UNIVERSITY OF COPENHAGEN
NOVO NORDISK FOUNDATION
CENTER FOR PROTEIN RESEARCH

Annual Report 2021

Novo Nordisk Foundation
Center for Protein Research

COLOPHON

ABOUT

Novo Nordisk Foundation Center for Protein Research (CPR) was founded in 2007 at the Faculty of Health and Medical Sciences, University of Copenhagen, to promote basic and applied discovery research on human proteins of medical relevance.

The establishment, growth and continuation of the center has been possible thanks to unprecedented and repeated financial support by the Novo Nordisk Foundation as well as through significant contributions from the University of Copenhagen.

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Becoming a world-leading protein explorer

The ambition of CPR is to be a world-leader in exploring how proteins drive fundamental biological processes in humans. The research can ultimately lead to new ways to diagnose, prevent and treat diseases.

CPR has a unique strategy to tackle the challenge of how proteins drive fundamental biological processes in humans by interdisciplinary research and the development of new technologies. The center combines three different approaches to reach its goal to become a world-leading protein explorer:

- Develop and combine under one roof the broadest possible spectrum of state-of-the-art protein technologies combined with high-end computation and big data management
- Perform highly effective technology-driven and mechanism-oriented protein research
- Translate basic discoveries to health care.

CPR STAFF

At the end of 2021, CPR employed 235 staff members from 39 different countries compared to 222 at the end of 2020. CPR employees fall into three main categories: scientific personnel, research support and administrative support, of which scientific personnel constitute 73%.

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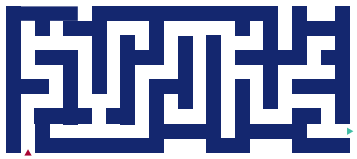
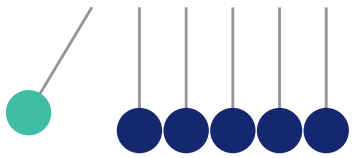
AMBITION

TECHNOLOGIES



CHALLENGE



IMPACT

NUMBERS

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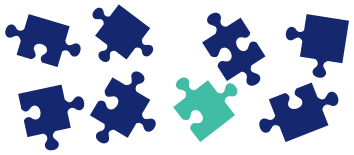
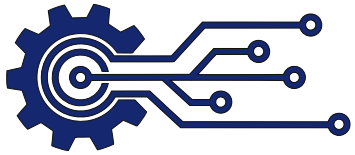
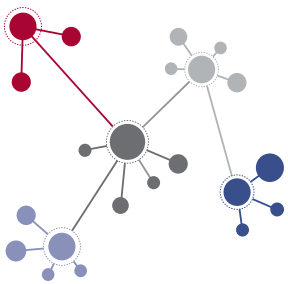
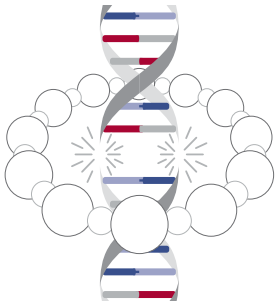
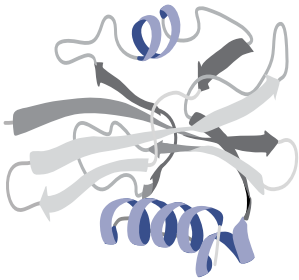
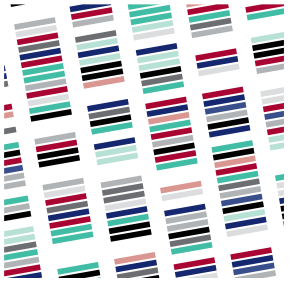




