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Issue 95 Summer 2020

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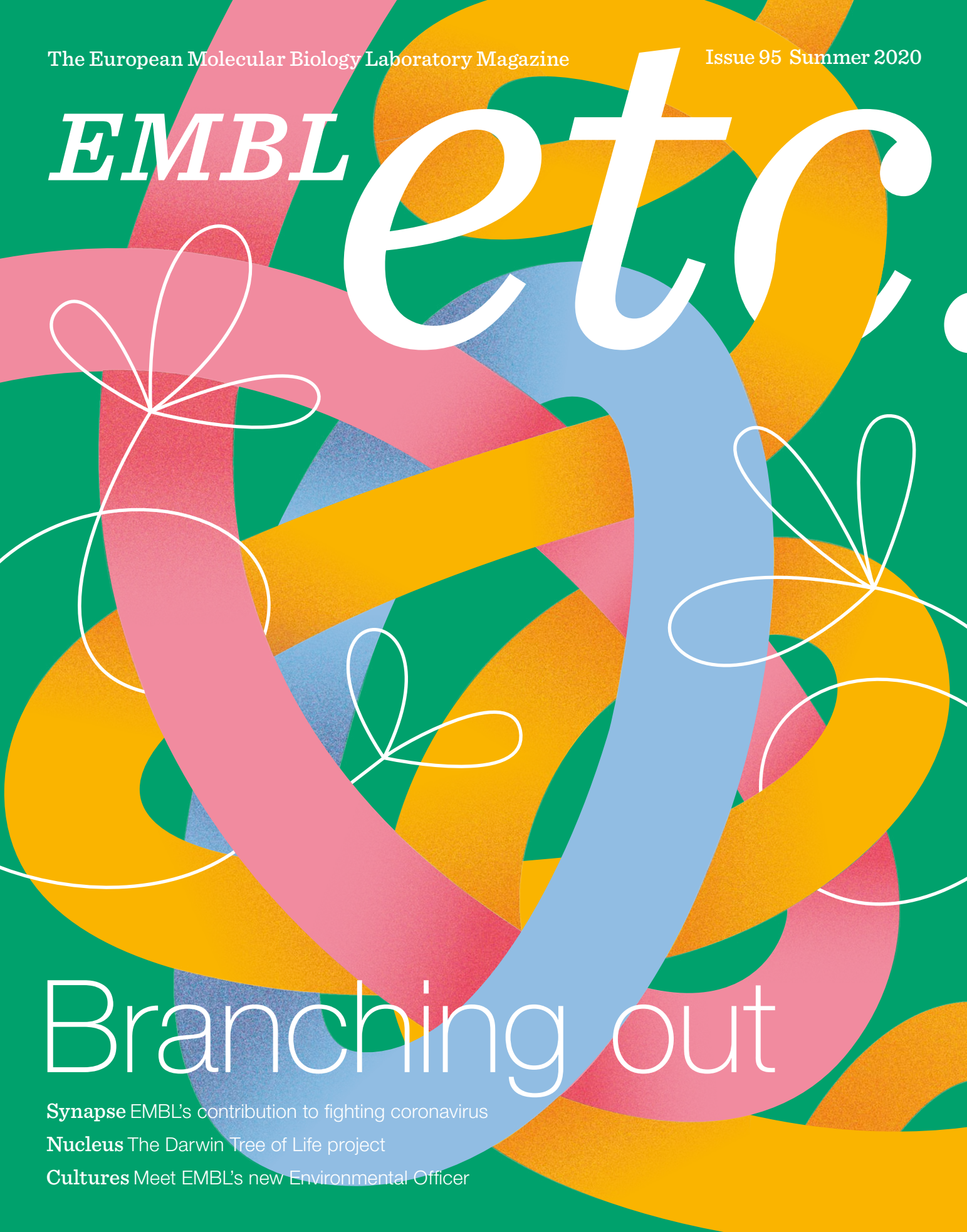

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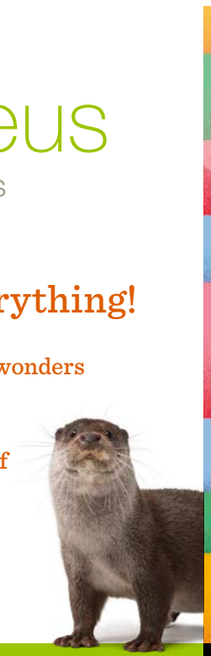

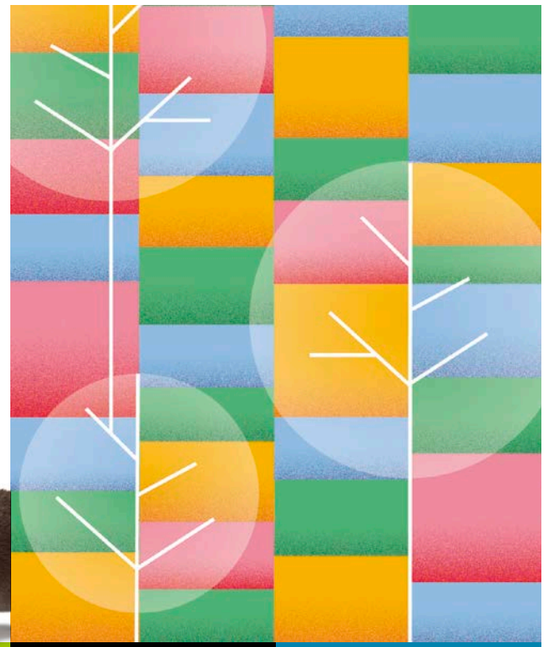

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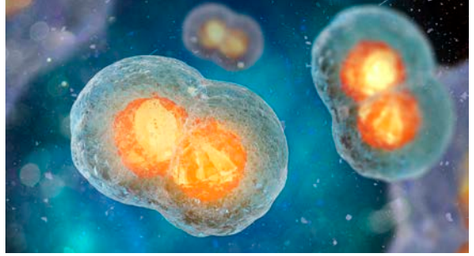

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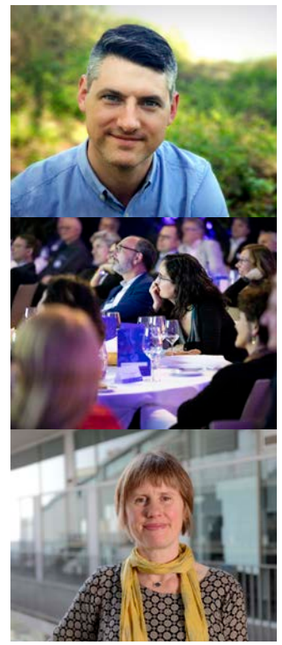
Alumni



Editorial

I could not have imagined, when we chose 'branching out' as the theme of this issue, what kind of world we'd be living in when the magazine was published. For many of us, the past few months have felt not like a branching out but a retreat into our homes and a narrowing of the way we live our lives. But these times have given us other kinds of opportunities to branch out; to break our routines and do things in a different way.

In this issue, many of our stories are about applying research in new contexts. We report on the EMBL research groups and core facilities using their expertise to study coronavirus (pp. 5–9), and Stephen Cusack, Head of EMBL Grenoble, discusses how the insights his group has gained into the influenza virus can be applied to combat other viruses, such as Lassa virus (p. 22). We also hear how scientists at EMBL-EBI are working with NASA on a new branch of microbiome research – in space (p. 26).

Branching out is a vital part of forming new collaborations and communities. This issue features several large collaborative projects involving EMBL, including the Pan-Cancer project (pp. 10–11) and a range of initiatives in which EMBL is sharing expertise and supporting training and research internationally (p. 16). We also report on EMBL-EBI's involvement in the Darwin Tree of Life project, which is providing new insights into the dynamics of ecosystems at the molecular level (p. 18).

Ecosystem research is important in the work of EMBL scientist Katja Ovchinnikova, who is applying her skills in computer science to study the health of coral reefs. Her participation in an innovative leadership programme helped her find a network of people with whom she could work on projects that are important to her, and made her more open to learning new things and facing unfamiliar challenges (p. 28).

As our lives slowly begin to branch out again, I hope we can all emerge from this crisis with a renewed sense of what really matters to us, and with the courage to go on doing things differently to bring positive change for ourselves and our world.

Edward Dadswell
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EMBL-EBI launches COVID-19 Data Portal

EMBL-EBI and partners launch the COVID-19 Data Portal to help scientists, public health and healthcare professionals to tackle the coronavirus pandemic

BY OANA STROE

Since the start of the COVID-19 pandemic, thousands of researchers across the globe have been working tirelessly to understand the new coronavirus, SARS-CoV-2. They have generated an enormous amount of information, but until now there has been no central repository for this information.

To address this need, EMBL's European Bioinformatics Institute (EMBL-EBI) and partners have launched the COVID-19 Data Portal, which enables the sharing and analysis of data related to the new coronavirus. The initiative aims to facilitate international collaboration to accelerate scientific discovery, monitor the pandemic, and help develop treatments and a vaccine for the virus.

The COVID-19 Data Portal contains numerous datasets submitted by collaborators or pulled in from other EMBL-EBI resources. The portal covers a wide range of data types including genomic, protein, and microscopy data, as well as scientific literature.

Scientists from all over the world can upload their data to the portal to share it with the scientific community. In the coming weeks and months, data from other European projects will be added.

The COVID-19 Data Portal is the entry point to the wider European COVID-19 Data Platform initiative, which involves the creation of multiple SARS-CoV-2 Data Hubs. These hubs are currently being built and, once ready, will organise the flow of sequence data from the outbreak and provide comprehensive open data sharing for the European and global research communities via the Data Portal.

"Launching the European COVID-19 Data Platform is an important concrete measure for stronger cooperation in fighting the coronavirus," says European Commissioner Mariya Gabriel. "Building on our dedicated support for open science and open access over the years, now is the time to step up our efforts and stand united with our researchers. Through our joint efforts, we will better understand, diagnose, and eventually overpower the pandemic."

The European COVID-19 Data Platform is one of ten projects included in the first iteration of the ERAvsCORONA Action Plan launched by the European Commission.

COVID-19 DATA PORTAL:
covid19dataportal.org

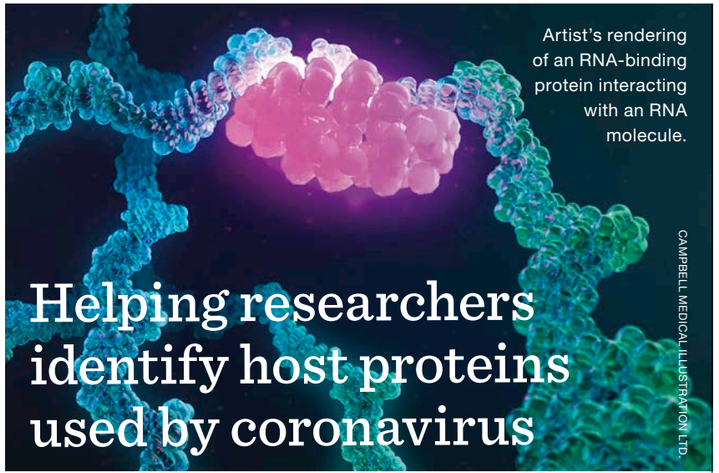
EMBL's contribution to fighting coronavirus

EMBL is using its skills, expertise, and resources to assist the global response to the coronavirus pandemic

EMBL's European Bioinformatics Institute (EMBL-EBI) is leading an international collaboration to develop the European COVID-19 Data Platform, an initiative to improve and accelerate the exchange of data among researchers globally. The platform consists of SARS-CoV-2 Data Hubs and the COVID-19 Data Portal (p. 5).

Many projects are in progress at EMBL sites to contribute to the global research effort, for example by identifying antibodies that can bind to SARS-CoV-2 and prevent it from infecting cells, studying drugs that have shown potential against the virus, or developing new and scaled-up testing methods. A selection of these projects are covered in the following pages.

ADDITIONAL CONTENT AND THE LATEST UPDATES ONLINE:
embl.org/topics/coronavirus



Artist's rendering of an RNA-binding protein interacting with an RNA molecule.

CAMPBELL MEDICAL ILLUSTRATION LTD.

Helping researchers identify host proteins used by coronavirus

EMBL scientists release database to help identify proteins that interact with the SARS-CoV-2 genome

BY MARIUS BRUER

RNA viruses, such as SARS-CoV-2, require cellular RNA-binding proteins (RBPs) as host factors to create more copies of themselves and influence cellular functions. The cellular proteins that bind to SARS-CoV-2's RNA genome have not yet been identified.

EMBL scientists in the Hentze and Huber groups have created the RBPbase database, which stores information on more than 4 000 proteins that have been identified as RBPs across multiple studies. The scientists hope that RBPbase will help researchers worldwide to identify candidate proteins in infected cells as coronavirus-interacting RBPs. This may lead to a better understanding of how SARS-CoV-2 multiplies in cells, and may enable the design of novel therapeutic strategies.

