered before or with antibiotics to inactivate anti-microbial resistance in bacterial pathogens.

These Nemesis Symbiotics will make existing antibiotics work again, prevent the spread of resistance genes, and protect the efficacy of new antibiotics. The technology is applicable to all antibiotic classes, resistance mechanisms and bacteria.

To deliver the Symbiotics, our novel Transmids[©] vectors are encapsidated in a bacteriophage coat. Transmids can also spread directly between bacteria by conjugation. Other applications include reduction of chemotherapeutic toxicity, inactivation of virulence factors, and in vivo synthesis of biofuels and therapeutics. Our current Symbiotics use RNA-guided endonuclease technology to inactivate eight families of betalactamase (bla) resistance genes — so resurrecting sensitivity to a broad range of beta-lactams. We have validated the (i) efficacy of Transmid delivery by phage coat infection and of consequent AMR inactivation in mouse models and (ii) also prophylactically inactivated AMR following plasmid conjugation from an introduced commensal strain to AMR bacteria in the gut flora. We are now developing our Transmids for delivery to, and AMR inactivation in, pathogenic E. coli and other Enterobacteriaceae.

Our multi-functional gene targeting systems may obviate the need for prior diagnostic screens for antibiotic resistance and be used generally as a companion biological therapeutic together with well-established antibiotics for therapeutic treatment of infection as well as for prophylactic treatment to prevent the spread of AMR.

Contact: massam@nemesisbio.com | www.nemesisbio.com

OBRIZUM



OBRIZUM®

The CamBioScience team have created OBRIZUM®, an enterprise level cloud platform that allows companies in high-skill areas like healthcare, engineering, finance, law, and software, to automatically create, deliver and monitor adaptive online courses and assessments, on a global scale. The hyper-modular courses are powered by deep proprietary Artificial Intelligence technology which personalises the presentation of content and assessments in real time based on the unique needs of the end-users. Using OBRIZUM®, managers can automatically create e-learning courses quickly and easily simply by 'dragging and dropping' content into the platform. Beyond formal e-learning, OBRIZUM's AI technology makes complex or high volume content exchange between colleagues and departments faster and more efficient. The personalised learning experience is user friendly and considerably faster than traditional linear e-learning. Tracking the performance of individuals and teams using the platform's analytics dashboards is easy and global data is updated instantaneously.

The OBRIZUM® platform is poised to disrupt the corporate learning and development market and transform the trading of knowledge both within and between organisations.

OBRIZUM® is built to meet the demands of a fast-evolving work place and change the way eLeaning is produced, consumed, and monitored. It allows companies and employees to acquire new skills on-demand in a highly targeted manner.

Smart assessments and analytics dashboards report on user performance topic by topic, overcoming the unsustainable traditional learning of broad subjects to demonstrate the acquisition of a particular skill.

Contact: www.cambioscience.com

OPPILOTECH



Oppilotech are utilising systems biology and machine learning to build computational models of cells. Our pathway modelling methodology is different from traditional approaches (Flux Based Analysis) in that we go into a much higher level of detail incorporating parameters such as catalytic rates, metabolite levels and half-lives. The high level of detail allows us to reveal new biology and identify first-in-class non-intuitive drug targets. We initially focused our modelling efforts on E.coli identifying four first-in-class antibacterial drug targets and generated active chemical matter against three of them. The company intends to develop these programmes towards the clinic. We are now expanding into pathways in human cells, allowing us to address a wider range of diseases. Oppilotech is actively seeking partnerships with Pharma/ Biotechs/Academic Groups to model specific biological pathways to identify viable drug targets and new biology.

Contact: www.oppilotech.com

O2H



o2h Discovery was founded in 2005 and has an integrated drug discovery platform operating from our state-of-theart research centre in India and our office in Cambridge, UK. We have the in-house capability to execute hit-leadoptimisation programmes leading into patent and IND filing from our state-of-the-art biotechnology incubator with expertise in discovery chemistry, biology, pharmacology and the on-going project management of pre-clinical development. o2h Discovery has developed and launched its proprietary application AI Chemistry in the Cloud[™] the world's first app to revolutionise the project management of external drug discovery programmes. The app enables communication between the various scientific stakeholders essential to successful project advancement, leading to faster decision making. It negates the onerous tasks of weeding out critical information that is required to take a complex decision by extracting the information from large data intensive reports and databases. These crucial decision points are now just a 'tap/swipe-of-the-finger' in the Al Chemistry in the Cloud[™] app so that they can speedily execute tasks anytime, anywhere. The DNA of o2h is centered around the nurturing of its people, values and culture; it reflects in the way we work with each other, as well as our collaborators and partners.

Contact: tejas@o2h.com | www.o2h.com

PELAGO BIOSCIENCE



Pelago Bioscience AB was founded in 2013 to develop and provide services based on the patented Cellular Thermal Shift Assay (CETSA®). This assay is uniquely able to measure drug-target interactions in-situ within the cellular environment and can be applied against a specified protein target for compound screening and lead optimization (CETSA Classics and CETSA HT) or in a non-targeted proteomics study (CETSA Mass Spec).

Critically CETSA require no modification to the ligand or target as it utilizes the natural thermodynamic properties of the protein itself and can be applied to any cell or sample type. CETSA MS is ideal for un-biased proteomics studies and is now used routinely for determining compound liabilities and for mode of action studies. A recent development has been its use to identify novel biomarkers. Pelago works exclusively on CETSA and is able to offer full assay development and screening services to its customers, using its own dedicated laboratories in Sweden.

PHOREMOST



PhoreMost is a Cambridge UK-based biotech company. Founded in 2014, PhoreMost has developed SITESEEKER, its proprietary phenotypic screening platform that exploits biological shape diversity inherent in proteins, to discover new functional pockets on target proteins — enabling the development of first-in-class drug discovery programs.

SITESEEKER is a phenotypic screening platform that systemically probes protein-protein interactions using hugely diverse, DNA encoded libraries with full coverage of the human proteome and beyond. The SITESEEKER platform identifies novel, phenotype-driven drug targets, functional binding pockets and peptide binding partners, which accelerate and de-risk small molecule drug discovery.

PhoreMost is currently advancing novel drug discovery programs in Cancer and Immuno-Oncology and is progressing a target ID pipeline in Aging and Neuro-degeneration.

PhoreMost also collaborate with Pharma and Biotech partners to enable access to the SITESEEKER platform. Through these collaborations PhoreMost work collaboratively to screen pathways of interest and deliver validated targets with functional, binding peptides suitable for entry into the drug discovery pipeline.

Contact: www.phoremost.com

POLYPROX

POLYPROX

PolyProx Therapeutics is a biotechnology company focused on the discovery and development of a new class of drugs, Polyproxin™ molecules, to treat cancer and neuro-degenerative diseases. Polyproxin™ molecules are biopharmaceuticals that selectively target disease-causing proteins and use natural cellular pathways to degrade or remove these proteins.

Our initial focus is in developing Polyproxin™ drug candidates for use in the treatment of cancers, targeting aberrant proteins that have previously proven difficult to target using conventional drug classes, such as small molecules or monoclonal antibodies.

Polyproxin[™] molecules were discovered during over a decade of research in the field of protein structure, folding and stability at the laboratory of founder Professor Laura Itzhaki, Department of Pharmacology, University of Cambridge UK. Working with co-founders Dr Pamela Rowling and Dr Albert Perez-Riba, they discovered that a novel class of designed proteins can be repurposed to direct disease-causing targets for destruction.

The Company was formed in 2018 based on these inventions, which are protected by a strong intellectual property portfolio that has been exclusively licensed from Cambridge Enterprise. Professor Itzhaki serves as Chief Scientific Officer, working with serial entrepreneurs Andrew Sandham, Executive Chairman, and Dr Kevin Moulder, Chief Operating Officer. Our laboratories are located at the prestigious Babraham Research Campus, Cambridge UK.

Contact: www.polyprox.com

REPOSITIVE



Repositive is committed to accelerating the development of precision cancer therapies to the clinic by working with biopharmas and Contract Research Organisations (CROs) to improve the predictivity of preclinical cancer research. Through its Cancer Models Scout service, Repositive is helping biopharmas to optimise their preclinical cancer projects by identifying the most suitable cancer models for their requirements from its world-leading inventory of over 4,500 models. In addition, Repositive is connecting researchers with the right CRO partners, which have first-class expertise and years of experience running similar studies, to ensure biopharmas receive the best advice for planning and conducting their projects.

Contact: www.repositive.io

SELVITA



Selvita is one of the largest drug discovery companies in Europe. The company was established in 2007 and currently employs almost 600 scientists, among whom 30% are PhDs. Selvita is headquartered in Krakow, Poland, with a second research site in Poznan, Poland and foreign offices located in Cambridge, MA and San Francisco Bay Area, in the US, as well as in Cambridge, UK.

Our scientists have extensive experience in life sciences, and we offer the following: contract chemistry services, biology services, integrated drug discovery projects, comparative studies of biosimilar medicinal products

Selvita's laboratories are GLP and GMP-certified.

Contact: www.selvita.com

STORM THERAPEUTICS



Harnessing the power of RNA epigenetics

Storm Therapeutics is a spin out of the Gurdon Institute at the University of Cambridge, created to commercialise the work of founders Professors Tony Kouzarides and Eric Miska in RNA epigenetics.

Several large families of RNA-modifying enzymes have been identified that impact key biological processes by changing the activity of RNA through catalysing epigenetic RNA modifications. Storm is working at the forefront of this new field, collaborating closely with our scientific founders and their research groups at the Gurdon Institute to elucidate the functional role of diverse RNA modifications. Advances in the understanding of RNA modification and its role in the development of cancer offer the prospect of identifying novel therapeutic targets. Using cutting-edge techniques such as CRISPR screens, chemical biology, RNA-Seq and RNA mass spectrometry, we have established a unique target discovery platform for the identification of small molecule modulators of RNA modification pathways.

Since inception in May 2015, Storm has raised £16m in seed and Series A funding. The company uses the proceeds to establish a pipeline of drug discovery programmes to develop novel, first-in-class drugs for the treatment of specific cancers with high unmet medical need.

Contact: info@stormtherapeutics.com www.stormtherapeutics.com

STANDIGM

Standigm

Standigm is a drug discovery company that searches therapeutic lead compounds using advanced artificial intelligence trained on biomedical big data. Standigm currently focuses on designing novel compound structures to bind specific protein targets. We developed an Al-based lead generation platform (Standigm BEST®) based on which we have several in-house target-based drug discovery pipelines as well as collaborative drug discovery projects. We are seeking further collaboration partners who are interested in discovering novel scaffolds for their specific targets.

Standigm have also developed an AI platform for new indication prediction and novel target discovery using an ensemble of multiple AI models and a comprehensive biomedical graph database, based on which tens of drug candidates for cancers, Parkinson's disease, autism, fatty liver diseases (NASH) and more have been experimentally validated with several collaboration partners and CROs.