Understanding the role of our genes in SARS-CoV-2 infections

EMBL scientists will contribute to the new German COVID-19 OMICS Initiative

BY MARIUS BRUER

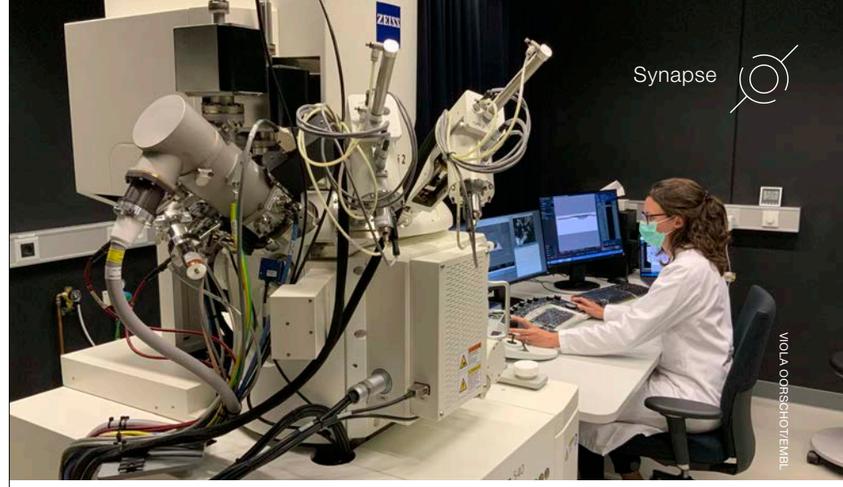
While SARS-CoV-2 infection only causes mild symptoms in some patients, others suffer from severe illness. Large clinical studies and detailed analysis of the data they generate are necessary to understand the biological factors that lead to these differences. To address these challenges, experts from more than 20 universities and research institutes, including EMBL, have joined forces in the German COVID-19 OMICS Initiative (DeCOI). EMBL group leaders Jan Korbel and Oliver Stegle will contribute to DeCOI by coordinating the set-up of IT infrastructures for secure storage and access to human genome sequencing data. This will be necessary to determine the influence of our genes on coronavirus infections.

Identifying how potential COVID-19 drugs work

EMBL researchers are studying how drugs that have shown good results against COVID-19 work in living cells

BY FABIAN OSWALD

To identify drugs that are effective against COVID-19, we need to understand how they work. EMBL researchers are using a technology called thermal proteome profiling, which can systematically identify targets for potential drugs in living cells. This will help scientists to quickly propose other efficient drugs or drug combinations to treat COVID-19, which are urgently needed until a vaccine is developed and made available globally. The project will rely on services provided by EMBL's Proteomics Core Facility.



VIOLA OORSCHOT/EMBL

Taking a closer look at coronavirus-infected cells

Scientists study the changes in cell structures after coronavirus infection

BY ANNE-MARIE ALLEAUME

Little is known about the mechanisms used by coronavirus to infect and destroy its target cells in humans. To better understand the changes in cell structures occurring in cells infected by SARS-CoV-2, scientists at Heidelberg University Hospital have shared samples of infected lung cells and biopsies from COVID-19 patients with members of EMBL's Electron Microscopy Core Facility and Schwab team, who will visualise and identify structures in cells that undergo changes after infection with the virus.

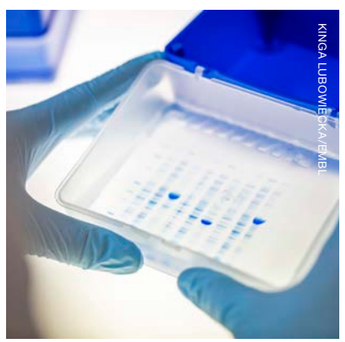
(Above) Laboratory Officer Nicole Schieber working in EMBL's Electron Microscopy Core Facility.

Producing proteins for coronavirus research

EMBL Protein Expression and Purification Core Facility will produce proteins for coronavirus-related research projects

BY MARIUS BRUER

Testing samples for coronavirus requires enzymes – proteins that perform a specialised task. The Protein Expression and Purification Core Facility (PEPCF) at EMBL Heidelberg will produce these enzymes using bacteria as host organisms. This will allow colleagues at EMBL to develop new coronavirus testing methods. PEPCF will also provide proteins that are required for several other coronavirus-related research projects at EMBL, to assist the development of new strategies to fight the virus.



KINGA LUBOMIŃSKA/EMBL

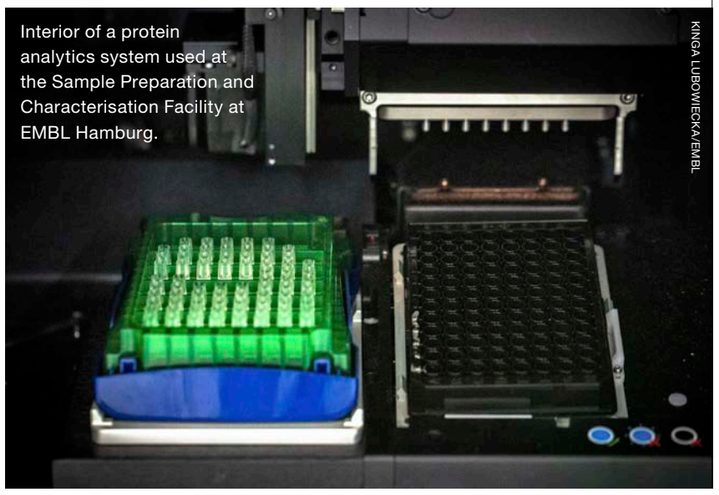
Purified proteins on a gel.

Exploring synthetic antibodies to stop coronavirus

EMBL scientists aim to identify nanobodies that could prevent SARS-CoV-2 from entering human cells

BY MARIUS BRUER

Scientists in the Löw group at EMBL Hamburg and collaborators at Karolinska Institutet aim to find synthetic antibodies – known as nanobodies – that bind to a surface protein of SARS-CoV-2. Once bound, the nanobodies make it impossible for the coronavirus to attack human cells. The scientists will use a large library of synthetic nanobodies and a piece of a SARS-CoV-2 protein to figure out which nanobodies bind most tightly to the virus. These candidates will then be further tested. In the future, nanobodies have the potential to be used as compounds to stop SARS-CoV-2 from infecting humans, or as tools in coronavirus diagnostic tests.



Interior of a protein analytics system used at the Sample Preparation and Characterisation Facility at EMBL Hamburg.

KINGA LUBOWIECKA/EMBL

EMBL SPC Facility supports COVID-19 projects

Facility at EMBL Hamburg reopens to support scientists working on COVID-19 research

BY SARA VERSTRAETEN

The Sample Preparation and Characterisation (SPC) Facility is an integral part of EMBL Hamburg's user facilities, and is in high demand from external users for COVID-19 projects. Alongside colleagues from EMBL Hamburg, scientists from other institutes like DESY and the Heinrich Pette Institute – which carries out research on experimental virology – have requested access to the SPC Facility for research projects related to COVID-19. Reopening the facility allows experts at EMBL to measure how strongly potential drug molecules bind to SARS-CoV-2 proteins, which could support the identification of drug treatments for coronavirus infections.

Helping to scale up coronavirus testing

EMBL scientists contribute expertise to develop large-scale coronavirus testing methods

BY MARIUS BRUER

Increasing the capacity and speed of testing is crucial for containing the coronavirus pandemic. To help reach these goals, scientists in EMBL's Genomics Core Facility and Genome Biology Unit are contributing their expertise in a community effort involving partners at Heidelberg University. A pilot project is under way to develop large-scale testing methods, using liquid-handling robots and high-throughput DNA sequencing machines. This approach would make it possible to automatically analyse thousands of samples in parallel.

Silencing the SARS-CoV-2 receptor with epigenetic modifications

EMBL scientists develop a new molecular tool to prevent SARS-CoV-2 infection in mice

BY ROSSANA DE LORENZI

Epigenetic modifications can turn genes on and off by affecting the chemical structure of the DNA or its associated proteins, rather than the DNA sequence. Scientists in the Hackett group at EMBL Rome have developed a new version of a CRISPR molecular tool used for epigenome editing. They will use this tool in mice to target airway cells and prevent them from expressing the ACE2 protein – the receptor that binds the SARS-CoV-2 spike protein and allows the virus to enter the cell. This is expected to block the entry route for the virus. The project will investigate the wider potential of epigenetic editing as a strategy for future prevention or treatment options.

Editing the mouse genome to study SARS-CoV-2 infection

EMBL scientists will produce transgenic mice with potential to advance antibody and vaccine preclinical trials

BY ROSSANA DE LORENZI

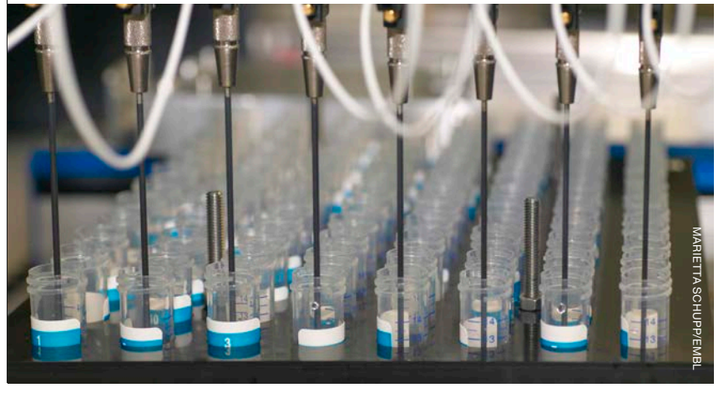
Researchers can study SARS-CoV-2 infection by using mice that have had their genome modified to express a human version of a protein called ACE2, which SARS-CoV-2 binds to. However, the transgenic mice currently available do not show the full disease spectrum observed in human patients. To solve this problem, scientists in the Gene Editing and Embryology Facility at EMBL Rome will subtly edit the mouse version of the gene so that the protein it produces is like the human version only at critical points where it interacts with SARS-CoV-2. The expression levels and function of this protein should then be the same as in non-transgenic mice. The new mouse line will be shared with preclinical research collaborators carrying out vaccine and antibody trials.

Remote access to EMBL structural biology pipelines to support research on SARS-CoV-2

Fully automated pipeline allows scientists to operate facilities at EMBL Grenoble via the internet

BY SARA VERSTRAETEN

The Marquez team has restarted operations at the High-Throughput Crystallisation (HTX) Lab at EMBL Grenoble. The team has developed a fully automated protein-to-structure pipeline, which can be operated by any scientist from a computer with an internet connection. Scientists can send samples via post from anywhere in the world and access their results via the Crystallographic Information Management System (CRIMS). CRIMS is able to communicate with the ESRF synchrotron in Grenoble and the PETRA III synchrotron in Hamburg, to support automated and remote X-ray data collection. These capabilities are unique and provide valuable support for structural biology projects focusing on SARS-CoV-2 and other coronaviruses.



Crystallisation reagents being prepared by a pipetting robot at the HTX Lab.

MARIETTA SCHUPP/EMBL

The Pan-Cancer project

EMBL co-leads most comprehensive study of genetic causes of cancer

BY MATHIAS JÄGER

An international team, including scientists from EMBL, has completed the most comprehensive study of whole cancer genomes to date, significantly improving our fundamental understanding of cancer and marking out new directions for its diagnosis and treatment. The results of the project have been published in more than 20 papers in *Nature* and its affiliated journals.

The Pan-Cancer Analysis of Whole Genomes project is a collaboration involving more than 1300 scientists and clinicians from 37 countries. More than 2 600 genomes of 38 tumour types have been analysed, creating a huge resource of primary cancer genomes. This was the starting point for 16 working groups to study multiple aspects of cancer development, causation, progression, and classification.

The Pan-Cancer project has extended and advanced methods for analysing cancer genomes. Most previous studies have focused on the 1% of the genome that codes for proteins. The Pan-Cancer project has explored in considerably greater detail the remaining 99% of the genome. This has revealed new knowledge about cancer biology and confirmed important findings from previous studies.

The first wave of results shows that the cancer genome is finite and knowable, but enormously complicated. By combining sequencing of the whole cancer genome with a suite of analysis tools, the researchers were able to characterise every genetic change found in a cancer, all the processes that have generated those mutations, and even the order of key events during a cancer's life history.