Founded in 2015 by experts in artificial intelligence and systems biology at the Samsung Advanced Institute of Technology in Korea, Standigm has grown into a team of elite researchers including 11 PhDs with multi-disciplinary expertise in chemistry, biology, pharmacology, and high-performance algorithms and data structures. It has recently raised \$11.5 million in a Series B funding round which brings its total financing to \$15 million so far. Standigm will use the funds to scale the AI technology platforms and advance its drug discovery pipelines toward license-out. Our vision is a full-stack pharmaceutical company that could ease the pains of patients all over the world.

Contact: www.standigm.com

STREM CHEMICALS UK



Another growth year for Strem Chemicals UK, we have seen an increase in customers relying on key product lines, such as metal catalysts, ligands (especially phosphines), organometallics and N-heterocyclic carbenes for organic synthesis. More recently, Strem Chemicals has introduced a line of biocatalysts, which includes enzymes, enzyme carriers and a selection of biocatalyst kits for screening of various processes.

There has been advancement in the 4th Generation of Buchwald Palladacycle technology that has seen some amazing successes in developing anti-diabetic drug development, migraines, autoimmune diseases, myeloproliferative and inflammatory disease, major depressive disorders, treatment of hepatitis c, oncology, and it is wonderful to show how our chemicals can make a difference.

Many of our kits are used in Pharma research and contain a variety of chemicals commonly combined when screening experiments and our license allows us to provide this technology for R&D and commercial applications. We offer patent-free and proprietary catalysts and ligands for organic synthesis, often at kilo-scale, including many for asymmetric transformations. Our licensed technologies come royalty-free for R&D purposes.

New research materials have been released for all our customers this year in 18 booklets focused on heterogeneous catalysts, kits, metal catalysts for organic synthesis including organocatalysts, MOCVD, CVD & ALD precursors, new products, other ligands, phosphorus ligands and compounds, photocatalysts and PURATREM™. These are available for download in pdf format.

Contact: 01223 870584 | enquiries@strem.co.uk

TWIST BIOSCIENCE



At Twist Bioscience, we work in service of customers who are changing the world for the better. In fields such as medicine, agriculture, industrial chemicals and data storage, by using our synthetic DNA tools, our customers are developing ways to better lives and improve the sustainability of the planet. The faster our customers succeed, the better for all of us, and Twist Bioscience is uniquely positioned to help accelerate their efforts.

Our innovative silicon-based DNA Synthesis Platform provides precision at a scale that is otherwise unavailable to our customers. Our platform technologies overcome inefficiencies and enable cost-effective, rapid, precise, high-throughput synthesis and sequencing, providing both the quality and quantity of the tools they need to rapidly realize the opportunity ahead.

Contact: www.twistbioscience.com | @TwistBioscience

UBIQUIGENT



Ubiquigent enables and supports protein degradation focused drug discovery via modulation and exploitation of the ubiquitin system. Our chemistry and biology platforms allow us to design and develop novel compounds as part of strategic partnerships. In parallel we also provide access to our platforms and capabilities for the evaluation of our partners' compounds. Deubiquitylase (DUB) enzymes provide a rich seam of protein degradation regulation and chemically tractable drug targets relevant across many therapeutic areas including neurodegeneration, oncology and fibrosis. Ubiquigent have developed a capability to design and deliver novel small molecule DUB targeting chemistry utilising our in-house proprietary computational and medicinal chemistry 'DUB toolkit' platform integrated with our comprehensive biology workflow. This DUB inhibitor screening capability enables the characterisation of molecules to determine their affinity, selectivity, mechanism of action and in-cell target engagement. We are also building a wider platform for supporting not only DUB targeting but also drug discovery employing other protein degradation modalities such as PROTACs and molecular glues. Commercial relationships with Ubiquigent may be both on a CRO or an exclusive Collaborative Drug Discovery basis. In the latter case Ubiquigent can provide exclusivity around both the target and our novel chemistry. Ubiquigent is therapeutic area agnostic working with an array of companies and groups. Partners range from those with significant expertise and activity in the ubiquitin and protein degradation field to those with little experience in the area. Typically partners bring strong therapeutic area expertise and Ubiquigent the ubiquitin system and protein degradation drug discovery capabilities.

Contact: www.ubiquigent.com

VERNALIS



Vernalis Research is recognised as a world leader in fragment- and structure-based drug discovery. Based in Cambridge, UK, Vernalis has been developing and applying these methods to challenging projects since 2003. Vernalis has a strong emphasis on combining innovative structural biology, biophysics and medicinal chemistry to tackle targets across therapeutic areas ranging from oncology to inflammation and neurodegeneration.

Vernalis balances an internal portfolio of drug discovery projects with fully integrated research collaborations; these include working with academic partners, biotechnology companies and large pharmaceutical companies. Vernalis currently has seven NCEs in clinical development, and a number of other compounds in pre-clinical development.

Contact: www.vernalis.com

VIROKINE THERAPEUTICS



Virokine Therapeutics Ltd (VTL) is a biotech start-up, developing patent-protected discoveries by the founder in targeting immune cells by virus immunomodulators, known as our VTL 'virokines', with the potential for major applications in immunotherapeutics. These new class of immunostimulants and immunosuppressors, molecular 'ON/OFF switches', could lead to novel treatments for infectious disease, autoimmunity, and cancer. VTL is establishing a laboratory at the London Bioscience Innovation Centre (LBIC) and a programme of pre-clinical evaluation in USA as supported by a National Institutes of Health (NIH) programme.

The associated studies conducted prior to incorporating VTL in Cambridge and the London School of Hygiene & Tropical Medicine were funded by grants to the Founder as Professor including Royal Society Industry and Wellcome Trust Senior Fellowships, and awards from BBSRC, Bill and Melinda Gates Foundation plus the Higher Education Innovation Fund.

Contact: info@virokine.com

AFFILIATED INSTITUTIONS

The Affiliated Institutions programme, established in October 2017, now includes 14 academic institutions across four continents. These partners share our vision of developing new models for research collaboration across industry and academia to transform pioneering science into therapies.











JOHNS HOPKINS

UNIVERSITY & MEDICINE





















BIO-SYNERGY RESEARCH CENTER (BSRC), KAIST



As a Korean national research center, BSRC has been developing a virtual human system called CODA, with which we can explore potential efficacy and candidate mode-of-action pathways of single or combination drugs, and natural product-derived medicinal extracts. CODA contains more than 50 million physiological associations among genes, metabolites, cellular functions, and phenotypes in a unified XML-like format called CODA-ML. BSRC has been applying this system to develop combination drugs and functional foods in collaboration with several Korean pharmaceuticals and food companies. BSRC expects to find international collaboration partners in the Milner Symposium, who might utilize CODA in their research and development projects. (http://biosynergy.re.kr/eng_main)

CRUK OXFORD CENTRE



Established in 2010, the CRUK Oxford Centre (formerly the Oxford Cancer Research Centre) is a network and partnership between Oxford University, Oxford University Hospitals NHS Trust and Cancer Research UK, based on the University's Translational Biomedical Research Campus. It harnesses Oxford's world-leading cancer research with the core aim of facilitating collaboration to ensure rapid translation from scientific discovery to treatments for patients.

The ultimate aim of the Centre is to enhance cancer research activity to increase cancer cure rates. The Centre currently comprises over 500 members from 25 different Departments, Units, Institutes of the University as well as the NHS Trust. The partnership provides a cumulative investment of approximately £55m each year for science in Oxford for research to save and improve peoples' lives.

The Oxford Centre is an inclusive network of organisations in Oxford for whom cancer research is a priority focus. We support and connect people working across a range of disciplines and aim to facilitate research collaboration on a local, national and international scale to speed up translation from scientific discovery to treatments in patients.

CENTRE FOR GENOMIC REGULATION (CRG)



The Centre for Genomic Regulation (CRG) is an international biomedical research institute of excellence located in Barcelona, Spain, whose mission is to discover and advance knowledge for the benefit of society, public health and economic prosperity.

CRG believes that the medicine of the future depends on the groundbreaking science of today. The breadth of topics, approaches and technologies at CRG permits a broad range of fundamental issues in life sciences and biomedicine to be addressed. Research at CRG falls into four main areas: gene regulation, stem cells & cancer; cell & developmental biology; bioinformatics & genomics; and systems biology.

With around 500 scientists from 41 nationalities and ranking 5th worldwide in research quality, the CRG excellence is based on an interdisciplinary, motivated and creative scientific team that is supported by high-end and innovative technologies.

CRG offers numerous and varied (often unique) possibilities for collaboration in various areas of human health and personalized medicine (e.g. novel targets and mechanisms in oncology; exosomes and genome sequencing; tissue regeneration and engineering; and the study of the microbiome), as well as access to cutting-edge expertise and infrastructure for Advanced Light Microscopy, FACS, Genomics, Proteomics, Bioinformatics, Screening/Protein Technologies and Tissue Engineering. Since 2015 the CRG also integrates the National Centre for Genomic Analysis (CNAG), the 2nd largest centre in sequencing capacity in Europe. Tools and technologies are also available for partnering and licensing in the fields of cancer and immunology, lung and infectious diseases, rare diseases, neurodegeneration, protein engineering, regenerative medicine and vaccination.

SPANISH NATIONAL CANCER RESEARCH CENTRE (CNIO)

cnio stop cancer

The Spanish National Cancer Research Centre (CNIO) is a world-class centre for basic and translational cancer research located in Madrid. Our mission is to gain knowledge and apply it to prevent, diagnose and treat cancer with over 450 researchers at the forefront of cancer research.

The CNIO ranks in first position for monographic cancer centres in Europe, and our expertise and capabilities extend to ageing and oncology. In 2018, 90% of our staff were scientists and 17% were foreigners. Nurturing an ecosystem for translational research and innovation, we help researchers maximize the value of their science and bring their discoveries to society as new technologies and therapies.

A strategy to accommodate different partnership models with industry and facilitate knowledge transfer is at the core of our goals. We have a dedicated Academic Drug Discovery Programme with the expertise to carry out chemical validation of potential new targets and development of lead compounds into preclinical drug candidates.

Our current portfolio includes 8 active proprietary programs in oncology, and our value in drug discovery is supported by our unique research with genetically-modified and xenograft disease mouse models and our state-of-the-art biotechnology units. CNIO investigators are leaders in oncology and ageing (regenerative medicine) with special emphasis in DNA damage, cell cycle and telomeres, metastasis and microenvironment, inflammation and immuno-modulation, metabolic disorders and fibrosis, gene therapy, breast cancer, prostate cancer, melanoma, brain cancer, haematological tumours and lung cancer.

The CNIO seeks public-private research partnerships and licensing of a number of small molecule discovery programs at the hit-to-lead or lead optimization stage.

ELECTRONICS AND TELECOMMUNICATIONS RESEARCH INSTITUTE (ETRI)



The Electronics and Telecommunications Research Institutes (ETRI), as the Federal Research Agency of Korea for ICT and related technologies, has launched the Cognitive Informatics Research Program, as a strategic institutional agenda, for research and development of novel technologies to enable cognitive reasoning in artificial intelligence.