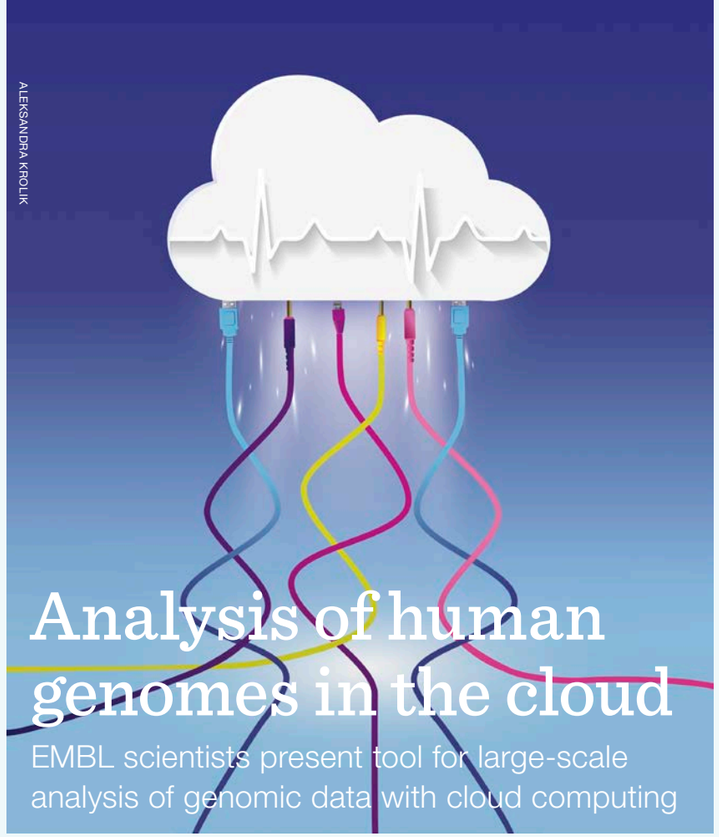
A key finding is that it's possible to identify mutations in the genome that occurred years, or even decades, before a tumour appears – theoretically opening a window of opportunity for early cancer detection.

On top of the discoveries that have already been made, the Pan-Cancer project equips scientists with a comprehensive resource for cancer genomics research, including the raw genome sequencing data, software for cancer genome analysis, and multiple interactive websites exploring various aspects of the Pan-Cancer project data.

RAYNE ZAAYMAN-GALLANT/EMBL

LEARN MORE ABOUT THE PAN-CANCER PROJECT:
bit.ly/embletc-95-pcawg

The Pan-Cancer project showed that cancer mutations can be identified years, or even decades, before a tumour appears.



ALEKSANDRA KROLIK

Analysis of human genomes in the cloud

EMBL scientists present tool for large-scale analysis of genomic data with cloud computing

BY MATHIAS JÄGER

Most bioinformatics software used for genomic analysis is experimental in nature and has a relatively high failure rate. In addition, cloud infrastructure itself, when run at scale, is prone to system crashes. To solve these problems, EMBL scientists led by Jan Korbel have developed a tool, called Butler, that identifies and fixes crashes efficiently. The tool was developed for the Pan-Cancer project.

Butler differs from other bioinformatics workflow systems because it constantly collects health metrics from all system components. Its self-healing modules use these health metrics to figure out when something has gone wrong, and can take automated action to restart failed services or machines. Butler thereby dramatically reduces the time needed to execute large projects.

Butler can run on a wide variety of cloud computing platforms, including most major commercial and academic clouds. This allows researchers access to the widest variety of datasets while meeting stringent data protection requirements.

Yakneen, S *et al. Nature Biotechnology*, 5 February 2020. DOI: 10.1038/s41587-019-0360-3

Cancer mutations occur decades before diagnosis

A large-scale pan-cancer analysis of the evolutionary history of tumours reveals that cancer-causing mutations occur decades before diagnosis

BY VICKY HATCH

Researchers at EMBL's European Bioinformatics Institute (EMBL-EBI) and the Francis Crick Institute have analysed the whole genomes of over 2 600 tumours from 38 different cancer types to determine the chronology of genomic changes during cancer development.

The Pan-Cancer project used data from the International Cancer Genome Consortium and The Cancer Genome Atlas to create tumour development timelines for several cancer types including glioblastoma, and colorectal and ovarian adenocarcinoma. Their findings suggest that tumour development can span the entire lifetime of an individual, so the mutations that initiate cancer progression may arise decades before diagnosis.

Understanding the sequence and chronology of mutations leading to cancer may help clarify the mechanisms of cancer development. Being able to determine whether a mutation typically occurs early or late during cancer progression may also help to guide early detection. This would make it possible to define the sets of alterations to screen for, and to detect pre-cancerous cells at different stages of transformation.

Gerstung, M, Jolly, C, Leshchiner, I, Dentro, SC, Gonzalez, S *et al. Nature*, 6 February 2020. DOI: 10.1038/s41586-019-1907-7

Tracing the origins of cells

EMBL scientists develop an improved method to reconstruct a cell's history

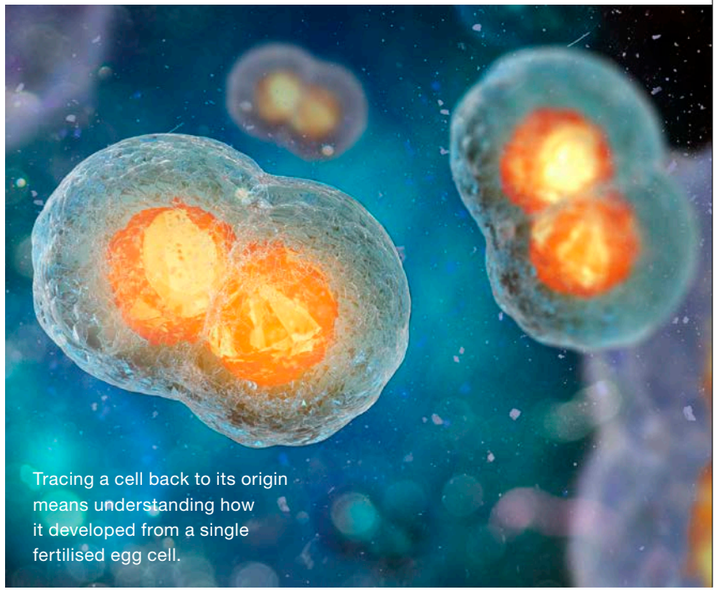
BY FABIAN OSWALD

Researchers from the Sharpe group at EMBL Barcelona have published a method to track the developmental history of a cell using the gene editing tool CRISPR–Cas9, but without the need to create transgenic organisms.

Every cell has a lineage: its developmental history, traced back through every cell division to the first cell from which it began. One method for cellular lineage tracing uses CRISPR–Cas9, the so-called 'genetic scissors', to generate mutations and use them as lineage markers. This method usually requires the creation of transgenic organisms: their genome is edited so that it contains specific DNA sequences that serve as targets for CRISPR–Cas9.

The Sharpe group developed software and used it to identify sequences that exist naturally in the genomes of mice and zebrafish that could be used as CRISPR–Cas9 targets. Their new method simplifies the lineage tracing approach and can be applied to any species with a published genome.

Cotterell, J *et al. Development*, 12 May 2020. DOI: 10.1242/dev.184481



Tracing a cell back to its origin means understanding how it developed from a single fertilised egg cell.

Unprecedented single-cell studies in virtual embryo

EMBL scientists create first complete description of early embryo development

BY MATHIAS JÄGER

Researchers from the Neveu and Hufnagel groups at EMBL Heidelberg and from the University of Padua School of Medicine have created the first complete description of early embryo development, accounting for every cell in an embryo. They constructed a 'virtual embryo' of *Phallusia mammillata* – a marine organism known as a sea squirt.

The virtual embryo describes the gene expression and morphology of every single cell in the embryo, at every cell division in the early stages of development – showing the evolution from a single cell to the 64-cell stage. To generate this comprehensive atlas, the researchers combined high-resolution single-cell transcriptomics and light-sheet imaging. The virtual embryo will help to show how the different cell types in an organism originate from a single egg cell.

Gene expression is generally thought to be a noisy process – in other words, one that shows an element of randomness – yet the new results show that it is remarkably reproducible and coordinated across cells in the embryo.

Sladitschek, H *et al. Cell*, 20 April 2020. DOI: 10.1016/j.cell.2020.03.055

How females shut off their second X chromosome

Researchers at EMBL Heidelberg and Institut Curie show that the protein SPEN plays a crucial role in X-chromosome inactivation

BY MEHDI KHADRAOUI

To avoid an imbalance in gene expression in mammals – in which more than a thousand genes on the X chromosome would be expressed in a double dose in females (XX) compared to males (XY) – females shut down the expression of genes on one of their two X chromosomes.

Scientists in the Heard group have identified how a protein called SPEN functions to induce gene silencing. A long non-coding RNA called *Xist* – known to initiate X-inactivation – binds SPEN, which then accumulates along the X chromosome and interacts with the regulatory regions of active genes. As soon as gene silencing occurs, SPEN disengages. Genes then remain inactive for the rest of the cell's lifetime.

The researchers found that a specific domain of SPEN called SPOC played the lead role in gene silencing. It represses the transcription of DNA into RNA and interacts with several proteins involved in RNA synthesis, as well as chromatin remodelling and modification.

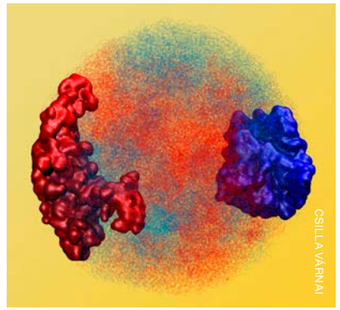
Dossin, F *et al. Nature*, 5 February 2020. DOI: 10.1038/s41586-020-1974-9

How chromosome structure influences development

EMBL researchers explore the interaction between DNA organisation and gene expression in the early embryo

BY FABIAN OSWALD

Scientists in the Heard group at EMBL Heidelberg have investigated the three-dimensional organisation of DNA in early embryos. They discovered that, during the first stages of an embryo's life, hundreds of regions of the genome are active on only one copy of a chromosome – either the one received from the mother or the father – but almost never on both at the same time. Their study is the first to report a complete map of paternal and maternal chromosome organisation during early mouse development, generated at single-cell resolution in a large number of cells – hundreds in this case



A 3D reconstruction of maternal (red) and paternal (blue) chromosomes from a single mouse embryo cell after three and a half days of development.

Collombet, S, Ranisavljevic, N, Nagano, T *et. al. Nature*, 25 March 2020. DOI: 10.1038/s41586-020-2125-z

Tissue dynamics provide clues to human disease

EMBL scientists examine the molecular causes of a rare hereditary disease of the spine and ribs

BY MITSUHIRO MATSUDA, JAMES SHARPE, AND EDWARD DADSWELL

The repetitive structure of the vertebral column is created in the embryo by a group of genes called the segmentation clock, which show oscillating patterns of gene expression. Errors in the segmentation clock can cause hereditary disorders of the vertebrae, such as spondylocostal dysostosis (SCD).

Scientists in EMBL Barcelona's Ebisuya group and collaborators created cell lines that each lacked a gene thought to be the causative mutation of SCD, and cultured these cells to create simplified versions of an embryo. They found that oscillations in these systems did not properly coordinate across the tissue. Their next goal is to use their new *in vitro* model to identify a novel causative gene of SCD.

Matsuda, M, Yamanaka, Y *et al. Nature*, 1 April 2020. DOI: 10.1038/s41586-020-2144-9

EMBL co-develops new method that could facilitate cancer diagnosis

scTRIP can detect small-scale changes and many types of genetic variation that are undetectable with other methods

BY MATHIAS JÄGER

Researchers led by EMBL and the Center for Bioinformatics at Saarland University have developed a cheaper and faster method to check for genetic differences in individual cells. The new method, called single-cell tri-channel processing (scTRIP) makes it possible to detect small-scale changes, along with many types of genetic variation that were invisible using other single-cell methods.

The researchers tested their method by studying patient-derived leukaemia cells. They found four times more variants in their sample than were detected by standard clinical diagnostics. These included a missed clinically relevant translocation that drove the overexpression of a cancer-causing gene. They also observed a catastrophic chromosome rearrangement that was missed in the initial leukaemia diagnosis.

The team has begun to expand their use of the method to analyse different forms of leukaemia and evaluate its potential clinical utility. They also plan to study mutational processes in various human cell types, and to assess their consequences in terms of human disease.

Sanders, AD, Meiers, S, Ghareghani, M, Porubsky, D *et al. Nature Biotechnology*, 23 December 2019. DOI: 10.1038/s41587-019-0366-x

TOBIAS WUSTEFELD

Innovative method delivers new insights into the stem cell microenvironment

Researchers identify previously unknown cell types involved in regulating blood cell production

BY MATHIAS JÄGER

A group led by researchers from EMBL and the German Cancer Research Center (DKFZ) in Heidelberg has developed new methods to reveal the 3D organisation of bone marrow at the single-cell level. Bone marrow harbours blood stem cells that are responsible for lifelong blood cell production, and there is a growing interest in exploiting the bone marrow environment as a target for novel leukaemia treatments.

The researchers combined single-cell and spatial transcriptomics with novel computational methods. By analysing the RNA content of individual bone marrow cells, they identified 32 distinct cell types, including some that are rare or previously unknown. It is thought that these rare 'niche cells' establish unique environments in the bone marrow that are required for stem cell function and production of new blood and immune cells.

The data is freely accessible in a 3D atlas via a user-friendly web app, and will facilitate the refinement of future genetic studies.

Baccin, C, Al-Sabah, J, Velten, L *et al. Nature Biotechnology*, 23 December 2019. DOI: 10.1038/s41556-019-0439-6

ARTURO AGOSTINO; EDITED BY SPENCER PHILLIPS/EMBL

DNA damage and faulty repair jointly cause mutations

Whole-genome sequencing in *C. elegans* gives new insights into cancer genomics

BY MEHDI KHADRAOUI

A cell's DNA is constantly exposed to physical and chemical stresses – or genotoxins – that can damage it and cause mutations. Many genotoxins were thought to cause a unique suite of mutations, recognisable as a mutational signature. A team including researchers at EMBL-EBI has tested the effects of combinations of genotoxins on *C. elegans* worms. They found that different types of DNA alterations induced by the same genotoxin are often fixed by different DNA repair pathways, some error free, others error prone. As a result, a single genotoxin may leave a variety of mutational signatures at various rates, depending on the repair process.

Volkova, NV, Meier, B, González-Huici, V *et al. Nature Communications*, 1 May 2020. DOI: 10.1038/s41467-020-15912-7

(Above) Artistic interpretation of mutational signatures in *C. elegans*.

€2.45 m to investigate leukaemia causes and therapies

EMBL part of LeukoSyStem consortium investigating leukaemia stem cells in acute myeloid leukaemia

BY MATHIAS JÄGER

The Heidelberg-based junior research alliance LeukoSyStem, which includes EMBL scientists, has obtained research funding of €2.45 million from the German Federal Ministry of Education and Research (BMBF). The aim of their project is to investigate the cells that are the origin of acute myeloid leukaemia. The scientists intend to use isolated single cells from patient samples to investigate characteristic markers, mutations, functional data, and metabolic pathways, to gain a better understanding of leukaemia stem cells and their environment in bone marrow. Leukaemia stem cells are considered to be the starting point of leukaemia, so their elimination is a basic prerequisite for a successful long-term therapy.

EMBL hosts its first virtual conference

Virtual symposium 'The Four-Dimensional Genome' attracts 470 participants

BY MARIUS BRUER

The EMBO | EMBL Symposium 'The Four-Dimensional Genome', originally planned as an on-site meeting at EMBL Heidelberg, became the first virtual conference of the EMBL course and conference programme from 30–31 March.

The meeting included four virtual sessions with 13 live talks from invited speakers. The sessions also included 20 pre-recorded short talks, and a virtual gallery system was used to make posters viewable online.

The organisers had expected 250 pre-registered attendees, but reopening registration for the virtual conference attracted nearly twice as many participants. The conference also brought other advantages by reducing carbon emissions associated with the event and reaching participants who would have been unable to attend a meeting on site.

DETAILS OF FORTHCOMING VIRTUAL CONFERENCES: embl.org/events

Note: This was the first virtual conference of the EMBL course and conference programme; however, an EMBL PhD symposium did take place as an online meeting in December 2006.

Nordic EMBL Partnership awarded €210 000 funding

Funds for the next generation of specialists in molecular medicine in the Nordic countries

BY MATHIAS JÄGER

The Nordic EMBL Partnership for Molecular Medicine has been awarded €210 000 by NordForsk as part of the Nordic Research Infrastructure Hubs initiative. The funds will be used to train the next generation of specialists and research leaders in molecular medicine in the Nordic countries. The grant will allow EMBL and its partners to further strengthen research in molecular medicine in the Nordic countries and will reinforce the connection between the Nordic countries and EMBL. The grant enables EMBL to offer further benefits to the EMBL member states in the partnership, by supporting career development opportunities at the six EMBL sites.

(Above) The Nordic EMBL Partnership for Molecular Medicine includes EMBL and partner institutes in Denmark, Finland, Norway, and Sweden.

Chan Zuckerberg grant for Global BioImaging

New grant will increase collaboration between imaging centres and fuel scientific discovery

BY EDWARD DADSWELL

The Chan Zuckerberg Initiative has announced over $1.3 million (€1.2 m) in funding to support Global BioImaging, an international network of bioimaging facilities and communities coordinated by EMBL. The three-year grant will support Global BioImaging's work to promote community building and training worldwide, enabling scientists to access the latest imaging technologies.

Global BioImaging was founded in 2015 to bring together imaging facility operators, technical staff, scientists, managers, and science policy officers to network, share expertise, and build capacity in biological and biomedical imaging. By promoting access to the latest imaging technologies and facilitating training and data analysis, Global BioImaging drives forward research and enables breakthrough discoveries in the life sciences and beyond.

EMBL shares expertise with European institutes

European Commission grants funding for new Twinning projects involving EMBL scientists

BY MARIUS BRUER

Three international teams involving various research groups and core facilities at EMBL Heidelberg have been granted funding from the European Commission for three Twinning projects with institutes in Portugal and the Czech Republic. The projects will enable the creation of new research networks and collaborations across Europe. They are funded with €1 million each and will run for three years.

Twinning is part of the EC's 'Horizon 2020' widening programme. At least two advanced partners, like EMBL, team up with an institute to share their expertise. Twinning projects foster the exchange of knowledge between participants and enable new areas of expertise to be developed and sustained at research institutes based in regions that are less established in research and innovation. The participation in three new Twinning projects underscores EMBL's continued efforts to promote collaborative research across Europe and bring together the European life science community.

ALEKSANDRA KROLIK

New branches

EMBL scientists are applying their knowledge in new contexts to drive forward discovery

Let's sequence everything!

Genome sequencing has done wonders for helping us understand human health and disease, but can it help us make sense of our environment and protect biodiversity?

ALEKSANDRA KFOLIK

BY VICKY HATCH

With sequencing costs continuing to fall, it was only a matter of time before scientists came up with a plan to sequence all life on Earth. This initiative, which started in 2019, is called the Earth BioGenome Project, and is one of the most ambitious projects in biology today.

One part of this initiative is the Darwin Tree of Life (DToL) project, a huge collaborative effort to sequence, assemble, and annotate the genomes of all 60 000 eukaryotic species found in the Atlantic archipelago of Britain and Ireland; in other words, all species except for bacteria and another group of microbes known as archaea. EMBL's European Bioinformatics Institute (EMBL-EBI) has joined the project to store, curate, and share the data that will be generated.

Our planet is currently experiencing a wave of extinctions as a result of human interventions such as deforestation and activities that lead to global warming. As a species, we have drastically altered the Earth's ecosystems, so it is now more important than ever to carefully document and protect the species currently living.

DToL, funded by Wellcome and the UK's Biotechnology and Biological Sciences Research Council, aims to use the genomic data collected to help scientists better understand the diversity of life and to aid conservation efforts.

The first 2 000 species

Phase 1 of DToL began in November 2019, with the aim of sequencing the genomes of 2 000 species. This initial period allows researchers to collect and catalogue samples, and to build up the expertise required to complete this enormous project, which is expected to take at least 10 years. After this initial phase, the project will significantly scale up to get the genomes of all 60 000 species sequenced, annotated, and shared with the global research community.

The red squirrel (*Sciurus vulgaris*) was one of the first species to be sequenced, followed closely by the grey squirrel (*Sciurus carolinensis*). Red squirrels are a native species in the UK and Ireland, but their populations in these countries have declined significantly since the introduction of the grey squirrel from North America in the nineteenth century.

Grey squirrels have a selective advantage over their red counterparts due to their immunity to squirrelpox, a disease that is diminishing the red squirrel population. Sequencing and compiling reference genomes for these squirrel species will help scientists understand more about immunity to squirrelpox and could aid future conservation efforts. The red squirrel genome is set to become available in EMBL-EBI's Ensembl database in July 2020. >>

Another of the first genomes sequenced by DToL is that of the Eurasian river otter (*Lutra lutra*). This otter species came close to extinction in the UK and Ireland during the 1970s, due to the use of pesticides, which polluted the otters' natural habitat. The use of many of these chemicals has since been banned, and the otter has been able to make a comeback. Sequencing the genome of the Eurasian river otter will help scientists to understand the genetic effects caused by such environmental changes.

Open data for all

Much of the work on DToL is taking place in rural Cambridgeshire on the Wellcome Genome Campus, which is home to EMBL-EBI. In an effort reminiscent of the Human Genome Project, EMBL-EBI and the Sanger Institute have teamed up again. Along with a wide range of collaborators, they have begun sequencing the genomes of thousands of species and sharing the data with the rest of the world.

EMBL-EBI's neighbour, the Wellcome Sanger Institute, will serve as a hub for sequencing and assembling the genomes of species collected by numerous collaborators in the UK and Ireland. Once sequenced, the genomic data will be passed on to EMBL-EBI for further steps to ensure it is safely stored and easily accessible to scientists for ever.

One of the most important goals of DToL is to make all the genomic data generated freely accessible to scientists around the world. Every genome sequence from DToL will be freely available through EMBL-EBI's European Nucleotide Archive (ENA), one of the largest and most comprehensive databases in the life sciences. The ENA will create a sort of virtual waiting room in which collaborators can place the assembled genomes alongside the appropriate metadata, which provide further context. All of these will then be rapidly ingested into the ENA, which will serve as a public archive for the data from the project. This makes the data openly available for current and future generations of scientists.

The reference genomes produced from the ENA data will also be annotated, stored, and shared through EMBL-EBI's Ensembl database. The team is setting up efficient data flows to enable the raw sequencing data to instantly pass to the ENA and Ensembl, so the data for thousands of species can be processed faster than ever before.

"Thanks to the efforts of the ENA and Ensembl teams, researchers will be able to access fully annotated genomes and, using the Ensembl genome browser, ask complex scientific questions based on genomic data," says Leanne Haggerty, Developer at EMBL-EBI.

Scaling up the data infrastructure

Big data collaborations such as DToL have only recently become possible thanks to advances in sequencing technologies, the reduced costs of sequencing, and more efficient solutions for data storage.

"EMBL-EBI has been scaling up its infrastructure to prepare for the Darwin Tree of Life data," explains Fergal Martin, Vertebrate Annotation Coordinator at EMBL-EBI. "The Ensembl gene annotation pipeline has undergone substantial changes to speed up the annotation process.

"Annotating the location of the genes within a genome used to be a manual process that could take months. It now only takes a few minutes to configure the annotation pipeline for a species, and the results are ready within a matter of days. We're continually reviewing and updating the pipeline to make sure it will be ready once the number of genomes sequenced in DToL begins to ramp up."

It's also important to optimise the genome data analysis for different species. For example, some species of salamander can have up to ten times more DNA than humans. Wheat has multiple copies of each of its chromosomes, compared to the two copies typically found in mammals. These differences must be taken into account for data analysis pipelines to run efficiently.

A new understanding of ecosystems

DToL will provide a complete genomic record of most ecosystems in the UK and Ireland; the first time a complete record of eukaryotic genomes will be made available on such a scale. This will give researchers and conservationists new insights into the dynamics of ecosystems at the molecular level. Such information can help us understand the survival needs of different species and how they have adapted to their environments. It can also improve conservation efforts for individual species and entire ecosystems.

Scientists studying comparative genomics and evolutionary biology will also find the data gathered by DToL extremely beneficial for defining differences between species. Comparing genomic species data can help scientists reconstruct the evolutionary history of genes or genomes. And having access to data from as many species as possible provides a better understanding of how species have evolved and how they might change in future.

The discoveries don't stop there. Data of this kind can help further our understanding in many branches of science, such as gaining new insights into the genes driving crop and livestock yields, which could increase food production in future. Projects like DToL bring enormous potential for future discoveries and benefits to human and planetary health.

Future endeavours

DToL is only just beginning. Many new genomes will be sequenced in the next few years. One group the researchers are particularly excited about are British butterflies and moths. These are interesting to conservation experts because they act as indicators of climate change. Deeper investigation of butterfly and moth genomes will further our understanding of the ways they have adapted to cope with the effects of human activity on the environment.

DToL is also gearing up to sequence entire ecosystems. One of the first such ecosystems to be explored is that of British and Irish shorelines. Sequencing the genomes of molluscs, including snails and sea slugs, will give new insights into the impact of climate change and pollution on the islands' shores.

As DToL and the Earth BioGenome Project scale up, researchers can expect to see more new genomes released in the ENA and Ensembl. These projects also provide fantastic opportunities to bring people closer to nature and give us a better understanding of how we can protect our beautiful and diverse planet.

The Darwin Tree of Life project is a collaboration between EMBL-EBI; the Wellcome Sanger Institute; the Natural History Museum, London; the Royal Botanic Gardens, Kew; the Royal Botanic Garden Edinburgh; the Marine Biological Association; the Earlham Institute; the University of Oxford; the University of Exeter; the University of Edinburgh and Edinburgh Genomics; and the University of Cambridge.

Understanding the influenza virus

Stephen Cusack, Head of EMBL Grenoble, discusses how the influenza virus infects cells, and shares his most recent discoveries

BY FABIAN OSWALD

The infectious disease commonly known as flu is caused by the influenza virus. It spreads around the world in seasonal outbreaks, causing millions of infections and hundreds of thousands of deaths each year. Stephen Cusack, Head of EMBL Grenoble, has been studying various aspects of the influenza virus for 30 years. He recently published a paper describing the function of influenza polymerase – a key enzyme of the virus – in unprecedented detail. Here, he describes how the influenza virus functions, the technologies that are helping researchers to understand it, and why it's necessary to constantly develop new drugs.

Stephen Cusack, Head of EMBL Grenoble.

Tell us about your research on the influenza virus.