The human civilization is going through another technological revolution, which is referred to as The 4th Industrial Revolution, to augment our mental capabilities while the previous industrial revolutions were aimed to augment our physical capabilities.

CybreBrain consists of a set of novel ICT technologies to enable The 4th Industrial Revolution, with focus on the self-adaptive real-time Artificial Intelligence. This self-adaptive artificial intelligence with plasticity is capable of deductive reasoning, real time inferencing from in-motion data as well as at-rest data, progressive and incremental learning from outcomes, and self-adaptation to new findings and decision making.

The R&D approach we are taking is to reconstruct and simulate the human brain for cognitive reasoning, prediction and prescriptive decision making by reverse engineering the cerebral cortex of human brain. We call this novel machine learning and artificial intelligent system "The Thinking Machine" or "CybreBrain".

THE INSTITUTE OF CANCER RESEARCH (ICR)



The Institute of Cancer Research, London, is an independent research institute based across two London sites: one in Chelsea in the heart of the UK capital, and one in Sutton, 30 minutes from Gatwick international airport. A member of the University of London, we have an outstanding record of achievement dating back more than 100 years.

Around 800 scientists work here, across the full spectrum of cancer research: from basic cancer biology and drug discovery to clinical trials. We also have a unique partnership with The Royal Marsden NHS Foundation Trust: together, we are rated in the top four centres for cancer research and treatment worldwide.

The Institute of Cancer Research (ICR) is ranked top for research, research impact, biological sciences, clinical sciences and research intensity in the definitive REF rankings of UK university research. We are also world-leading in the commercialisation of our research, seeing collaboration with industry as a vital component of our success.

We have more than 200 active partnerships with a range of companies, from small, specialised biotech and medtech firms to big pharma. We are consistently ranked by international league tables as one of the world's most successful higher education institutions for academic innovation and effective collaboration with industry.

We are also among the top 10 universities worldwide for the proportion of our papers published with industry, and are first globally for the proportion of academic papers cited in patent applications.

INSTITUTE FOR RESEARCH IN BIOMEDICINE (IRB BARCELONA)



IRB Barcelona is a world-class research centre devoted to understanding fundamental questions about human health and disease. It was founded in October 2005 by the Government of Catalonia (Generalitat de Catalunya) and the University of Barcelona (UB), and is located at the Barcelona Science Park

(Parc Científic de Barcelona). IRB Barcelona forms part of the Barcelona Institute of Science and Technology.

The Institute's missions include conducting multidisciplinary research of excellence at the unique interface between biology, chemistry and medicine, providing high-level training in the biomedical sciences to staff, students and visitors, driving innovation through active technology transfer to the benefit of society, and actively participating in an open dialogue with the public through a series of engagement and education activities.

Exceptional scientific results deserve to be transferred to society. With this in mind, IRB Barcelona has devised a proactive strategy to ensure that the discoveries made in its labs are developed into products and technologies that serve the scientific and healthcare communities, as well as society at large.

Advised by an international Business Advisory Board, specialists from the Innovation Department work shoulder to shoulder with our researchers to identify results with commercial potential and to protect, develop and commercialize them, with the aim to establish strategic public-private sector collaborations, licensing agreements, and spin-off companies.

JOHNS HOPKINS UNIVERSITY & MEDICINE

JOHNS HOPKINS

UNIVERSITY & MEDICINE

Johns Hopkins Technology Ventures (JHTV) is the intellectual property administration center of The Johns Hopkins University. In addition to serving as the licensing, patent and technology commercialization office for Johns Hopkins researchers and inventors, JHTV also supports the growth of startup companies in and around the university and is an active liaison to parties interested in leveraging university research or materials for academic or corporate endeavors.

JHTV aims to maximize the impact of The Johns Hopkins University's research excellence by facilitating the translation and commercialization of discoveries into accessible technologies, products and services that benefit society.

The JHTV website is: ventures.jhu.edu and can provide more details.

MEDICINES DISCOVERY CATAPULT



The Medicines Discovery Catapult is a national centre of applied Research and Development expertise, uniquely designed to promote and support innovative, fast-to-patient drug discovery in the UK through collaborative projects.

It is one of a network of elite, not-for-profit technology and innovation centres established by Innovate UK as a long-term investment in the UK's economy. The Medicines Discovery Catapult will work with industry, academic teams, technology experts, charities, regulators and others.

We provide unique scientific capabilities and act as a gateway to specialist facilities, technology and expertise within the UK, supporting SMEs to drive the development of new approaches for the discovery and early development of new medicines. Helping to transform ideas into commercial products and services for the wider health and wealth of the country.

By developing and validating new ways of discovering new medicines, and promoting key talent and expertise across sectors, it can help the UK maintain its heritage position as a global leader in this key industry.

PETER MACCALLUM CANCER CENTRE



Peter MacCallum Cancer Centre is Australia's only public hospital solely dedicated to caring for people affected by cancer and is one of the world's leading cancer research, education and treatment centres. We have over 2,500 staff, including more than 580 laboratory and clinical researchers. We aim to lead a new era of cancer prevention, care and discovery, supported by state-of-the-art facilities at our new home within the Victorian Comprehensive Cancer Centre building.

The Peter MacCallum Cancer Centre houses the largest group of laboratory-based cancer researchers in Australia working in close collaboration with multi-disciplinary teams comprising medical, surgical and radiation oncologists, nurses, radiation therapists and allied health professionals. We offer industry a range of opportunities for collaborative research and development across the spectrum from discovery through to clinical trials. Our laboratory scientists offer pre-clinical drug development expertise, with access to sophisticated animal models of cancer, cutting edge genomic facilities and a range of human tissue banks. Many of our laboratories have also pioneered new technologies in-house that are open to licensing and further development.

65+ years after our establishment, this sense of purpose and commitment to making life better for people affected by cancer continues at our centre today.

SAMSUNG GENOME INSTITUTE



Personal genome information is essential for patient care in a precision medicine clinic. The Samsung Genome Institute (SGI) is mainly working on cancer genomics to understand tumor heterogeneity and microenvironment. CancerSCAN is a diagnostic service for precision cancer medicine with comprehensive annotation on any variant in patients. We provide information about the treatment response to each variant in certain tumor types in the Samsung Medical Center (SMC). CancerSCAN analyzes 377 cancer-related genes for SNV, Indel and CNV and also 661 genes for gene fusions and immune profiling. Until now, we have analyzed more than 10,000 cases, which is also linked to a patient's clinical information through a clinical data warehouse in SMC (Nature Communications, 2017). Based on frequent somatic mutation in SMC patients, we designed a focused NGS panel for circulating tumor DNA liquid biopsy (Genome Biology, 2017). We have designed cancer type-specific panels to maximize the detection sensitivity for tumor monitoring in clinical trials in SMC. Single cell genome analysis provides invaluable information about the tumor microenvironment in patients.

We found cell-type markers for immuno-therapy in lung, colon and breast cancer (Nature Communications, 2017; Nature Genetics, 2017). We are also working on undiagnosed disease in the neonatal intensive care unit to uncover pathogenic mutations in sick babies. The clinical sequencing lab operates four Illumina sequencers and a Oxford Nanopore with a CAP-accredited pathology lab. The bioinformatics lab provides an analysis pipeline, and also runs projects on cancer genomics. We are now interested in the utility of clinic-genomic data for the discovery for drug targets.

SYLVESTER COMPREHENSIVE CANCER CENTER, UNIVERSITY OF MIAMI HEALTH SYSTEM



Since its inception as a dedicated, comprehensive cancer center, then significantly supported by a naming gift from the Harcourt M. and Virginia W. Sylvester Foundation, Sylvester Comprehensive Cancer Center (UM/Sylvester) has been the cancer brand for the University of Miami Leonard M. Miller School of Medicine. As the only university-based cancer center in South Florida, Sylvester has transformed cancer research and treatment in South Florida and beyond.

We seek to reduce the human burden from cancer and other serious illnesses through research, education, prevention, and the delivery of quality patient care.

- Sylvester will become a fully integrated program of patient care, education, and research with an international reputation for excellence.
- Sylvester will provide new hope for cancer patients in our extended community, which includes South Florida, the southeastern United States, the Caribbean, and South America.
- Sylvester will promote efficient, community-responsive health care, and generate resources to sustain and enhance innovative cancer programs.

UNIVERSITY OF PENNSYLVANIA: PENN CENTER FOR INNOVATION



As the nation's first medical school and home to the first teaching hospital, the Perelman School of Medicine (Penn Medicine) has a long tradition of academic excellence and scientific discovery. Building on this tradition, our innovative, interdisciplinary research programs continue today to pave the way for a future of new paradigms in cutting-edge science.

As an internationally renowned community of scientists and physicians, we are dedicated to both advancing knowledge and fostering a culture of excellence in training the next generation of scientific leaders. Our faculty are at the forefront of the biomedical revolution, and we are committed to sustaining a vibrant intellectual environment, with the ultimate goal of translating ground-breaking discoveries into medical therapies that will eradicate disease and improve health care around the world. The Penn Centre for Innovation (PCI: www.pci.upenn.edu) helps to translate Penn discoveries and ideas into new products and businesses for the benefit of society by facilitating connections with the private sector. Whether the end result is a technology license, an R&D alliance, the formation of a new venture, or an integrated combination of these activities, PCI serves as a dedicated one stop shop for commercial partnering with Penn.

YONSEI UNIVERSITY COLLEGE OF MEDICINE



The history of the Yonsei University College of Medicine starts from the opening of "Kwanghyewon" in 1885. Kwanghyewon was established to provide western-style medical treatment to the people of Chosun (Korea's former name) suffering from disease, as well as to serve as a teaching facility for its youth to learn western medicine and sanitary science. Then in 1886, the Chejungwon Medical School was established and formalized medical education began. As Korea's first institution of western medicine, our College of Medicine has been a leader in medicine here for the past 120 years.

In order to create a leading medical college, we are striving to provide an environment where researchers can passionately achieve their greatest potential. In addition, to further develop our education and research potential, we will expand the college's essential support functions, as well as distribute and apply resources in the most efficient manner.

Ultimately, it is our goal to increase the level of medical education and services in order to become a hub medical institution in the world. We will do this by identifying the most capable individuals at our institution, supporting research and continuing our efforts to lead the way in the latest methods in clinical treatment.

POSTER ABSTRACTS

See poster number listing on p86

Domainex Successfu — from vi This overvi discovery of to virtual so optimisatio

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RAY BOFFEY

Successful academic drug discovery collaborations — from validated target to candidate

This overview of Domainex's successes with academic drug discovery collaborations will showcase our approaches to virtual screening, hit finding, hit-to-lead and lead optimisation. The poster will describe how results achieved using our unique technologies and integrated solution led to successful funding applications, enabling further research that delivered drug candidates which have been outlicensed to pharma.

Domainex is an integrated drug discovery CRO, with a reputation for speed and innovation, that can offer assistance in medicinal chemistry, molecular modelling, protein science, protein crystallography, assay development and screening.

Built on an exceptional track record of drug candidate delivery, it has a world-class discovery team with an unrivalled track record of an average of one drug candidate delivered every year.