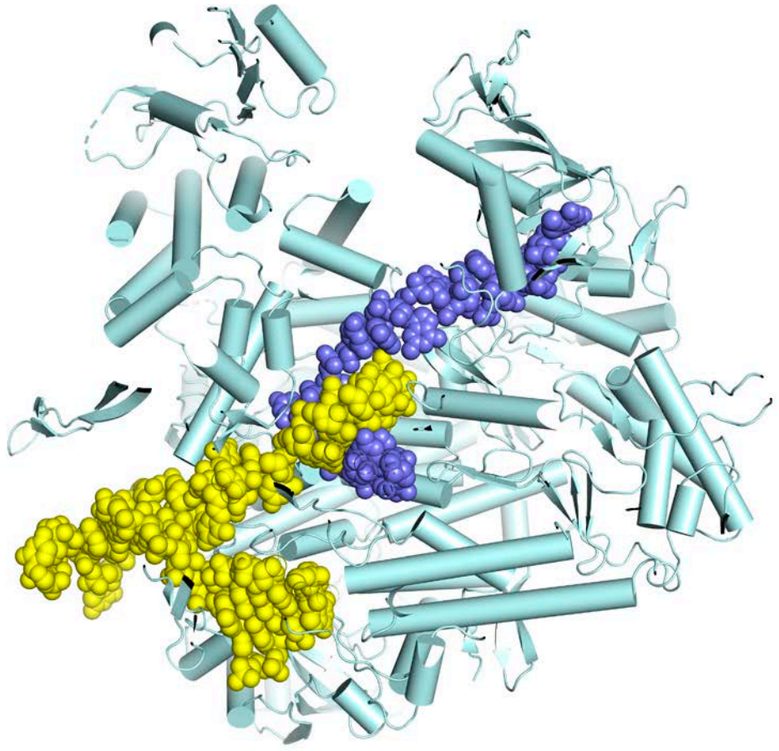
We study how the influenza virus proliferates in an infected cell; in particular, how the genome of the virus is copied by the viral polymerase. Most cellular organisms and some viruses have a genome made of DNA. The influenza virus is an RNA virus, which means that its genome is made of RNA – a molecule similar but chemically distinct to DNA. The viral genome serves two purposes. Firstly it is *transcribed*: this is the process by which it is used to make what's called messenger RNA, or mRNA. This mRNA carries instructions to the protein-making machinery of the host cell to make viral proteins. Secondly, the viral genome has to be *replicated*, which means that exact copies of it are made. These are packaged, together with the newly synthesised viral proteins, into the next generation of viruses, which bud at the cell surface.

"A few years ago, we would never have believed this was possible"

And what is the focus of your recent research?

The polymerase is a molecular machine, moving along the RNA genome as it copies it. We want to find out what all the moving parts are and thus understand how the machine works. Then we will be in a good position to develop antiviral drugs that stop the polymerase in its tracks. To do all that, we use structural biology to determine the atomic structure of the polymerase. However, you need not just one structure, but many snapshots of the machine in action. That's what we've been doing, step by step, for the past 12 years. We started out by determining the structure of fragments of the polymerase. This was in itself interesting, as some of these fragments are targets against which highly potent anti-influenza drugs have been developed. Then, in 2014, we were able to determine by X-ray crystallography the structure of the complete polymerase, which is a really big and complex molecule, made of three separate protein chains folded >>

(Opposite) Artist's representation of the influenza virus.



STEPHEN CUSACK/EMBL

Influenza polymerase (cyan) in the process of making messenger RNA (blue) by transcribing the viral RNA template (yellow).

together. At that time, it was still unclear how it really worked, because the first structures didn't show the polymerase in an active state – when it's actually copying the genome. Since then, we've spent a lot of time figuring out how to determine structures of the functioning enzyme. That has only really become possible since the so-called cryo-electron microscopy *resolution revolution.*

Why was this essential?

Cryo-electron microscopy, or cryo-EM, is a technique that now allows us to get structures of protein complexes at near atomic level. This has only been possible in the last five or so years, thanks to spectacular technical advances. Prior to that, we used X-ray crystallography, a powerful technique that can also give high resolution, but to do it you need to grow crystals of your sample. In the crystal, all the molecules are constrained to be in the same state, and that's not always possible when the molecule is very flexible. With cryo-EM, the sample in solution is applied to grids and then rapidly frozen, trapping the polymerase particles, each in its particular state, in a thin layer of ice. The grids are then placed in the electron microscope and many images captured of different parts of the grid where there are particles. We use sophisticated image processing software to process the data to obtain a high-resolution structure. That's what we've been doing for the past three years, with the support of the Cryo-EM Service Platform at EMBL Heidelberg, and it's worked beyond all expectations. A few years ago, we would never have believed this was possible.

Could you explain your most recent publication?

We've now managed to understand how the influenza polymerase carries out the complete transcription process. We set up a transcription reaction in the test tube in a way that meant it would stall at different points in the process. For each stalled reaction, we determined the structure of the polymerase bound to the genomic RNA and to the partially made product mRNA. In this way, we obtained a series of snapshots of eight successive stages, from the beginning to the end of transcription, resembling a molecular movie. This has never been done before in such detail for a large viral polymerase. We were able to reveal some unique features of influenza polymerase for the first time. For instance, we show how the polymerase copies the genome, but never lets go of the genome ends, which enables rapid recycling for the next round of transcription. This is really breakthrough research, and has now been published in *Cell*. It's mainly the work of PhD student Joanna Wandzik and EMBL Interdisciplinary Postdoc Tomas Kouba.

"We're currently extending our studies from influenza to other related viruses"

What avenues does this open for your future research?

There are a few things we want to do next. First, we want to apply this method to the other activity that the polymerase has, when it replicates its genome to be packaged into new viruses. This is more complicated, as there may be two polymerases involved. Then, we want to move towards the more physiological aspects. Until now, we've used influenza polymerase made in the lab and working in a test tube. This enables you to understand the basic mechanisms. But, in reality, the RNA genome is never naked but at all times packaged together with the polymerase and many copies of the viral nucleoprotein in the so-called viral ribonucleoprotein particle (vRNP). The processes of replication and transcription actually take place in the vRNP context. We want to understand how that happens. The third step will be to go really into the cell and look directly at the polymerase working in the nucleus, as certain host proteins are crucial for transcription and replication as well. This is very challenging, but is becoming possible using the developing technique of cellular cryo-electron tomography. There's a lot of exciting work on that going on at EMBL Heidelberg, particularly in the group of Julia Mahamid, who's pioneering this technique.

Another important project we will focus on is developing new drugs that help to treat influenza. The virus evolves quickly, thanks to errors that the polymerase makes in copying the genome, and can develop resistance to drugs, so there's always a need for the next generation of drugs. All the studies we've done have opened up opportunities for developing new ways of targeting the polymerase as part of an antiviral drug development programme.

Can your methods for studying influenza be adapted to other types of viruses?

Yes, very much so. We're currently extending our studies from influenza to other related viruses that have a similar kind of polymerase, but infect the cell in very different ways. Together with the Virology Department at the Bernhard Nocht Institute for Tropical Medicine in Hamburg, we're studying the Lassa virus, which sporadically produces local epidemics of Lassa fever in Western Africa, and is very dangerous. More generally, all RNA viruses have an RNA-dependent RNA polymerase, and they're all evolutionarily related. The structure of the core of the enzyme is always the same, and in principle the methods we used can be applied to any of them. Many human pathogens are RNA viruses, including the common cold virus, Ebola, HIV, and SARS-CoV-2, which is causing the current COVID-19 pandemic. SARS-CoV-2 is not in the same family as the influenza virus, but it also has an RNA polymerase that fundamentally works in the same way, because it has to copy its RNA genome. Many people are trying to gain structural insights that will help target the SARS-CoV-2 polymerase for drug development. Developing a completely new drug will take a long time. However, some polymerase inhibitors already developed and tested against influenza or Ebola viruses seem to be active against SARS-CoV-2, and this brings some hope that treatments for COVID-19 may become available soon.

Space oddities: how microbes change beyond Earth

Scientists from EMBL-EBI are working with NASA to design an interactive tool for microbiome data analysis and visualisation

BY OANA STROE

For the vast majority of people, going into space is just a dream or a childhood fantasy. However, a team at EMBL's European Bioinformatics Institute (EMBL-EBI) is helping researchers to get one step closer.

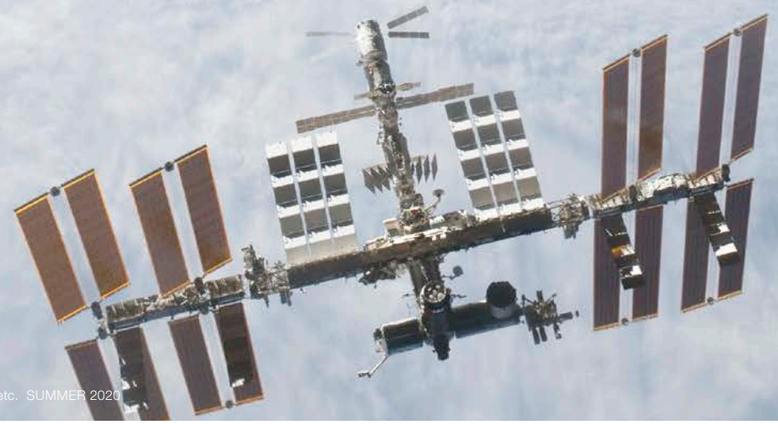
The team that runs EMBL-EBI's MGnify data resource is working with NASA-funded principal investigators on a project called Microbiome Analysis of NASA GeneLab Omics (MANGO). The aim is to collect samples from the International Space Station (ISS) and a range of other environments selected by scientists from the Biotechnology and Planetary Protection Group at NASA's Jet Propulsion Laboratory (JPL), and by members of the team who run NASA's GeneLab project: an interactive, open-access resource where scientists can upload, download, search, share, and analyse spaceflight and spaceflight-relevant omics data.

The data have been collected to help researchers understand how microbial communities adapt to spaceflight, and to explore similar stresses on Earth. Some of the MANGO datasets are openly available in EMBL-EBI's MGnify.

What can space microbes tell us?

On Earth, microbes have adapted to live in almost every environment, and wherever there are humans, there are also microbes. This includes the ISS.

"Project MANGO started by investigating the responses of plants in outer space," explains Richard Barker, Research Scientist at the University of Wisconsin–Madison and a lead team member on the MANGO project in collaboration with the "interplanetary protection team" at JPL. "You can't have plants without microbes, so we decided to investigate the entire ecosystem; that was when monitoring the microbiome on the ISS became really important.



Scientists are studying the microbiome of the International Space Station (pictured) and similar environments.

NASA

"Personally, I think microbiomes in plants are really interesting even on Earth, but framing it in an extraterrestrial context makes it even more exciting. Sometimes you can learn a lot by looking back down from the space station."

Growing plants in space is possible. One of the most recent projects to show this was NASA's Vegetable Production System, affectionately known as the Veggie: a space garden the size of a carry-on piece of luggage, which resides on the ISS. The Veggie can produce lettuce big enough to eat and there are now even more sophisticated systems for growing plants in space. Yet many questions remain about how to make this activity sustainable, not least of which is how the microbiome develops in space and how this then contributes to the plant's success or failure.

The microbial environment is also an important – but not well understood – part of human health. We need certain microbes to survive, while others are known to cause disease. Analysing the communities of microbes on the ISS can help researchers understand how living in space for long periods of time affects the health of astronauts. And this could help us plan for longer journeys.

GeneLab and MGnify join forces

The aim of NASA's GeneLab project is to speed up scientific discoveries from extremely rare and valuable space biology experiments by making the data from these experiments openly available.

"NASA colleagues approached us because they wanted to compare the metagenomic data they were collecting from the ISS to similar data available on Earth," says Alex Mitchell, EMBL-EBI alumnus and previously MGnify Coordinator. "After a few conversations, we agreed that the idea was just crazy enough to work."

MGnify is an EMBL-EBI open data resource that allows researchers to submit, analyse, discover, and compare metagenomic data on genetic material recovered from environmental samples. It's one of EMBL-EBI's fastest growing resources, with over 340 000 publicly analysed datasets, including data from large studies like Tara Oceans and the Earth Microbiome Project.

"Having these MANGO samples analysed in a standardised way by MGnify means the analysis results are easily available for further investigation by the community, but crucially it allows them to be compared with other relevant datasets within MGnify," explains Lorna Richardson, Microbiome Resource Coordinator at EMBL-EBI. "While we know that microbes can and will exploit a variety of habitats, by comparing these space station samples with equivalent terrestrial samples, it's possible to identify any variations in composition or functional potential of the microbiomes in each habitat."

Within the first six months of the collaboration, 10 datasets were added to the MANGO project in MGnify. These datasets include raw sequence reads from swabs from the ISS and the Mars500 habitat during simulated Mars flight and landing. The number of datasets is set to grow over the coming months and years.

Inside closed habitats

The Mars500 project, which took place between 2007 and 2011, was the first full-duration simulation of a manned flight to Mars. For 520 days, six crew members lived like astronauts in a specifically designed and hermetically sealed spacecraft-like environment. One dataset available in MGnify covers the microbial community within the facility during the simulation.

Since the majority of microorganisms identified were not harmful, there were no health concerns. The scientific information obtained by the study is essential for evaluating biosafety risks, predicting and mitigating possible corrosion caused by microbes, and improving the sanitary and hygienic quality of life for crews inside closed habitats.

A universe of possibilities

"It's early days still for this collaboration, but the potential is enormous; we're opening up some incredibly interesting data to the research community," says Alex. "We're hoping people will have a look and be inspired to pursue new and creative research avenues."

While most of us will probably never get a chance to travel into space, the data NASA GeneLab and MGnify are making available are helping life science researchers inch a little bit closer to the stars.

Connecting for a sustainable future

EMBL scientist Katja Ovchinnikova reflects on her participation in the Homeward Bound leadership programme

BY FABIAN OSWALD

The women were making their way through the snow when suddenly the whole group came to halt. In Antarctica, there are many obstacles to consider when travelling by land. The trails are narrow and few, and the unpredictable weather makes it hard to plan ahead. In this case, however, the path was obstructed by nothing more than a tired penguin. Antarctica is full of so-called penguin highways, which humans are not allowed to walk on. Penguins, on the other hand, are free to use human trails – or even lie down on them to get some rest. Instead of disturbing the bird, the group decided to wait for it to get up and continue its journey. For EMBL computer scientist Katja Ovchinnikova, this was an important experience – a glimpse of how humans have to limit their intrusion into nature if they want to coexist with it. This was one of the impressions she took home from a three-week expedition to Antarctica – the highlight of a year-long mentoring programme to prepare women for leadership roles in fields related to science, the environment, and sustainability.

Codes and coral

Katja works as a computer scientist specialising in artificial intelligence. At EMBL Heidelberg, she is a postdoc in the Alexandrov group. Here, she focuses on the computational analysis of data from mass spectrometry – a technology used to analyse the structures of molecules. During her academic career, Katja's work has involved language processing, robotics, artificial intelligence, and computational biology. She has always been driven by a desire to contribute to causes she believes in, which is why she also applies her skills to environmental science. Her current projects include developing software to automatically detect scallops in images of the seabed, in collaboration with the University of St Andrews in the UK, and a project on coral health in collaboration with the University of Hawai'i at Hilo.

When ocean temperatures rise, as a result of climate change, for example, corals expel the algae that live inside their tissues. This is known as coral bleaching. Corals live with these algae in a close relationship, known as symbiosis, in which both species benefit. Without the algae, corals lose their colour and begin to starve, although it is possible for them to recover. "The idea of our initiative is to study the global health situation of coral reefs," says Katja. "We do this using imagery taken by divers and underwater drones. My part in the project is developing computer science methods to analyse these images of coral and detect bleaching." The challenge for Katja and other computer scientists is to develop algorithms that can determine the state of coral health. To do this, they need large amounts of data from different regions of the world, as the species and the conditions in which corals live are very diverse. The project aims to unite various universities and research groups and encourage them to share their data. Coming from computer science, Katja is very aware of the importance of open and shared information. "I need a lot of data to train my algorithms," says Katja, "so I hope I can get people to see the value of sharing and taking on these big projects together."


KARI LYDERSEN

Katja Ovchinnikova in Antarctica.

Antarctica provides a strong example of open collaboration. During her expedition, Katja visited two research stations: Argentina's Carlini Base and China's Great Wall Station. Here, she learned about the Antarctic Treaty of 1959, an agreement that sets aside Antarctica purely for open scientific collaboration, ignoring political differences between nations. Information, data, and even food: scientists share what they need in the harsh conditions of the Southern Continent. >>

"I hope I can get people to see the value of sharing and taking on these big projects together"

Switching scales

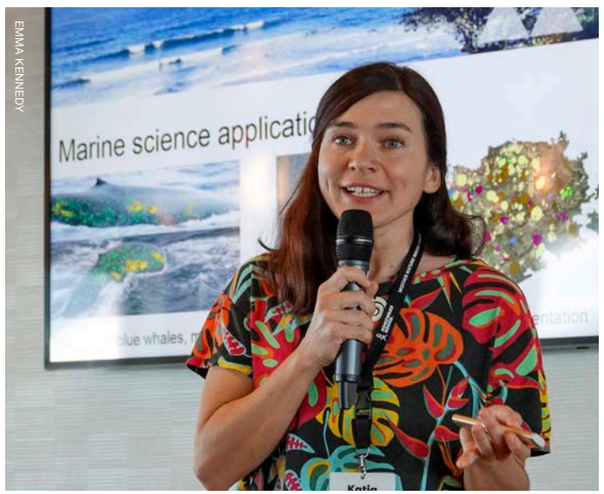
Katja has always been interested in topics relating to diversity and inclusion, and is constantly looking for ways in which science can help human communities and the planet. In October 2019, she organised a Climathon at EMBL Heidelberg. This is an annual event held on the same day all over the world, bringing together developers, engineers, and scientists to tackle local climate-related challenges. During 24 hours, several teams worked on solutions for environmental issues facing Heidelberg.

"I had various ideas and was trying some of them out," says Katja. "But everything was happening on a small scale. I realised that I needed a network of people who are like minded and share my values, but have a different set of skills."

Katja came a step closer to finding that network when her husband received a postcard from Antarctica. It was from a colleague who was participating in a leadership programme called Homeward Bound, aimed at women with a background in STEMM – science, technology, engineering, mathematics, and medicine. This was the first time Katja had heard of the programme. At first, she was sceptical about the kinds of leadership values it might promote, but after reading through the programme description, she realised that the philosophy behind it was very compatible with her own. "Leadership in the context of Homeward Bound refers to being empowered, bringing forward your ideas while staying true to your values, and striving towards positive change," says Katja. Homeward Bound aims to help build a society that is led by men and women equally, with people in leadership positions focusing on a sustainable future, caring for relationships between people, and seeing the world as a home that is shared by everyone. The philosophy of the programme, especially its focus on the environment, is what convinced Katja to apply. After passing three selection rounds, she was invited to join Homeward Bound in November 2018.

Building a tribe

One of the goals of Homeward Bound is to build a strong network of current and former participants. These connections can be used to organise projects and realise ideas with input from people in a diverse range of STEMM fields. In the long run, the aim is for Homeward Bound's support network to include over a thousand women. "We were in the fourth year of the programme, so there were already three groups who had completed it," Katja explains. "And we had access to all of them. It's great because you have your tribe, a community of passionate people – that's so important." Katja's group consisted of 100 women at very different stages of their academic careers; the programme has no age restrictions. Participants ranged from PhD students to institute directors and even retired scientists, who can provide a lifetime of experience to the support network. "The point is that there's absolutely no hierarchy," says Katja. "We're all on the same page, and I think that's just great. It's very difficult to find an environment where a young person, very early in their academic life, can speak like a friend to a senior scientist and share their experience."



EMMA KENNEDY

On the ship, Katja gives a talk about her work.

"I'm much more open to learning new things, taking on new challenges"

The programme was held mostly online, with monthly calls to bring everyone together. The women would listen to talks, communicate via chat, and later be given assignments, which increased over the year. In various online channels they gathered books, videos, and links that offered ideas to consider and discuss. After a year, the programme reached its highlight: the journey to Antarctica.

The Homeward Bound participants met in Ushuaia, the southernmost city in Argentina. From there, they set off on a ship headed south. The three weeks spent together on board built a strong bond between the participants. Expeditions on land were often limited by the unpredictable weather and by strict environmental regulations, so most of the group's time was spent in the confined space of the ship, where they participated in workshops and talks on various subjects, including leadership and the science of climate change. "The range of topics was huge," says Katja. "We talked about marine science and sustainability, how to recover from failure, and how fields like biology and physics can contribute to environmental protection. And we developed a lot of >>

KATJA OVCHINNIKOVA

A group of penguins (foreground) amid the Antarctic landscape.


KARI LYDERSEN

A total of 100 women joined the Homeward Bound group of 2019.

ideas for future collaborations." While the talks and workshops taught them about the Antarctic ecosystem and how important it is to the health of the planet, seeing it with their own eyes created a connection on a much deeper level. It enabled Katja to experience what the Earth might have been like before it began to be shaped by human activity.

Optimism and action

The Homeward Bound programme has inspired Katja to take action in many ways, from organising the Climathon at EMBL to running workshops on climate change and on confronting implicit biases. The network she built up during the programme also offers many possibilities for future projects. One example is the coral bleaching research project, in which several Homeward Bound participants are involved.

"I think the biggest change that came through the programme is my mindset about my future plans," says Katja. "I used to look at what I can do short term, with my skills, in my current life situation. Now, I focus on what I deeply care about, and how I can make a difference in that area. I'm much more open to learning new things, taking on new challenges. And I'm much more optimistic about facing big tasks."

KATJA'S PERSONAL WEBSITE, INCLUDING DETAILS OF HER RESEARCH PROJECTS AND A LINK TO HER BLOG ON HOMEWARD BOUND:
bit.ly/embletc-95-katja

LEARN MORE ABOUT HOMEWARD BOUND AND HOW TO APPLY:
bit.ly/embletc-95-hb

Cultures

Alumni

ALEKSANDRA KROLIK

Welcome: Brendan Rouse

EMBL's new Environmental Officer discusses the role of organisations in responding to the challenges of climate change

BY MARIUS BRUER

Brendan Rouse came to Heidelberg in March as EMBL's Environmental Officer, tasked with monitoring the organisation's environmental impact and promoting sustainable practices. Here, he discusses his plans for the new role.

How did you first get interested in issues relating to the environment and sustainability?
At a very young age, thanks to an old cartoon called *Captain Planet and the Planeteers*. It taught me that polluters are the bad guys and environmentalists are the good guys! I've tried to be a good guy ever since, and decided to study environmental science at university.

What's your professional background?
I've been a sustainability manager for 10 years now. I started at Great Ormond Street Hospital for Children in London, where I was the first Sustainability Manager and was able to develop a sustainability programme from scratch. We saved a lot of money and reduced our carbon footprint. Most importantly, we successfully engaged staff in using sustainability as a way of improving the outcomes for our patients and their families. It was a really inspirational place to work. After five years, I moved into the private sector and worked for two real estate companies in London. It's been interesting to see how private companies now recognise sustainability as a critical factor for their long-term success.

Tell us about your role. What will be your main tasks and projects at EMBL?
I'm joining EMBL at a critical time in the fight against climate change and I see my role as ensuring EMBL responds appropriately to this challenge. I'll be supporting the projects of the Green EMBL Working Group, which was set up in 2019 by EMBL group leaders Detlev Arendt and Kiran Patil. I also want to develop a strategy that demonstrates our commitment to reducing our impacts in line with the United Nations Paris Agreement. Some of the early work will include talking to colleagues throughout the organisation about developing a new travel policy, as well as setting up energy monitoring and reporting tools for the EMBL sites.

How do you think research at EMBL could help to tackle environmental issues?
Around the world, there's been a lot of research on the impact climate change will have on different species and habitats, and EMBL research could also help us to understand these changes by studying their effects on organisms at the level of genes and molecules. It's also vital that EMBL continues to improve our understanding of microorganisms, especially with regard to a warming climate. And it's great to see EMBL's involvement with the Tara Ocean Foundation, which has carried out research on marine biodiversity and the impact of microplastics on marine organisms.


K. LEINWEBER

Brendan Rouse will monitor EMBL's environmental impact.

Do you think we're seeing an increase in people's awareness of climate change?
I definitely think there's been a change in awareness over the past year, fostered by activist movements and environmental disasters. In my work, there was a sudden switch from trying to get people to engage with the subject to being inundated with questions. We can all see how the world is changing around us and feel the uncertainty this brings to our children's futures. The corporate world has responded, too. For example, last year the chief executive of my previous company was giving his annual results presentation, and his second slide was on our sustainability programme. This would have been unheard of only two years ago.

What are the major challenges for organisations in tackling issues around sustainability?
The level of change that's needed is quite hard to grasp. There's often a fear that tackling these issues will lead to organisations losing some competitive advantage. Once this mindset changes and people see the opportunities that being sustainable can bring, that's one major hurdle overcome. There can also be a lack of political continuity, which hinders companies and organisations in developing long-term plans and investing with confidence.

What can research institutes like EMBL do to reduce their energy usage and carbon footprint?
So much! Direct energy emissions from combustion activities can be reduced by making sure our heating plant is running efficiently. For energy that's generated by someone else, we can reduce emissions by controlling our air conditioning systems, turning off lights and equipment when they're not needed, and moving to renewable energy sources. Finally, emissions are generated by the goods and services we use. This category can include a huge number of activities, so one of our tasks will be to decide which of these have the biggest impact on our carbon footprint.

How do you spend your leisure time?
I have two children under the age of three, so I spend most of my leisure time being a father. One of the reasons we were excited to move to Heidelberg was to escape the London rat race and have more outdoor quality time. I'll be looking to join a football or rugby team, take up cycling, and maybe even dust off my skis in the winter.