LUIGI ALOIA

Wellcome Trust—Cancer Research UK Gurdon Institute, Dept of Physiology, Development and Neuroscience, Wellcome Trust—Medical Research Council Stem Cell Institute, University of Cambridge

Epigenetic remodelling licences adult cholangiocytes for organoid formation and liver regeneration

Upon severe or chronic liver injury, adult cholangiocytes contribute to regeneration by restoring both liver epithelial cell types, hepatocytes and cholangiocytes (or ductal cells). Recently self-renewing organoid cultures have been

established enabling long-term clonal expansion of mature cholangiocytes isolated from primary adult liver tissue. However, the molecular mechanisms by which mature cholangiocytes initiate organoid cultures and regenerate the tissue upon damage remain unknown.

Here we describe that non-proliferative cholangiocytes undergo epigenetic remodelling mediated, at least in part, by TET1, during formation of liver organoids and upon tissue damage *in vivo*.TET1 is a member of the TET1/2/3 family of methylcytosine dioxygenases oxidizing the repressive DNA mark 5-methylcytosine (5mC) to 5-hydroxymethylcytosine (5hmC), which has been associated with gene activation. *In vitro*, TET1 promotes cholangiocyte de-differentiation to a progenitor state by regulating proliferation and stem-cell genes. *In vivo*, TET1 is required for cholangiocyte expansion and cholangiocytemediated hepatocyte regeneration upon liver injury. Moreover, decreased TET1 levels *in vivo* induce liver fibrosis upon chronic damage.

Altogether, we demonstrate that adult mature cholangiocytes undergo transcriptional and epigenetic changes enabling them to initiate organoids and regenerate the liver after tissue damage induced by a toxic diet.

SHAO-TUAN CHEN

Dept of Engineering, University of Cambridge

Device physics modeling of microfluidic ion pumps

Following recent advances of microfluidic ion pumps (μ FIPs), it has been demonstrated that drugs can be delivered to targeted cells with temporal and spatial precision with an applied electric field. In the μ FIP, charged drug molecules are electrophoretically pumped from the microfluidic reservoir through an ion exchange membrane, where the membrane can selectively allow only the drug of interest to be delivered while preventing undesirable passive diffusion of drugs when no applied electric field is

present. As we continue to improve the design of $\mu FIPs$, there is an urgent need for deeper understanding of the physics of such devices.

Here we report a finite-element based model for μ FIP platforms. The device physics of μ FIP are described by governing equations for both the ion concentration and the charge carrier transport when external electric potential is applied. We investigate device parameters including fixed charge concentration in the ion exchange membrane, initial drug concentration and diffusion coefficient of the transported drugs by constructing an ionically/electronically coupled computational model.

The computational model allows us to have clear insights of the ionic and electronic transport phenomena across the μ FIPs, further enabling us to design next-generation μ FIP platforms and push forward the development of targeted drug delivery treatments.

GILLIAN LIVOCK

Definiens

Generating insights from the tumor microenvironment using tissue phenomics to drive cancer immunotherapy

Immunotherapeutic approaches have revolutionized cancer therapy over the last few years, thereby increasing the clinical benefits to responders. However, response rates for many indications are still limited. Although genetic conditions such as mutational status might show increasing relevance for immune therapy stratification, it has become evident that the specific composition of an individual's immune cell populations in space and time, as well as their complex interaction with the neoplastic fraction, is decisive for therapy performance.

Therefore, a comprehensive understanding of tumor heterogeneity and immune contexture is a key determinant

for developing and optimizing therapeutic approaches, identifying predictive signatures, and selecting the most adequate treatment option for a given patient. Definiens Artificial Intelligence-driven approach is a methodology to gain mechanistic insights into the tumor microenvironment. This integrates a continuum of procedures, and this process extracts biological structures from virtual histology slides at different hierarchical scales, from cellular and subcellular entities to higher-order structures, allowing a systematic quest for relevant phenes.

Readouts from virtual slides are mined for local expression profiles; this spatial data aggregation detects categories of local environments, which are subsequently submitted to an interactive pattern analysis. Correlation to clinical, genomic or other -omics data helps identify relevant cohort subpopulations.

SARANTIS CHLAMYDAS

Active Motif

Novel high throughput tools for detecting age associated epigenetic changes in liquid biopsies

Aging-associated epigenetic changes such as global DNA hypomethylation, loss of histones, and alterations in specific histone marks, have been described in humans and other organisms, and likely contribute to aging-associated cellular dysfunction. Liquid biopsies show promise for biomarker identification and treatment evaluation as clinical researchers use cfDNA to assess risk, disease progression, and treatment strategies prospectively. Here, we highlight Active Motif's high-throughput approaches to detect epigenetic alterations in human serum samples from healthy young and old individuals.

Studies have shown that methylation levels of long interspersed nucleotide element I (LINE-I) repeats serve as reliable proxy for assessing global DNA methylation. We demonstrate that aging-associated decreases in

DNA methylation in LINE-I repeats can be quantified in cfDNA using an ELISA-based assay to assess global DNA methylation. Differentially methylated regions are confirmed with MeDIP-Seq in a subset of samples. We also determined the levels of intact nucleosomes circulating in serum using a novel ELISA-based approach.

Next, we plan to use a histone H3 bead-based multiplex ELISA to screen relevant histone marks, to inform downstream ChIP-seq analyses. We aim to show that these tools can be used to aid in discovery and detection of biomarkers and screening patient samples using clinically relevant biopsies, as well as to inform mechanistic studies.

PAULA MACGREGOR

Dept of Biochemistry, University of Cambridge

A single dose of antibody-drug conjugate cures a stage I model of African trypanosomiasis

Here we show that antibody–drug conjugates (ADCs) can be re-purposed from cancer immunotherapeutics to anti-protozoals by changing the specificity of the immunoglobulin to target a parasite cell surface receptor.

Infections of humans and livestock with African trypanosomes are treated with drugs introduced decades ago that are not always fully effective and often have severe side effects. Here, the trypanosome haptoglobin-haemoglobin receptor (HpHbR) has been exploited as a route of uptake for an ADC that is completely effective against Trypanosoma brucei in the standard mouse model of infection, using only a single dose (0.25 mg/kg). We have strategically used toxins and conjugation chemistry that are identical to anti-cancer ADCs demonstrating the ability to piggy-back onto the huge research efforts and resources that are being invested in the development of such ADCs.

The potential for development of ADCs against a wide range of human pathogens is vast, where only epitope binding sites need vary in order to provide selectivity. This provides a far-reaching opportunity for the rapid development of novel anti-protozoals for the targeted killing of a wide range of pathogens that cause disease worldwide, especially in developing countries.

SUSANNA LOVELL

Diagenode

Epigenomics profiling services — RNA-seq, ChIPmentation and DNA methylation analysis

Epigenetics is crucial for the regulation of gene expression and has broad relevance in biological processes like development, disease and response to the environment. Epigenomics, the study of the epigenetic state of the genome, is therefore a key layer of biological systems. For more than 10 years, Diagenode has been offering innovative tools to study epigenetic marks such as histone post-translational modifications and DNA methylation. Moreover Diagenode facilitates the use of next-generation sequencing by developing advanced library preparation protocols dedicated to epigenetics analysis. Standard library preparation techniques, which are based on ligation, are long assays, with numerous steps and reduced efficiency on low input samples. To overcome this, Diagenode now presents two new ligation-free protocols for epigenomic studies: the Capture and Amplification by Tailing and Switching (CATS) for RNA-sequencing and ChIPmentation for chromatin immunoprecipitation coupled with highthroughput sequencing (ChIP-seq).

DANEL TAMS

Censo Biotechnologies

Patient derived iPSC for high grade glioma

PDI:HGG is an InnovateUK funded project to create an iPSC resource from primary high grade glioma for use in phenotypic screening. High grade glioma makes up 45.2% of

malignant primary brain and CNS tumours, typically affects patients aged 50-60 years and is currently incurable.

Glioma cell lines were isolated from primary tumour tissue at Leeds Institute of Medical Research at St James's and expanded as per published protocols. Each glioma line was reprogrammed using Yamanaka factors. Whole genome sequencing at 60x resolution of tumour tissue, isolated glioma and reprogrammed iPSCs was performed at Edinburgh Genomics. Phenotypic screening was performed on the ArrayScan VTI HTS and statistical analysis using GraphPad.

Reprogramming of glioma was achieved using a feeder-dependent system and colonies of cells were shown to express the stem cell markers SSEA3, OCT4, NANOG, SOX2 and TRA-I-60. Each iPSC-line derived from glioma was whole-genome sequenced, providing data on tumour mutations in the iPSC-line and comparison to mutations in the original tumour tissue.

Differentiation of the iPSC-lines derived from glioma to neural progenitor cells was achieved and demonstrated loss of terminal differentiation. A pilot screen of 80 compounds was completed and 8 compounds identified that statistically significantly increased terminal glioma differentiation.

HENRIETTE WILLEMS

ALBORADA Drug Discovery Institute, University of Cambridge

Phenotypic screening of the ALBORADA Institute annotated library

Phenotypic drug discovery involves screening with a functional cellular assay or a cell-based disease model, where the drug target protein is not known. This approach can present us with cellular or animal screening formats that are closer to the human disease models. However, when screening small molecules, subsequent drug development and lead optimization steps can be more challenging because of the absence of a primary target, biochemical assay, protein structure or pharmacophore

hypothesis to guide design. One approach to enabling the identification of potential targets that mediate the response observed for a phenotypic hit is to screen annotated, or chemogenomic, libraries.

This report describes our efforts to create an annotated library consisting of compounds with potent, selective activity for mammalian protein targets by mining the ChEMBL and chemical probe databases. This library of 750 compounds covering 419 primary protein targets has so far been screened in 4 phenotypic assays. Our strategies for analysing the annotations of the hits to identify protein targets that may be involved in inducing autophagy or disrupting protein aggregation will also be discussed.

MICHAEL WHITEHEAD

Dept of Clinical Neurosciences, University of Cambridge

Murine retinal transduction using novel exosomeassociated AAV2 gene therapy modalities

Gene therapy for retinal disease currently centres on the use of adeno-associated virus serotype 2 (AAV2) for the delivery of therapeutic genes into the retina. Whilst this approach has seen some significant success in the clinic, the application of the AAV2 platform in patients is limited by modest transduction efficiencies and anti-capsid immune responses following intraocular AAV2 injections. These issues limit therapeutic efficacy, pose safety/toxicity concerns and negate the opportunity for repeated gene transfer strategies.

We have developed a novel AAV2 formulation, exosome-associated AAV2 (ExoAAV2), in which AAV2 viral particles are associated with exosomal plasma membrane. Here we report that ExoAAV2 exhibits log-fold increases in transduction efficiency compared to titre-matched conventional AAV2 viral particles. We also showed that ExoAAV2 induces much lower neutralising antibody responses than high titre conventional AAV2, and

significantly reduced CD4+ and CD8+T-cell infiltration into the retina.