EMBL's Corporate Partnership Programme celebrates 10 years of impact

As EMBL's Advanced Training Centre passes its 10th anniversary, Corporate Partnership Manager Jonathan Rothblatt reflects on the ATC Corporate Partnership Programme and how it promotes training for outstanding scientists

BY DR. JONATHAN ROTHBLATT

Innovations and breakthroughs in the molecular life sciences thrive on the exchange of new ideas, data, approaches, and tools. Since its opening in March 2010, the EMBL Advanced Training Centre (ATC) has served as a forum for such scientific exchange. An important component of this is the ATC Corporate Partnership Programme (CPP), which aims to connect companies with the latest developments in molecular biology and to build successful long-term relationships between EMBL and corporate partners. Membership in the CPP offers a mechanism for partners to connect and collaborate with EMBL. In so doing, they provide opportunities for talented young research scientists to develop and branch out scientifically. This could include extending their experimental knowledge or tools, honing their analytical or computational skills, or developing personal connections that enable new collaborations.


COURTESY OF JONATHAN ROTHBLATT

Jonathan Rothblatt, Corporate Partnership Manager at EMBL.

The support that industry partners provide, through their membership in the CPP, ensures that outstanding scientists – from PhD students to established investigators – are not excluded from attending a course or conference, or working in an EMBL laboratory as a visiting scientist, because of a lack of funds to cover conference fees or travel expenses. Since 2010, CPP funding has provided fellowships covering registration fees and travel costs to more than 2 100 participants from more than 90 countries, attending more than 350 EMBL or EMBO courses, conferences, or symposia. In addition, the CPP provides funding for the Christian Boulin Fellowships, which help to cover travel and accommodation costs for young research scientists wishing to access EMBL's scientific facilities.

In addition to the significant impact of their financial support, the engagement and collaboration of corporate partners is crucial in the development and delivery of EMBL's courses and conferences. For example, of the 33 training courses held at EMBL Heidelberg in 2019, 11 were co-organised with CPP partners. Another example is the EMBL Conference 'Expanding the Druggable Proteome with Chemical Biology', which took place in February. This conference, co-funded by the CPP, explored advances at the interface between academic and industry research. The scientific organisers included two CPP partners alongside academic leaders in the field.

The CPP works closely with the EMBL International Centre for Advanced Training (EICAT) External Scientific Training team, supporting EICAT's commitment to offering the highest quality of scientific training and the broadest access to its programmes for outstanding life scientists from EMBL's member states and around the world. The strong involvement of EMBL scientists at all levels is another crucial factor in enabling the CPP to establish and develop mutually beneficial relationships with its corporate partners. Internal cooperation and teamwork sustain the spirit of open scientific communication and support for technology transfer that attracts CPP partners to begin collaborations with EMBL.

The alliance of the CPP with its corporate partners is one facet of EMBL's engagement with industry – in particular the life sciences business sector. This compliments the activities of EMBL's technology transfer partner EMBLEM, the EMBL Course and Conference Office, the EMBL-EBI Industry Programme, and direct interactions with industry partners by EMBL group and team leaders and heads of core facilities.


MASSIMO DEL PRETE/EMBL


MASSIMO DEL PRETE/EMBL

A signature scientific networking event bringing together CPP company leadership and a cross-section of the EMBL scientific community, the annual Corporate Partnership Programme Meeting, held in February, centred on the theme of infection biology.

With two new partners joining the CPP in 2019 and another already this year, the CPP has grown to 19 members, bringing together EMBL and global leaders in a range of business sectors, including biopharmaceuticals, diagnostics, information technology, research and clinical instrumentation, and laboratory products. We look forward to seeing the programme continue to evolve and grow in future years, always striving to deliver outstanding value and maintain its impact on the future of science.

For further information, contact Jonathan Rothblatt (jonathan.rothblatt@embl.de, +49 6221 387 8799), or visit embl.org/cpp.

Local science news

EMBL alumnus Veli Vural Uslu tells his story of branching out to talk and write about science

BY VELI VURAL USLU

(Above) Dalyan is a small farming and fishing town surrounded by pomegranate fields, high rocky mountains, and the Mediterranean.

Explaining science to non-scientists is a challenge. But a bigger challenge for me is explaining it in my native southwestern Turkish dialect. For almost a year, I've been writing a weekly science column in a local newspaper – *Güneyege* – distributed in Dalyan, the small fishing town where I grew up. The column has already reached 45 000 online clicks and the payback has been priceless: while walking through the main street on the first day of my holiday in Dalyan, a fisherman ran out of his tiny shop with his apron on. He said he loved the column and handed me a bag full of fish as a present. In the following days I kept on receiving other gifts, like oranges from a very old farmer and a bag of eggs from my parents' neighbour, just for writing a weekly science column. How did this happen?

One of the most life-changing experiences during my PhD at EMBL took place in the last two minutes of my second-year thesis advisory committee meeting. My legs were shaky and my ears were burning after our intense discussion of the project. EMBL alumnus Jochen Wittbrodt – a group leader at Heidelberg University and chair of the committee – put his brand new iPad on the table very gently. He took a deep breath and I knew that he was phrasing a remark in his head in the most polite and constructive way possible. He was sure the project was very promising, he said, and there had been substantial progress since the year before. But the way I delivered the presentation was bad. Very bad.

At the end of the meeting, as I was about to follow Jochen and the other committee members out of the room, my boss – François Spitz – held my arm. I felt a cold shiver, but François gave an encouraging speech and suggested that I join an EMBL course on presentation skills. It was this course that fired my passion for science communication. Not only did I learn how to communicate science, but I realised how much I enjoy using science to create everyday stories.

During my postdoc years at Heidelberg University, I began writing science stories and giving scientific talks for non-scientists around Germany. In 2018, I joined FameLab, one of the biggest science communication competitions in the world. After regional qualifications, I became national champion and represented Germany in the international final in England. There, I talked about how viruses have become a vital part of our genome. This story made me the runner up, bringing an award to Germany for the first time in the history of the competition. A few days later, a journalist in my hometown wrote about my success in FameLab in *Güneyege*.

Coming from a small town of 5 000 people, such media coverage makes the inhabitants very proud, although most people in Dalyan didn't have the slightest idea about the content of the science stories I told in the competition. But maybe it was not simply a lack of interest; rather that science had never been presented in the local dialect using everyday language in an entertaining way. So, in July 2019, I wrote my first column, on a *Nature* paper about quantum entanglement. The reaction was totally unexpected. Nebi Tunç, a chauffeur who used to work for the mayor, wrote me a beautiful message: probably he understood the text, for sure he loved it, certainly he would share it. I got several other encouraging messages from readers. Since then, I've written more than 40 articles on subjects ranging from retroviruses to the Higgs boson, X-chromosome inactivation to CRISPR and coronavirus.

Recently the editor of *Güneyege*, Cihat Cura, told me that the readers of my column are mostly between 40 and 65 years old, which came as a surprise to me. He said that they were not necessarily craving science at the beginning, but they were happy to read a column written by a successful person from the region. Almost a year after my first article, the readers have grown preferences for certain subjects. Some of them like reading about illnesses and are fascinated by the diversity of tumour cells, while others are amazed by bigger projects like the Large Hadron Collider or LIGO, which comprises two kilometre-scale instruments that were the first to detect gravitational waves. Of course, there have also been some negative comments: that the articles are still too complicated or that some of them focus on very specialised subjects – like the history of restriction enzymes – for which some readers said they couldn't care less.

To make sure the content is accurate, Dr. Zeynep Sena Agim, a Turkish scientist at the University of Massachusetts Medical School, does the fact checking and final editing of the texts. And, depending on the subject, several specialists – including another EMBL alumnus, Dr. Murat Iskar at the German Cancer Research Center (DKFZ) – give extensive feedback.

The column is a rather short text of 500–600 words. In the newspaper layout, it's surrounded by local news like "watermelon prices have gone up", "policemen warn motorcyclists who were not wearing helmets", or "daughter of previous mayor gets married". I'm fascinated that science is not a separate section, but anyone who is curious about their neighbourhood will come across science too. I really wish that science and scientific thinking could become a part of everyday life.

Since February 2020, I've been writing similar articles with Dr. Agim in *Diken*, a national newspaper with more than a million Twitter followers. Now we reach many more people with our science stories. But the local science column in *Güneyege* is still running. I think nothing is more fascinating than seeing my article about Peer Bork's *Nature* paper on enterotypes – cited over 4 500 times – right next to a column about a girl who found her cat again after three weeks.

DMYTRO DVORNIKOV

Veli Vural Uslu speaking at a science communication event in the Theater im Romanischen Keller at Heidelberg University.

EMBL Director General Edith Heard.

Awards & honours

Group leader **Isidro Cortés-Ciriano** has received the second MGMS Frank Blaney Award from the Molecular Graphics and Modelling Society, UK. The Award supports outstanding postdoctoral and young independent researchers.

Associate Director of EMBL-EBI Services **Paul Flicek** has been named a Fellow of the International Society for Computational Biology, in recognition of his status as a leading figure in the field of genomics, for his work to promote open data practices, and for his tireless efforts advocating for equal opportunities for women in science.

Edith Heard, EMBL Director General, has received a L'Oréal–UNESCO For Women in Science Award for her fundamental discoveries about the mechanisms governing epigenetic processes. The Awards are presented annually to five exceptional women scientists from different regions of the world. **Edith Heard** has also been made a Doctor of Science *honoris causa* by Cambridge University.

EMBL Director **Matthias Hentze** has received the 2020 RNA Society Lifetime Achievement Award, in recognition of his longstanding contributions in the fields of RNA biology and gene regulation. In addition to his scientific contributions, Matthias is recognised for his leadership, training, and mentoring of hundreds of young scientists at EMBL and throughout Europe.

Judith Reichmann, a Research Scientist in the Ellenberg group, has received the 2020 Paul Ehrlich and Ludwig Darmstaedter Prize for Young Researchers. The prize, awarded by the Paul Ehrlich Foundation, Germany, is given to scientists from anywhere in the world who have achieved outstanding results in biomedical research.

Group leader **Michael Zimmermann** has received a scholarship from the Daimler and Benz Foundation, Germany. These scholarships are awarded to selected postdoctoral researchers, junior professors, or heads of junior research groups, with the aim of reinforcing the autonomy and creativity of the next generation of scientists.

Alumni

Reaching out to the community

For us, like everyone, the coronavirus pandemic has brought new, unexpected challenges. But this challenging period has also been one of opportunity, togetherness, and creativity.

The new landscape has inspired us to utilise communication technology more than ever before, enabling us to reach alumni worldwide 'face to face'. Thanks to the launch of 'Coffee with EMBL', our regular digital discussion forum, we've reached groups who could otherwise not join our physical events due to geographical location, age, or other reasons. While most of our physical 'EMBL in...' event programme has been postponed until 2021, 'Coffee with EMBL' has quickly established itself as a popular platform through which to connect, share, and debate topical insights. Thank you to alumnus and moderator Angus Lamond for making this possible!

Stories of alumni supporting efforts to combat the pandemic have continued to inspire us (p. 46); a reminder of how the EMBL spirit endures through its community.

Before COVID-19 curtailed international travel, we were delighted to host the newly elected EMBL Alumni Association Board in Barcelona for their first meeting in January. Chair Fátima Gebauer shares future plans, and how EMBL can better support its alumni (p. 42). The next board meeting will take place online on 17 July. It will be followed by a live stream of the 2020 Alumni Awards (p. 44) and EMBL World Alumni Day, which this year will focus on planetary biology and environmental research, building on EMBL's expertise and moving towards an understanding of organisms in their environments from atoms to ecosystems.

Mehrnoosh Rayner
Head of Alumni Relations

Coffee with EMBL

In response to the keen and sudden demand among alumni for digital events, the first 'Coffee with EMBL' took place via videoconference on 24 April, with 150 participants joining from 35 countries across the globe.

It provided informal but rigorous debate, with guest speakers from EMBL and the alumni community offering expert insight into the biology of the coronavirus and the state of play globally.

Five further sessions have taken place since, covering topics ranging from how biotech companies are meeting new needs to whether drugs used for the treatment of flu can be repurposed to treat coronavirus patients.

EMBL is grateful to Angus Lamond for moderating the events, and to everyone who has joined as a speaker or participant.

We look forward to continuing and evolving this format to meet your needs. Alumni are encouraged to contact us with feedback and suggestions at alumni@embl.org.

How EMBL can support its alumni

Fátima Gebauer, Chair of the EMBL Alumni Association, discusses the results of the recent alumni survey

BY TOM FURNIVAL-ADAMS

After a new EMBL Alumni Association (EAA) Board was elected in May 2019, incoming members were keen for their activities and aims to be endorsed by feedback from the community. This is why incoming Chair Fátima Gebauer asked the Alumni Relations team to conduct their three-yearly alumni survey to coincide with the first meeting of the new board. "It enabled the board to have immediate feedback from the whole alumni body on initiatives the board wanted to introduce," she says.

Fátima, who was a postdoc and later a staff scientist in the Hentze group at EMBL Heidelberg, is now a group leader at the Centre for Genomic Regulation (CRG) in Barcelona. She has been an EAA Board member since 2016, and is keen to ensure that all alumni are aware of the opportunities available to them. "EMBL has helped me a lot," she explains. "I think it can have as positive an impact on the life of other alumni as it's had on mine. I'm very happy to work for the community to make this relationship better for everyone."