Overall, we have developed an exciting innovation that can achieve high transduction efficiency rates whilst limiting the immune response in the retina. Our data suggest that repeated gene transfer using ExoAAV2 will be possible, a novel finding that could have significant clinical implications and enable the delivery of multiple gene therapies into a single patient.

MYRA HOSMILLO

Dept of Pathology, University of Cambridge

Utilisation of human intestinal organoids to identify therapeutic approaches against human norovirus

Human noroviruses (HuNoV) and sapoviruses account for 20% of gastroenteritis cases worldwide. Outbreaks due to HuNoV have caused increasing socio-economic impact and significant morbidity and mortality of the immunocompromised patients including children, elderly and cancer or organ transplant recipients. Despite this large unmet need, there are no approved therapeutics for norovirus due, in part, to challenges in culturing the virus.

The establishment of an improved HuNoV organoid culture system has transformed our ability to propagate human norovirus in the laboratory. We have further used this system to characterise potential therapeutic approaches for human noroviruses in epithelial cells derived from 3D human intestinal cultures. We first evaluated innate immune regulators and demonstrated that HuNoV replication is restricted by the innate immune response. Modification of the innate immune response can impact on norovirus replication. Furthermore, we then evaluated the ability of a purine ribonucleoside analog (CMX521), identified by Chimerix, to inhibit HuNoV replication in the organoids. CMX521 was effective against HuNoV GII.3 and GII.4 in human mucosal stem cell-derived organoids. Additionally,

this compound has demonstrated pan-genotypic activity against all caliciviruses tested. Overall, utilisation of organoids facilitated a close to physiological system to directly evaluate approaches for the treatment and prevention of human norovirus infection.

KEVIN TEBURI

Genedata

Digitalization of translational research to facilitate efficient development of precision medicines

Recent studies have shown that clinical trials have a higher probability of success if subject selection is optimized. Utilizing a range of biomarkers, clinicians can select those patients most likely to benefit from a treatment, thereby significantly improving the response rate while simultaneously reducing toxicity within the patient group. Designing promising clinical trials that incorporate identification and validation of appropriate biomarkers requires integration, harmonization, and analysis of vast amounts of diverse low- and high-dimensional data, often siloed by type and source.

Using an example of the development of an immunooncology asset, we demonstrate how the enterprise software platform Genedata Profiler® breaks down data silos from clinical and pre-clinical trials to harmonize and integrate data of multiple types from distributed sources, enabling innovative approaches to analysis. The platform allows secure, controlled collaboration for multidisciplinary research teams across continents. Developed for use in the regulated clinical environment, the software maintains enhanced governance of patient and other data.

This automated approach to the exploitation of clinical, multi-omic, and digital pathology data frees up as much as 80% of investigators' time, allowing more focus on interpretation of results and implementation of solutions. Administrator-defined access controls enable self-service

analytics, allowing more team members to participate in decision-making.

ALBERTO MORENO DE LA GANDARA

PhoreMost

Phoremost: drugging the undruggable

Despite the increasing spend in drug discovery and the progress made on understanding the development and progression of debilitating diseases, the number of drug targets addressed with small molecules lags far behind. PhoreMost aims to remove these barriers to new drug development with its novel SITESEEKER® technology: a live cell, proteome-wide, phenotypic assay system that can rapidly identify unexpected druggable sites in specific disease-driving targets that can't be readily seen using conventional non-cell based analytical or genetic methods.

This technology uses Protein Interference (PROTEINi®) to identify cryptic sites across all human proteins. It differs fundamentally from other genome- or transcriptome-based target screening technologies such as CRISPR and RNAi by expressing a diverse and highly complex library of small 3-dimensional protein-fragment shapes in cells, one such peptide per cell, which interact with intracellular proteins to describe new druggable sites. This approach operates directly at the protein level, so that new druggable space can be defined as an inherent part of the target-function screening process.

PhoreMost is currently advancing novel drug discovery programmes in different areas of disease including cancer, immuno-oncology, ageing and neurodegeneration. Following a partnership model in collaboration with academia and industry, PhoreMost is building up an alternative ethical drug discovery model that brings a systematic pipeline of first-in-class drugs to market.

JANE REED

Linguamatics

Natural language processing to transform real world data for pharma decision making

In pharma and healthcare, understanding the real world impact of therapies on patients is critical. Real world evidence (RWE) can inform all phases of drug development, commercialization, and drug use in healthcare settings. RWE can shed light on real world clinical effectiveness or safety profiles of products across a broad patient community. RWE can be used to assess patient-reported outcomes, provide input for product reputation management, help with key opinion leader engagement, and more.

However, many real world data (RWD) sources, like electronic health records, patient forums, social media etc., contain unstructured text. Many of our customers are using the power of Linguamatics Natural Language Processing (NLP) platform to transform these unstructured sources of real world data into actionable structured real world evidence that can be rapidly visualized and analyzed. We will present an overview of customer success stories, to show best practise use of our NLP technology for real world understanding.

MATTHEW IVES

Abcam

Abcam strategy to support Parkinson's disease research

Parkinson's disease (PD) is the second most common neurodegenerative disorder. Despite intensive efforts, the etiology of PD remains largely unknown, and the establishment of early biomarkers of disease and the development of novel therapies remain challenging. PD is considered a complex multifactorial disease in which genetic and environmental factors are involved in the

pathology. To date, a total of 23 loci and 19 genes have been associated with PD, including SNCA, LRRK2, Parkin, PINK I, and DI-I, amongst others. To help researchers translate genetic discoveries into meaningful therapies and biomarkers, Abcam is taking several approaches: (1) Establishing a strategic partnership with The Michael J. Fox Foundation for Parkinson's Research (MIFF) to develop reagents and assays for preclinical and/or basic research studies; (2) Generating novel rabbit monoclonal antibodies (RabMAb® antibodies) against proteins related to PD, and validating them in knockout cell lines; (3) Providing researchers and partners with monoclonal antibodies and assay technologies in a format customized to their needs; (4) Promoting disease awareness by marking World Parkinson's Day through collaboration with academic experts and The Cure Parkinson's Trust. Through these avenues and the development of further collaborations and partnerships, we aim to help researchers and organizations to accelerate discoveries in basic research, diagnostics, and therapeutics for PD.

LAETITIA PELE

IBD BioResource, NIHR BioResource & Dept of Medicine, University of Cambridge

The Inflammatory Bowel Disease (IBD)
BioResource: progressing from genetics to function
and clinical translation in Crohn's disease (CD) and
ulcerative colitis (UC)

The UK IBD Genetics Consortium and the NIHR BioResource launched IBD BioResource in 2016 to expedite the clinical translation of recent genetics advances and support research in IBD. It is a national platform comprising individuals suffering from IBD with detailed genetic and phenotypic data available. The Main cohort includes individuals with established CD and UC. Both clinical and self-reported phenotype data are collected, alongside biological and DNA samples for sequencing

and genotyping. The Inception cohort recruits newly diagnosed IBD patients and provides detailed sampling unconfounded by drug treatment or effects of surgery. The IBD BioResource panel can be accessed by any investigators from science or industry for data/samples, or to recall genotype-selected participants to donate further samples or trial novel therapies. Three years in and a year earlier than anticipated, IBD BioResource has reached its initial 25,000 target and possesses an array of genetic data. To date, I2 studies have successfully applied to utilise the IBD BioResource, I I of which are currently active. We are yet to receive formal applications from the Life-Sciences Industry but are in early discussions and strongly encourage all potential industry partners.

ARWA RAIES

European Bioinformatics Institute, EMBL-EBI

Discovering novel therapeutic targets using large biomedical knowledge graphs

One of the main challenges in drug discovery is the high attrition rates late in development. Additionally, the large volume of biomedical data makes it more challenging for humans to gain useful insights. Therefore, there has been an increased interest in the application of artificial intelligence in several stages of the drug discovery pipeline starting with target identification. It has been shown that it is more likely for drugs to succeed clinically if these drugs have human genetic validation data. Hence, thorough knowledge of target and disease associations is the first and most critical step for drug discovery. Here, we present an application of machine learning to discover new therapeutic targets from large biological networks that consist of more than 28 million links between drugs, targets, diseases, and biological concepts extracted from biomedical literature. We applied graph embeddings algorithms to generate feature vectors for entities and edges, then we trained a classification model to predict new associations between

the targets and diseases. We generated and tested 4,500 models, and the best model achieved mean reciprocal rank score of 0.55, Hit@10 score of 91%, and area under curve scores of 96% using a hold out testing set.

THOMAS WILLIAMS

Experimental Medicine & Immunotherapeutics, University of Cambridge

High content high resolution confocal imaging to characterise mutations in the apelin receptor identified in patients from the 13,000 Genomes Project

The apelin receptor GPCR binds two endogenous peptide ligands, apelin and ELA, to regulate the cardiovascular system. The NIHR BioResource BRIDGE study is a prospective component of the Genomics England 100,000 Genomes Project that has performed case-control genomic analysis of ~7423 patients with rare cardiovascular diseases, identifying a number of mutations in the apelin receptor in this cohort. Here, 11 of these mutations were selected for further pharmacological assessment using high content imaging, in conjunction with binding and functional studies.

The Opera Phenix High Content Screening System was used to generate high-throughput triple fluorescence confocal images of fixed CHO-K1 cells transiently transfected with eGFP-tagged wild-type or mutant apelin receptor and stained with membrane and nuclear markers. Segmentation analyses were used to quantify fluorescence intensities of eGFP-tagged apelin receptor in the cytoplasm and membrane.

Images qualitatively demonstrated that mutation may profoundly affect the total amount, and localisation, of the apelin receptor. Quantification reconciled well with qualitative assessment and revealed that certain mutations induced significant effects on membrane expression. We report the successful use of high content imaging to empirically determine differences in expression and cell

surface distribution of the apelin receptor when naturally occurring mutations identified in the BRIDGE study are introduced.

SOPHIE ROSE

Metrion Biosciences

Metrion Biosciences: high quality ion channel drug discovery service provider

Metrion Biosciences is a UK-based Contract Research Organisation offering ion channel focused drug discovery services. Metrion combines in depth target class knowledge and high quality screening platforms and assays with experienced project managers to ensure that timelines and objectives are met. Metrion's core services include ion channel screening, cardiac safety and neurotoxicology profiling, translational and phenotypic assays and fully integrated drug discovery.

Metrion has validated screening assays against a comprehensive panel of ion channel cell lines using manual and automated patch clamp electrophysiology platforms. Cell lines can be selected from our in-house library, purchased commercially, or generated using transient or stable transfection. A case study regarding an optimised Na. I.8 assay is described.

A suite of neuroscience services is also offered, including work with native tissue such as rat DRG, hippocampal and cortical neurons. Microelectrode array (MEA) techniques allow characteristics of firing & network behaviour to be analysed.

Metrion also offers comprehensive cardiac safety profiling services against a validated panel of CiPA compliant human cardiac ion channels, *in silico*, and iPSC-derived assays.

The highly experienced interdisciplinary team can also manage fully integrated ion channel drug discovery programmes. Metrion's expertise is supported by selected

medicinal chemistry partners: AMRI, Concept Life Sciences and Assay. Works.

ROBYN MACRAE

Experimental Medicine and Immunotherapeutics, Wellcome Trust–MRC Cambridge Stem Cell Institute, University of Cambridge

Characterisation of the apelin receptor protein in human embryonic stem cell derived cardiomyocytes

Apelin receptor is expressed throughout the cardiovascular system, including in cardiomyocytes, where it promotes vasodilatation and has positive inotropic effects. Human embryonic stem cell (hESC)-derived cells can be used to investigate cellular signalling, disease pathogenesis and potential novel treatments. Our aim was to determine hESC-derived cardiomyocyte apelin receptor expression and density to ascertain potential for use as a phenotypic model for human diseases associated with apelin receptor mutations.

H9 hESCs were differentiated to beating cardiomyocytes. Saturation radioligand binding experiments were conducted and iterative curve fitting performed to determine receptor affinity and density. Immunocytochemistry was carried out using anti-apelin receptor or anti-cardiac marker antibodies.

Radioligand binding studies demonstrated receptor expression at the protein level in hESC-derived cardiomyocytes. Binding was saturable and [1251]apelin-13 bound with sub-nanomolar affinity (0.12 nM) and receptor density was 21 fmol/mg, comparable to human adult heart. Beating hESC-derived cardiomyocytes stained positive for apelin receptor, in addition to standard cardiac markers.

Apelin receptor mutations have been identified from the NIHR BioResource BRIDGE study that are associated with rare diseases. Ongoing experiments aim to pharmacologically characterise the apelinergic signalling

pathway in beating hESC-derived cardiomyocytes and we propose generating hESC-derived phenotypic models by introducing selected apelin receptor mutations via genetic editing.

OLIVER RAUSCH

STORM Therapeutics

Targeting RNA modifying enzymes for the treatment of cancer

Recent progress in the field of epitranscriptomics demonstrates that post-transcriptional modification is a key mechanism to control the processing, longevity and function of RNA. Several RNA modifications and their corresponding RNA modifying enzymes (RMEs) have been implicated in disease, suggesting the field represents an as yet unexplored novel opportunity for therapeutic intervention. STORM Therapeutics have established a pipeline of drug discovery programmes targeting RMEs for the treatment of cancer. We will discuss the key approaches and technologies we have developed to support the optimisation of our advanced lead molecules.

AMY ROCHFORD

Dept of Engineering, University of Cambridge,

Combining implantable electrodes and stem cellderived cell transplantation towards functional neurological restoration

Peripheral nerve injuries result in a disconnection in the nervous system communication and a consequent loss in neurological function. Currently, there are limited treatments for these conditions. Neuroprosthetics and cell transplantation are promising approaches to restore lost neurological function: the former aims to bypass the site of injury, connecting directly one part of the nervous system to another (or a prosthetic limb); while the latter

aims to repair the injury site. To date, both strategies have shown limited efficacy and lifetime due to several challenges. However, a combinational approach of implantable electronics and stem cell-derived cells for functional neurological restoration could address these issues. Attributes to this biohybrid implant are: an ability to host and interact with stem-cell derived cells; promotion of organised functional cellular integration with living tissue; and restoration of lost function.

Here we report the new design of a peripheral nerve multielectrode neural interface device, together with early *in vitro* culture studies. Our device contains gold electrodes, coated with a conducting polymer (PEDOT:PSS). The device hosts iPSC derived myocytes on the electrically active surface, allowing their efficient electrical stimulation and recording. We tested the proliferation and differentiation on our neural interface device and tested their morphological and electrophysiological behaviour.

TKALKAN

Elbis Biomed

Programming cell identity: enabling the next generation of human cell models from pluripotent stem cells

Challenges remain for utilizing induced pluripotent stem cell (hiPSC) lines in regenerative medicine and the pharmaceutical industry. Methods that enable faithful, homogeneous and scalable differentiation of hiPSCs to mature cell types are needed to replace current cell lines with limited functionality and biological significance. Coupled with modern genetic tools and the capacity of hiPSCs to reproduce human genetic diversity, hiPSC-derived cells present a pivotal tool for disease modelling and drug discovery.

Based on the principle that transcription factors (TFs) control cell identity, programming with TFs offer a

disruptive strategy for cell differentiation, with a growing number of programmed cell types described. We have developed an optimized inducible system (OPTi-OX) that enables homogeneous and tightly controlled expression of programming TFs in hiPSCs. This technology provides unprecedented scalability and purity for generating mature cell types, as demonstrated for glutamatergic cortical neurons, skeletal myocytes and megakaryocytes. While our programmed glutamatergic neurons are already used for drug screening and genome-wide genetic screens, our innovative high-throughput discovery platform will reveal novel master drivers of cell identity in order to rapidly expand our cell type portfolio. We aspire to provide state-of-the art, mature human cells that will improve basic research, drug discovery processes and hiPSC-based therapeutics.

ANASTASIOS POLYRAVAS

Dept of Engineering, University of Cambridge

Organic electrochemical transistors for neural interfaces

Understanding the operation of the human brain has always been a great challenge for the medical community. Despite the progress made so far, our knowledge on the different functions of the brain has been severely limited by the complexity of the nervous system and the quality of the information derived from recording devices. A device that holds great potential for recording high quality electrophysiology signals is the organic electrochemical transistor (OECT). OECTs can be fabricated from biocompatible materials and have been shown to exhibit a much higher signal-to-noise-ratio (SNR) compared to electrodes. Their unique properties can pave the way for enhanced performance neural interfaces while minimising the invasiveness of the recording method. In this study, we investigate how bias conditions and geometry affect the noise characteristics of OECTs, with the greater

aim of further improving their recording capabilities. We find that the overlap between the gold contacts and the semiconducting polymer film can be used to effectively tune the frequency response without affecting the transconductance and the noise level of our devices. We also demonstrate that OECTs with a thicker polymer film show a much higher SNR compared to their thinner counterparts.

WOOCHANG HWANG

Milner Therapeutics Institute, University of Cambridge

Artificial Intelligence for identifying novel therapeutic targets, biomarkers and drug repositioning opportunities

The challenges in drug discovery, including high attrition rates in the late development stage, are well documented. This has led to an increased interest and need for applying machine learning and artificial intelligence across the drug discovery pipeline from target identification to chemical lead selection and optimisation. It has also been demonstrated that drugs with human genetic validation data are more likely to succeed in the clinic. To address this, it is essential to unravel genetic networks to identify new or better targets for which the underlying mechanism is clear. Despite the significant advances in next-generation sequencing technologies and evolving databases of patient cohorts, the sheer complexity of these datasets makes their integration and interrogation a daunting task. Through the development and application of cutting-edge computational approaches, such as artificial intelligence, machine learning and mathematical modelling, to pharmacogenomics and drug discovery, we identify novel therapeutic targets, biomarkers and drug repositioning opportunities. We have developed a computational platform that performs (I) systematic integration and harmonisation of biomedical big data (2) a multi-omic disease association study and (3) network theory-based

analysis of targetable pathways which have significant potential to provide unprecedented insights into vital biological processes and the control hubs that underpin disease.

ALEJAND BRUNA

Cancer Research UK Cambridge Institute, University of Cambridge

Towards the derivation of a preclinical platform predictive of patient's drug responses

Breast cancer is a group of different diseases, displaying both inter- and intra-tumour heterogeneity. Our group has developed one of the largest and most comprehensive molecular-annotated biobanks of breast cancer patient-derived tumour xenograft (PDTX) models, which retain most of the originating cancer's heterogeneity. PDTXs, and their ex vivo counterpart PDTCs (or short-term cultures of PDTX cells) also capture the diversity of inter-patient drug responses seen in the clinic. We aim to expand our highly molecularly annotated living biobank of breast cancer samples and to improve our understanding of the molecular features that contribute to their phenotypes. A better understanding on cancer vulnerabilities and biomarkers of drug response will come from the integration of data from different molecular universes.

We further aim to explore the use of PDTXs as mouse avatars alongside ongoing clinical trials in the breast cancer neo-adjuvant setting, to leverage the development of a predictive platform of evolutionary trajectories of drug responses with high clinical predictive power paving the way towards a platform to help guide personalised clinical decision making.

In parallel, we aim to investigate whether mouse specific evolutionary pressures impact on drug responses by comparing molecular changes on match patient/PDTX longitudinal samples. As PDTXs are improved preclinical

models, we speculate that this resource will accelerate cancer research.

MING ZENG

Dept of Chemical Engineering and Biotechnology, University of Cambridge

Using computational biology to identify novel therapeutic targets for ion channel-related disease

Two-pore potassium (K2P) ion channels are expressed across neurons, muscle cells and endocrine cells. Studies showed that the modulation of these channels are related to a variety of disorders. The problem is, scientists have yet to identify any truly predictive methods that can be applied to any chemotype to increase their selectivity against a particular channel despite the critical role they play in the physiological function of cells. In this poster, we will I) explore how using gene expression profiling data from publicly available resources could narrow down top diseases associated with K2P channels, 2) construct a protein-protein interaction network between K2P genes with a list of genes known to be associated with potentially K2P-related diseases 3) identify key genes in the protein-protein interaction network and construct a more condensed network connecting K2P genes with the key genes 4) carry out pathway analysis to understand potential side effects that could arise from targeting K2P genes and 5) propose chemical structures potentially targeting K2P genes. These analyses provide a comprehensive understanding of target-disease association and testable hypotheses for LifeArc to probe deeper into K2P-related disease leading to the development of drug discovery pipelines effectively targeting these ion channels.

GEOFFROY DUBOURG-FELONNEAU

Cambridge Cancer Genomics

A framework for implementing machine learning on omics data

The potential benefits of applying machine learning methods to -omics data are becoming increasingly apparent, especially in clinical settings. However, the unique characteristics of these data are not always well suited to machine learning techniques. These data are often generated across different technologies in different labs, and frequently with high dimensionality. We present a framework for combining -omics data sets, and for handling high dimensional data, making -omics research more accessible to machine learning applications. We demonstrate the success of this framework through integration and analysis of multi-analyte data for a set of 3,533 breast cancers. We then use this data-set to predict breast cancer patient survival for individuals at risk of an impending event, with higher accuracy and lower variance than methods trained on individual data-sets. We hope that our pipelines for data-set generation and transformation will open up -omics data to machine learning researchers. We have made these freely available for noncommercial use at www.ccg.ai.

GEORGIA TSAGKOGEORGA

Milner Therapeutics Institute, University of Cambridge & STORM Therapeutics

Phylogenetic reconstruction of human RNA methyltransferases

RNA methyltransferases (RNMTs) play an important role in functional regulation of RNAs and have thus attracted an increasing interest as potential drug targets. The overall structure of RNMTs is conserved, binding the S-adenosylmethionine cofactor (SAM) as a methyl group donor to the substrate. Although SAM-binding sites are

localised at the same position of the fold, the chemistry of the SAM-binding interaction shows an important variation across RNMTs.