Career support, sabbaticals, and mentoring opportunities

The results of the survey, 'How EMBL can support you', highlighted some clear needs; the most widespread being demand for sabbatical opportunities at EMBL, as well as more career support and mentoring opportunities for staff and alumni. These formed the basis of discussions at the first meeting of the new EAA Board at EMBL Barcelona in January. The box at left gives the top five items alumni voted as most important to them.

Members decided that the first step would be to form working groups: one led by Anne-Sophie Huart and Ramesh Pillai on exploring opportunities for training, sabbaticals, and internships at EMBL, and another led by Marina Chekulaeva and Anne-Marie Glynn, on a potential alumni advisory programme for EMBL staff and alumni.

Most requested resources by alumni

1. Sabbaticals at EMBL
2. Help with grants
3. Leadership training
4. Mentoring

5a. EMBL faculty-level lectures at alumni institutes

5b. Alumni faculty-level lectures at EMBL

Fátima Gebauer, Chair of the EMBL Alumni Association.

"I think EMBL can have as positive an impact on the life of other alumni as it's had on mine"

"The working groups are now working closely with the Alumni Relations team to contact relevant people at EMBL," says Fátima, "and explore what already exists, what can be further developed and implemented, and how best to improve the way we communicate these." At their next meeting in July, the board will assess their findings and establish a plan based on their recommendations.

The survey also allowed EMBL to identify a large group of alumni volunteers offering concrete suggestions on how they can help with the initiatives that support alumni. This list is being reviewed and alumni who offered to volunteer will be contacted once the needs arise.

Better communication with alumni

The need to more effectively communicate about EMBL resources and opportunities for alumni was a point that came up both in the survey and in the discussions at the board meeting.

"Some of the needs identified through the survey could be simply addressed if alumni were made more aware of what already exists," says Fátima.

Work is already under way to improve the EMBL website, and a brochure is being developed that better presents the resources available to alumni. Furthermore, there will be articles and dedicated emails communicating opportunities and benefits available to all.

The Alumni Relations team will also conduct a survey exploring the effectiveness of EMBL's communications channels and content with its alumni, which will inform future communications strategy.

Meanwhile, Fátima is looking forward to leading the board in the coming years. **"**I hope that, during this term, we really strengthen the synergistic relationship between EMBL and its alumni," she says, "and that alumni realise how positive the impact can be, both on the life sciences and on them personally."

The new EMBL Alumni Association Board met for the first time in Barcelona in January.

EMBL Alumni Awards 2020

Committee recognises outstanding contributions of EMBL alumni to science journalism and genome editing

BY MARIUS BRUER

The winners of the 2020 EMBL Alumni Awards were selected earlier this year. Giorgia Guglielmi wins the John Kendrew Award for her journalism work focusing on the intersection of science and society, while John van der Oost wins the Lennart Philipson Award for his contributions to our understanding of the genome editing tool known as CRISPR–Cas. Here, the awardees discuss some of the defining moments in their careers.

AMANDA MACCHIA PHOTOGRAPHY

Giorgia Guglielmi, winner of the John Kendrew Award.

"It was at EMBL that I realised I could combine my passions"

Combining two passions

Giorgia Guglielmi has always been fascinated by how an embryo develops into a mature organism. In 2011, she joined the group of Stefano De Renzis at EMBL Heidelberg to investigate embryonic development. Besides her passion for science, Giorgia felt a strong interest in communication. "In high school, my dream was to become a journalist. Then I fell in love with science," she says. "It was at EMBL that I realised I could combine my passions."

In 2016, having earned her PhD, she applied successfully for a spot in MIT's prestigious Graduate Program in Science Writing. In the thesis she wrote as part of the course, Giorgia investigated how misinformation had led to the death of millions of olive trees in the Italian region of Apulia, where she was born. The report won her an MIT Stanley Klein Prize for Scientific Writing. After graduating from MIT in 2017, she had the opportunity to work in the newsrooms of *Science* and *Nature*.

Striving for facts

Covering the societal aspects of scientific research is at the heart of Giorgia's work. She wrote about alleged irregularities in a homeopathy study that was later retracted, and reported about a donation from the Italian National Order of Biologists (ONB) to a group that questions the safety of vaccines. The donation has since been withdrawn. "This kind of work can be stressful, but it's very satisfying to see that my stories are read by thousands of people, and that they sometimes even influence science policy," says Giorgia.

Giorgia now works as a freelance science journalist in Cambridge, Massachusetts. Her writing has recently focused on diversity, exploring gender imbalances in science and the under-representation of indigenous populations and other marginalised groups in genomic studies. Giorgia sees receiving the John Kendrew Award as a signal that rigorous science communication is important and valued. "I'm grateful to the committee for supporting independent science journalism," she says. "That's a huge encouragement for me to keep going."

Enabling genome editing

John van der Oost has spent most of his scientific career studying bacterial enzymes. In 1990, his postdoctoral training in the group of structural biologist Matti Saraste brought him to EMBL Heidelberg. John later started his own research group at the University of Wageningen in the Netherlands.

While studying *Sulfolobus*, a microorganism that lives in extreme environments such as hot springs, John and his team discovered unexpected stretches of repetitive DNA among its genes. These DNA regions appeared to contain fragments of viral DNA, an adaptive defence system against bacteriophages – viruses that infect bacteria. John had stumbled upon the system now known as CRISPR–Cas: a powerful genome editing tool that biologists can use to target a specific DNA region.

In the years that followed, John and his team made a series of seminal discoveries that explain how the CRISPR–Cas system works. Most importantly, they managed to transplant the entire system to another bacterial strain and succeeded in programming it to protect the recipient bacteria against a specific bacteriophage – a 'flu shot for bacteria'. With these results, John had found the key ingredients to enable genome editing applications. The initial results were published in 2008, but it took John and colleagues another 11 years to optimise their system to work in human cells. They finally succeeded in 2019.

PAULIEN VOS

John van der Oost, winner of the Lennart Philipson Award.

"I could never have predicted that I would end up where I am now"

Keeping an open mind

Meanwhile, John has continued to explore bacterial genome editing mechanisms. The potential applications are manifold. CRISPR has already revolutionised life science research and is likely to have a similar impact on biotechnology and healthcare. Reflecting on his career, John points out the huge impact that chance and unexpected developments have played. "I could never have predicted that I would end up where I am now. It's a matter of keeping your eyes open and looking for opportunities," he says. "But I think this uncertainty is also what makes science one big adventure."

WATCH THE VIRTUAL ALUMNI AWARDS PRESENTATION AS PART OF EMBL WORLD ALUMNI DAY ON 17 JULY: bit.ly/embletc-95-wad2020

Alumni responses to the coronavirus pandemic

EMBL is proud that members of its community are finding creative and impactful ways to support global efforts to tackle the COVID-19 pandemic. Here, we share stories from just a few of the many alumni who've been aiding research efforts and government responses where they are.

FURTHER STORIES AND THE LATEST UPDATES ONLINE:
bit.ly/embletc-95-responses

Fátima Gebauer

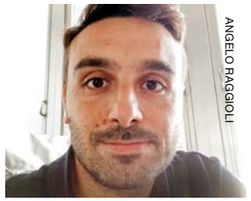
Group Leader, Centre for Genomic Regulation (CRG), Barcelona, Spain; Postdoc, EMBL Heidelberg, 1996–2000

"The CRG is doing SARS-CoV-2 tests for the citizens of Barcelona, has donated kits and other necessary materials (coats, gloves, masks) to hospitals, and has offered trained manpower to local and national authorities. We have a Crisis Committee that deals with all COVID-related issues relevant for our community and beyond, which operates 'on the minute', and in which EMBL alumni participate." (11 April)

Angus Lamond

Professor of Biochemistry, University of Dundee, UK; Group Leader and Senior Scientist, EMBL Heidelberg, 1987–1995

"I received a phone call from 10 Downing Street, as the UK government was busy setting up an emergency national virus testing lab. They decided to approach university research labs and ask if researchers were willing to donate equipment. I have two liquid-handling robots in my lab, which were described as being 'like gold dust'. Of course I agreed to give them to the government, so I packed them up and met a team from the Royal Navy who were sent to collect my equipment and rush it to the new facility near London. Fingers crossed it may help a little."
(22 March)



Angelo Raggioli

Head of Vectorology, ReiThera, Rome, Italy; Postdoc, EMBL Rome, 2014–2019

"At ReiThera we are developing a vaccine against SARS-CoV-2, named GRAd-COV2, using an adenovirus-based platform similar to the one that proved successful in 2014 during the Ebola outbreak in Africa. The GRAd-COV2 vaccine leverages the knowledge and expertise acquired, among others, by EMBL alumni Riccardo Cortese, Alfredo Nicosia, and Alessandra Vitelli, to design, engineer, and manufacture adenoviral vector-based vaccines. The vaccine against the novel coronavirus should hit phase I/II clinical trials starting July 2020. We are definitely thrilled by the opportunity to make available our know-how to find a solution to get out of this threatening pandemic."
(22 April)

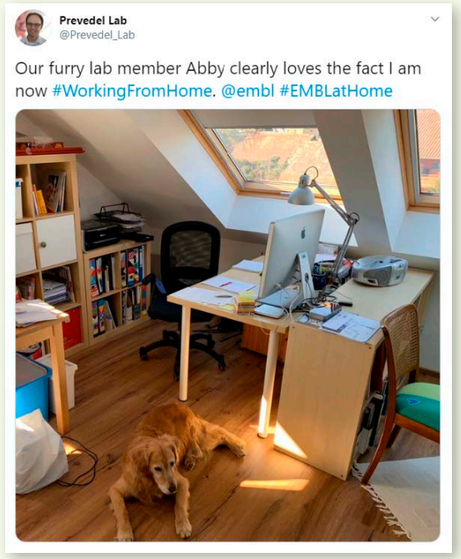
Xiushan Yin

Karolinska Institutet, Stockholm, Sweden; Postdoc, EMBL Heidelberg, 2009–2010

"Vicente Pelechano, Weihua Chen, and I – all EMBL alumni – are helping Africa, Pakistan, Israel, and other countries with test methods and kits. Our company also donated RT-qPCR kits [used to test for coronavirus] covering more than 20 000 people, and we will continue working with NGOs to provide donations and free technical support. If other countries urgently need this kind of help, we would be happy to provide it. Maybe through the alumni group we can expand the EMBL alliance against COVID-19."
(25 March)

#EMBLatHome

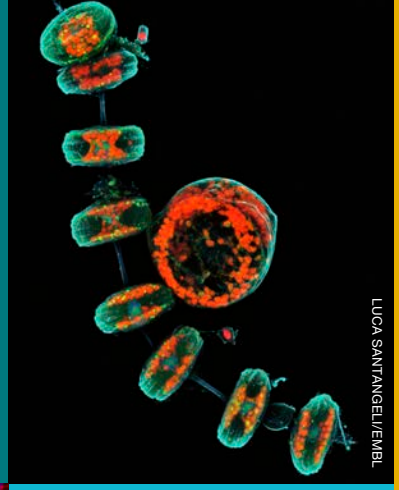
In March, as many of us made the transition to remote working, staff across EMBL's sites found new ways to connect. On Twitter, members of the EMBL community used #EMBLatHome to share how their daily life had changed and what they were doing to stay motivated.



Events

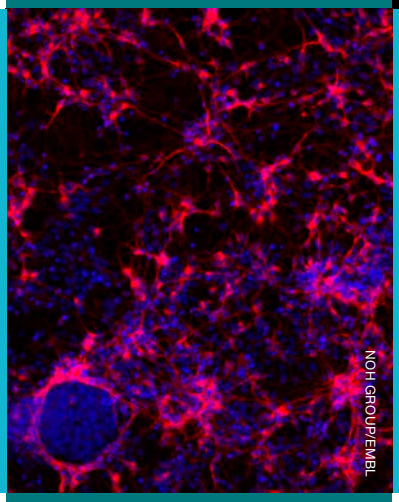
July
13–15

Virtual
EMBL Conference:
Microfluidics: Designing the Next Wave of Biological Inquiry


LUCA SANTANGELI/EMBL

August
27–29

Virtual
EMBL Conference:
Transcription and Chromatin


NOH GROUP/EMBL

September
1–4

Virtual
EMBL Course:
Gene Expression at Spatial Resolution

Upcoming meetings
Alumni

17 July
Virtual: EMBL World Alumni Day and Alumni Awards Ceremony

Virtual: Coffee with EMBL
31 July
18 September
16 October
13 November
11 December

bit.ly/embletc-95-cwe

September
3–5

Virtual
EMBO Workshop:
Chemical Biology 2020

September–October
28–2

Virtual
EMBL Course:
Mathematics of Life: Modelling Molecular Mechanisms

October
13–15

Virtual
EMBO | EMBL | HHMI Conference:
Gender Roles and their Impact in Academia


NICOLAS PESCHKE/EMBL

November
4–5

Virtual
EMBL Science and Society Conference:
Our House is Burning:
Scientific and Societal Responses to Mass Extinction

VIEW THE COMPLETE LIST OF EVENTS ONLINE:
embl.org/events