Here we aimed to infer the evolutionary relationships of RNMTs in our genome. We collected and collated structural and sequence information for human RNMTs to create three datasets for phylogenetic reconstruction: (i) a structural alignment of the conserved SAM-binding motifs; (ii) a multiple sequence alignment based on the full RNMT protein sequences; and (iii) a combined structural and sequence-based alignment of the binding domain across enzymes. We used Maximum Likelihood reconstruction to build phylogenies and assessed statistical support of each node using rapid bootstrapping.

Phylogenetic analyses yielded different tree topologies depending on the dataset used. All phylogenetic trees showed minimal statistical support for the interrelationships of RNMTs, which most likely stems from their extreme evolutionary divergence. Our results unequivocally support that RNMTs are highly variable in both structure and sequence, despite their conserved SAM-binding domain.

VIKRAM SUNDAR

Dept of Chemistry, University of Cambridge

Machine learning for predicting active ligands for previously unseen targets

Identifying candidate drugs that bind tightly to a given protein target is a crucial step in drug discovery. Experimental screens for this are costly and prone to failure, but the large quantity of screening data available has encouraged the development of machine learning algorithms for this problem. Algorithms to predict active molecules for a single protein target given prior data about that particular target (i.e. single protein models) have proven successful, but algorithms that make predictions

about many protein targets and try to generalize to previously unseen targets (i.e. drug/target interaction (DTI) models) have had less success. We build on the success of single protein models to improve the performance of DTI models. Specifically, we use single protein models to infer information about the interactions between known targets and all drugs, and then generalize using DTI models to unseen targets. Our methods are a significant improvement over the current state-of-the-art, achieving accuracies of greater than 0.9. Our work suggests a paradigm shift where we focus on initially making high-quality predictions for a single protein and then generalize to other unseen proteins. It is also a significant step towards reducing the reliance on screening in drug discovery.

SEAN TYACKE

Pelago Bioscience

The cellular thermal shift assay — target engagement measures for unbiased deconvolution of phenotypic assay hits

The Cellular thermal shift assay (CETSA) is a label-free method for measuring target engagement of compounds in intact cells. The method has proven to be a very valuable tool in the field of targeted drug discovery. Our mass spectrometry-based CETSA offers unbiased proteome wide analysis of a compound's effect on thousands of proteins.

Since drug treatment affects the primary cellular target(s) and have downstream pathway effects, the MS format makes it possible to understand the mode of action for a particular drug by following the global changes in protein stabilities that compound treatment causes. Moreover, comparing results from different cell matrices, various doses and incubation lengths makes it possible to understand key parameters such as cellular uptake, target specificity and importantly also if any unwanted targets are affected by the treatment and present a liability.

Here Pelago Bioscience present several examples showing how CETSA MS has enabled identification of primary hits and novel biomarkers as well as confirmed results from alternative phenotypic deconvolution programs. The results suggest that CETSA MS will allow both treatment response and liability monitoring on top of primary target engagement measures.

SHUYU LIU

Wellcome Trust—Cancer Research UK Gurdon Institute, Department of Pathology, Wellcome Trust—MRC Stem Cell Institute, University of Cambridge

Modeling branching morphogenesis with human embryonic lung organoids

Accumulating evidence shows that human embryonic lung development differs from mouse in molecular signaling. However, the details of the molecular regulation, and underlying cellular mechanisms, that occur in humans remain to be determined. Multipotent epithelial progenitor cells can be expanded from human embryonic lungs as organoids in a dish. These cells can be used to investigate many aspects of lung development that are specific to humans. For example, when grown in a chemically-defined medium the organoids remain as self-renewing progenitor cells. However, these progenitor cells retain the capacity to change cell shape and the organoids can undergo budding in vitro, which is closely related to branching morphogenesis in vivo. Human embryonic lungs undergo branching morphogenesis during the pseudoglandular stage of development to form the respiratory tree. Therefore, we are able to use the in vitro organoid-budding system to identify cytokines, signaling pathways and their downstream transcription factors that potentially regulate branching. State-of-art imaging and analysis, plus cutting-edge genetic engineering tools, enables presentation and interpretation of organoid budding. To date, we have identified EGF and several FGF family ligands as potent factors inducing lung

organoid budding and are developing ways to improve the morphological quantification of organoid budding and tracking cell shape changes.

DOUGLAS ROSS-THRIEPLAND

AstraZeneca

Launching the new Joint AstraZeneca and Cancer Research UK Functional Genomics Centre at the Milner Therapeutics Institute

The new Joint AstraZeneca and Cancer Research UK Functional Genomics Centre has been established to accelerate the development of new treatments for cancer. Opening in July this year it will become a world-leading centre of expertise in genetic screens, cancer models, CRISPR vector design and computational approaches to big data. All with the common goal of identifying novel targets and resistance mechanism to create new cancer medicines.

Located within the Milner Therapeutics Institute, the Functional Genomics Centre will be comprised of 16 cancer and computational scientists that will at its core, focus on developing and delivering pooled CRISPR screening to both the AstraZeneca portfolio and the Cancer Research UK network.

The synergistic combination of CRUK's deep expertise in cancer biology across an extensive network of scientists with AstraZeneca's leading position in new oncology medicines and strong background in functional genomics will together help to discover the right medicine and deliver it to the right patients to help beat cancer.

DAVID WALTER

Therapeutic Discovery Laboratories, Cancer Research UK

Functional Genomics Screening — how do you get involved?

The new Joint AstraZeneca and Cancer Research UK Functional Genomics Centre (FGC) is launching this July. It will both develop and deliver genetic screening (e.g. pooled CRISPR) across the AstraZeneca portfolio and CRUK's extensive academic and industrial network. Here we introduce some of the questions and challenges around genetic screening and present how we believe the FGC will lead the development and improvement of CRISPR screening tools and what underpins a successful and valuable screen. Also we describe some of the ways the CRUK academic network can bring their research into the centre:

- 1. What are leads to a successful pooled CRISPR screen?
- 2. You've a gene hit list, what do you do next?
- 3. What the FGC will do, and what it can't?
- 4. What are the next generation of genetic screens we want to develop?
- 5. How do you apply to have a project screened at the FGC?
- 6. What is the proposal process?

By addressing these basic questions, we aim to help researchers design the best possible CRISPR screens that will help answer deep biological questions underpinning their research.

IAN GROVES & DAVID TOUGH

Dept of Medicine, University of Cambridge GSK

Targeting latent HCMV infection via epigenetic intervention towards reducing virus reactivation in the transplant setting

Primary infection with HCMV rarely causes disease in immunocompetent individuals, and results in latent infection whereby the virus avoids immunosurveillance through epigenetic silencing of viral lytic gene expression. However, virus reactivation in the immunocompromised, such as transplant patients, can lead to severe morbidity/mortality. Whilst anti-virals do exist for HCMV, they only target lytically infected cells, suffer from poor bioavailability and have profound side effects. One novel strategy to decrease viral disease in the clinical transplant setting is to remove the ability of HCMV to reactivate by purging the transplant donor and/or recipient of latently infected cells. To this end, we have shown that inhibitors of histone deacetylases (HDACi) are able to relieve chromatin-regulated repression of the major immediate early promoter (MIEP). This induces transient expression of virus lytic antigens such that latently infected cells now become visible to preexisting HCMV-specific cytotoxic T cells (CTLs) in the carrier; this 'shock and kill' approach efficiently eliminates latently infected cells. We now show that a range of epigenetic modifying enzyme inhibitors are able to increase the proportion of latently infected cells that reactivate lytic gene expression. These include newer generation panspecific HDACi, and also myeloid-selective compounds, as well as bromodomain and extra-terminal domain inhibitors (BETi). The latter, by targeting bromodomain containing proteins BRD2/3/4, are able to not just induce high levels of virus IE gene expression but also inhibit HCMV genome replication at later time points, thereby limiting the ability of the virus to produce infectious progeny. Investigations are ongoing to assess any untoward consequences of these

treatments on T cell effector function. We believe that novel compounds employed with this strategy could reduce the latently infected cell reservoir in both an HCMV-positive donor and/or recipient prior to transplantation and decrease the chances of patients succumbing to reactivation event-related disease during clinical treatment.

EMMA KOPPE

GSK

The GSK Immunology Network: accelerating industry-academic collaboration

GSK launched the Immunology Network in 2015 as a novel industry-academic initiative to fully integrate immunology expertise between GSK and academia scientists. The mission is to deliver the best science and discover the next breakthroughs in immunology that can be developed into therapies for multiple diseases. Two key features of the network are important: one is the Immunology Catalyst, which hosts senior immunologists on sabbatical in GSK labs for up to 3 years where they and their postdocs collaborate with GSK scientists, share ideas, have exposure to drug discovery, and can access our tools and technology to pursue novel research; the other feature is an External Immunology Board comprising world class immunologists who participated in the design of the collaboration and who engage with GSK scientists and support the academics on sabbatical. Successes to date include high profile papers, unexpected opportunities to advance new therapies, the consideration of alternative applications for emerging therapies and to contribute to the formation of a new company, Sitryx. We will share further details around the collaboration model, our success and ideas for the future as GSK continues to invest in immunology and genetics for the discovery of new medicines.

YUTAKA YOSHIDA

Shionogi

Introduction of Shionogi's R&D and BD

Shionogi is a drug discovery-based pharmaceutical company making diligent efforts in the research and development of new drugs that are needed by patients around the world.

Pipeline. We have developed so-called blockbuster drugs such as Crestor (cholesterol lowering drug), Triumeq (anti-HIV drug), Cymbalta (anti-Depression drug) through the collaboration with Astra Zeneca, GSK/Viiv, and Eli Lilly. Very recently, we have launched the new anti-Influenza drug, Xofluza through partnering with Roche.

Development. At the moment, we have eight high-priority projects. In clinical stage, projects for Infectious diseases such as Tuberculosis, and projects for Pain/CNS such as Neuropathic pain and Depression, are ongoing. As for Projects in the pre-clinical stage, novel HIV drug and Nucleic acid adjuvant are ongoing.

Research. Our focus research areas are Infectious diseases and Pain/CNS disorders. Infectious diseases include three topics. I: three major infectious diseases such as HIV, Tuberculosis and Malaria, 2: Hard to treat bacteria such as Antimicrobial resistance and Fungus, 3: Prevention such as vaccine. Pain/CNS disorders include 2 topics. I: CNS disorders such as ADHD, Depression and Cognitive impairment, 2: Pain relief such as Cancer pain and Chronic pain.

Business development. We are also generating new opportunities for drug discovery, especially in the research areas mentioned above, through strategic investment. We are also challenging the new modalities for Regenerative medicine, Digital therapeutics and Al diagnostics. Shionogi would be very happy to discuss and share the ideas for the chance of new collaborations and partnering.

BIRGIT NIMMERVOLL

Cancer Research UK Cambridge Institute

Get to know the CRUK Cambridge Centre

The CRUK Major Centre at Cambridge University (CRUK CC) unites more than 700 laboratory and healthcare professionals around a common mission to end death and disease caused by cancer, through research, treatment and education. Our vision is to be the world-leader in the development of ways to detect, monitor and cure cancer. As a CRUK Major Centre we serve as a national and international resource for patients with cancer and their families; researchers and health care providers; and cancer professionals in training.

The Centre is focused on four strategic objectives:

- Conducting impactful interdisciplinary cancer research
- Adopting a proactive approach to cancer
- Developing the cancer leaders of tomorrow
- Partnering with the public

To achieve these strategic objectives, we have created a new organisational and governance structure for our Centre. Twelve Programmes pursue disease (n=8) or discipline-focused (n=4) cancer research, each comprising a critical mass of laboratory and clinic-based researchers.

SPOTLIGHT ON THE BABRAHAM INSTITUTE

ABRAHAM INSTITUTE

DAVID TURNER

Babraham Institute

Discovering novel roles for RNA binding proteins within the immune system by employing targeted CRISPR screens

Post-transcriptional regulation is essential for immune system function. RNA binding proteins expand proteome diversity and regulate the rate of gene expression by mediating differential mRNA stability and transcript translational efficiency. In the Turner lab, I have built comprehensive human and mouse sgRNA libraries for CRISPR/Cas9 knockout of messenger-RNA binding proteins. These sgRNA libraries enable high-throughput characterisation of mRBPs within many immunological contexts such as the lymphocyte signalling pathways governing proliferation, activation, and differentiation. Using in vitro cultures of primary mouse cells, I have screened for mRBP involvement with B cell differentiation towards plasmablasts, and for mRBPs that regulate cytokine expression in CD8+T cells. Furthermore, within human cell lines and primary B cells isolated from tonsils, I have screened for mRBP synergy with oncogenic stresses, as well as roles with conveying resistance or sensitivity to oxidative stress.

PAMELA LOCHHEAD

Babraham Institute

Paradoxical activation of the protein kinasetranscription factor ERK5 by ERK5 kinase inhibitors

The dual protein kinase-transcription factor, ERK5, is linked to poor prognosis in cancer and promotes acute cellular and systemic inflammation. Consequently, ERK5 is an emerging drug target, and small molecule ERK5 kinase inhibitors have been developed. A setback to these inhibitor programmes is that selective ERK5 inhibitors fail

to recapitulate ERK5 genetic ablation phenotypes. Here we show that ERK5 kinase inhibitors cause paradoxical activation of ERK5 transcriptional activity mediated through its unique C-terminal transcriptional activation domain. Using the ERK5 kinase inhibitor, Compound 26 (ERK5-IN-I) as a paradigm, we have developed drugresistant, kinase-active mutants of ERK5. With these mutants, we show that induction of ERK5 transcriptional activity requires direct binding of the inhibitor to the kinase domain. This in turn promotes nuclear translocation of ERK5 and stimulates gene transcription. This work shows that both the ERK5 kinase and transcriptional activation domains must be considered when assessing the effectiveness of anti-ERK5 therapeutics.

SIMON COOK

Babraham Institute

MEK I/2 inhibitor withdrawal reverses acquired resistance driven by BRAF^{V600E} amplification whereas KRAS^{G13D} amplification promotes EMT-chemoresistance

Acquired resistance to MEK I/2 inhibitors (MEKi) arises through amplification of BRAFV600E or KRASGI3D to reinstate ERK I/2 signalling. Here we show that BRAFV600E amplification and MEKi resistance are reversible following drug withdrawal. Cells with BRAFV600E amplification are addicted to MEKi to maintain a precise level of ERK I/2 signalling that is optimal for cell proliferation and survival, and tumour growth *in vivo*. Robust ERK I/2 activation following MEKi withdrawal drives a p57KIP2-dependent G1 cell cycle arrest and senescence or expression of NOXA and cell death, selecting against those cells with amplified BRAFV600E.

p57KIP2 expression is required for loss of BRAF^{V600E} amplification and reversal of MEKi resistance. Thus, BRAF^{V600E} amplification confers a selective disadvantage during drug withdrawal, validating intermittent dosing

to forestall resistance. In contrast, resistance driven by KRAS^{G13D} amplification is not reversible; rather ERK1/2 hyperactivation drives ZEB1- dependent epithelial-to-mesenchymal transition and chemoresistance, arguing strongly against the use of drug holidays in cases of KRAS^{G13D} amplification.

STEPHANIE NORWOOD

Babraham Institute

ORION Open Science: funding for collaborative co-creation projects

The ORION Open Science project is a European consortium of five research institutes, two funding bodies and two public-facing scientific organisations. We aim to embed open science and responsible research and innovation (RRI) principles in research and funding organisations. This year, we are launching a funding call offering up to 100,000 for new collaborative projects which bring together three or more of the following stakeholder groups: academia, industry, government, funders, regulators, educators, civil societies, charities, patient groups and the general public. We would like to encourage and support applications from companies and academics in the Cambridge bioscience community to develop exciting and innovative approaches to co-creation in the life sciences.

NO	POSTERTITLE	PRESENTER	INSTITUTION
T	Successful academic drug discovery collaborations — from validated target to candidate	Ray Boffey	Domainex
2	Epigenetic remodelling licences adult cholangiocytes for organoid formation and liver regeneration	Luigi Aloia	Wellcome Trust—Cancer Research UK Gurdon Institute, Dept of Physiology, Development and Neuroscience, Wellcome Trust—Medical Research Council Stem Cell Institute, University of Cambridge
3	Device physics modeling of microfluidic ion pumps	Shao-Tuan Chen	Dept of Engineering, University of Cambridge
4	Generating insights from the tumor micro-environment using tissue phenomics to drive cancer immunotherapy	Gillian Livock	Definiens
5	Novel high throughput tools for detecting age associated epigenetic changes in liquid biopsies	Sarantis Chlamydas	Active Motif
6	A single dose of antibody-drug conjugate cures a stage I model of African trypanosomiasis	Paula MacGregor	Dept of Biochemistry, University of Cambridge
7	Epigenomics profiling services – RNA-seq, ChIPmentation and DNA methylation analysis	Susanna Lovell	Diagenode
8	Patient derived iPSC for high grade glioma	Danel Tams	Censo Biotechnologies
9	Phenotypic screening of the ALBORADA Institute annotated library	Henriette Willems	ALBORADA Drug Discovery Institute, University of Cambridge
10	Murine retinal transduction using novel exosomeassociated AAV2 gene therapy modalities	Michael Whitehead	Dept of Clinical Neurosciences, University of Cambridge
11	Utilisation of human intestinal organoids to identify therapeutic approaches against human norovirus	Myra Hosmillo	Dept of Pathology, University of Cambridge
12	Digitalization of translational research to facilitate efficient development of precision medicines	Kevin Teburi	Genedata
13	Phoremost — Drugging the undruggable	Alberto Moreno de la Gandara	PhoreMost PhoreMost
14	Natural language processing to transform real world data for pharma decision making	Jane Reed	Linguamatics
15	Abcam strategy to support Parkinson's disease research	Matthew Ives	Abcam

NO	POSTERTITLE	PRESENTER	INSTITUTION
16	The Inflammatory Bowel Disease (IBD) BioResource: progressing from genetics to function and clinical translation in Crohn's disease (CD) and ulcerative colitis (UC)	Laetitia Pele	IBD BioResource, NIHR BioResource & Dept of Medicine, University of Cambridge
17	Discovering novel therapeutic targets using large biomedical knowledge graphs	Arwa Raies	European Bioinformatics Institute, EMBL–EBI
18	High content high resolution confocal imaging to characterise mutations in the apelin receptor identified in patients from the 13,000 Genomes Project	Thomas Williams	Experimental Medicine & Immunotherapeutics, University of Cambridge
19	Metrion Biosciences: high quality ion channel drug discovery service provider	Sophie Rose	Metrion Biosciences
20	Characterisation of the apelin receptor protein in human embryonic stem cell derived cardiomyocytes	Robyn Macrae	Experimental Medicine and Immunotherapeutics, Wellcome Trust–MRC Cambridge Stem Cell Institute, University of Cambridge
21	Targeting RNA modifying enzymes for the treatment of cancer	Oliver Rausch	STORM Therapeutics
22	Combining implantable electrodes and stem cell- derived cell transplantation towards functional neurological restoration	Amy Rochford	Dept of Engineering, University of Cambridge
23	Programming cell identity: enabling the next generation of human cell models from pluripotent stem cells	T Kalkan	Elpis Biomed
24	Organic electrochemical transistors for neural interfaces	Anastasios Polyravas	Dept of Engineering, University of Cambridge
25	Artificial Intelligence for identifying novel therapeutic targets, biomarkers and drug repositioning opportunities	Woochang Hwang	Milner Therapeutics Institute, University of Cambridge
26	Towards the derivation of a preclinical platform predictive of patient's drug responses	Alejand Bruna	Cancer Research UK Cambridge Institute, University of Cambridge
27	Using computational biology to identify novel therapeutic targets for ion channel-related disease	Ming Zeng	Dept of Chemical Engineering and Biotechnology, University of Cambridge
28	A framework for implementing machine learning on omics data	Geoffroy Dubourg- Felonneau	Cambridge Cancer Genomics

NO	POSTERTITLE	PRESENTER	INSTITUTION
29	Phylogenetic reconstruction of human RNA methyltransferases	Georgia Tsagkogeorga	Milner Therapeutics Institute, University of Cambridge & STORM Therapeutics
30	Machine learning for predicting active ligands for previously unseen targets	Vikram Sundar	Dept of Chemistry, University of Cambridge
31	The cellular thermal shift assay – target engagement measures for unbiased deconvolution of phenotypic assay hits	Sean Tyacke	Pelago Bioscience
32	Modeling branching morphogenesis with human embryonic lung organoids	Shuyu Liu	Wellcome Trust—Cancer Research UK Gurdon Institute, Department of Pathology, Wellcome Trust—MRC Stem Cell Institute, University of Cambridge
33	Launching the new Joint AstraZeneca and Cancer Research UK Functional Genomics Centre at the Milner Therapeutics Institute	Douglas Ross- Thriepland	AstraZeneca
34	Functional Genomics Screening — how do you get involved?	David Walter	Therapeutic Discovery Laboratories, Cancer Research UK
35	Targeting latent HCMV infection via epigenetic intervention towards reducing virus reactivation in the transplant setting	lan Groves & David Tough	Dept of Medicine, University of Cambridge GSK
36	The GSK Immunology Network: accelerating industry-academic collaboration	Етта Корре	GSK
37	Introduction to Shionogi's R&D and BD	Yutaka Yoshida	Shionogi
38	Get to know the CRUK Cambridge Centre	Birgit Nimmervoll	Cancer Research UK Cambridge Institute
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40	Paradoxical activation of the protein kinase- transcription factor ERK5 by ERK5 kinase inhibitors	Pamela Lochhead	Babraham Institute
41	MEK I/2 inhibitor withdrawal reverses acquired resistance driven by BRAF ^{V600E} amplification whereas KRAS ^{G13D} amplification promotes EMT-chemoresistance	Simon Cook	Babraham Institute
42	ORION Open Science: funding for collaborative co-creation projects	Stephanie Norwood	Babraham Institute