Combining technologies to grasp the protein world

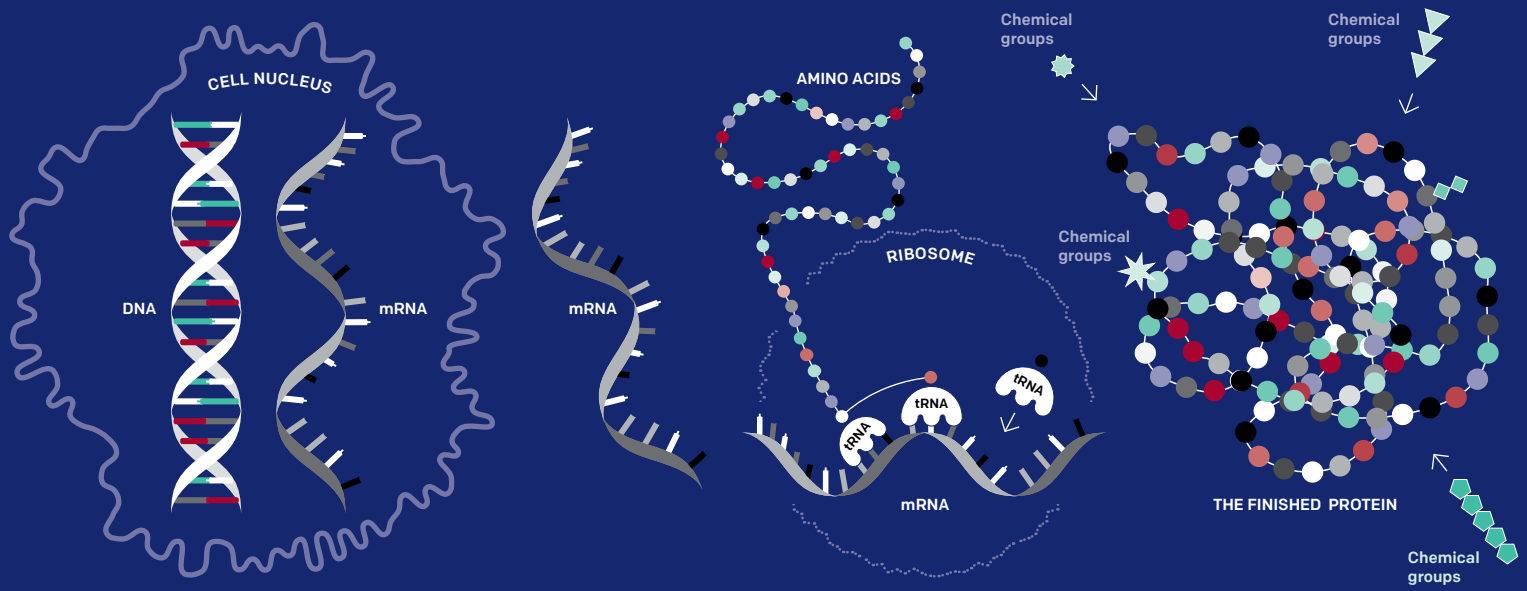
The technologies available in CPR span the entire spectrum from mapping all protein variants in a cell to vizualising how individual proteins assemble in functional networks that drive fundamental physiological processes. This allows for a highly collaborative and interdisciplinary research environment where the different research areas cross-fertilize and bring together different approaches to explore and understand proteins.

Technology	Mass spectrometry	Big data management and analysis	Protein imaging	Cryo-electron microscopy and x-ray crystallography	Functional genomics
	Analyzes all protein variants in a sample.	Predicts how proteins interact and cooperate.	Investigates protein function in living cells.	Deciphers the structure of individual proteins and protein complexes.	Explores genome organization and function.
					
What the technology can do?	Reveals the identity and amounts of proteins and their modifications in a biological sample by measuring the mass-to-charge ratio of ions.	Indicates how proteins function and vary across the population by generating and analyzing molecular interaction networks in health and disease.	Tests the function of selected proteins /protein networks in live cells by light microscopy and image analysis. Visualizes how proteins move around over time, how they interact and the effects on the cell.	Studies molecules and molecular interactions by the use of biophysical instruments. The structure and biophysical features of a protein reveal how it moves, how it interacts with other molecules, and more.	Uses DNA sequencing to understand genome function and how proteins provide epigenetic information, which is passed on to daughter cells to maintain cell identity and fate in next cell generation.
How the technologies interrelate at CPR	Mass spectrometry produces a list of proteins present in the sample for further processing by big data analysis.	Big data analysis integrates data sets collected from proteomics and other omics technologies, health data and more - and supports hypothesis generation for further testing in the laboratory.	Microscopy is used to investigate and functionally complement the results from mass spectrometry and big data analysis.	Protein characterization and structural studies contribute to the understanding of a protein's function, thus complementing all other protein technologies at CPR.	In a cross-disciplinary approach, functional genomics is combined with CPR technological strongholds such as proteomics, structural biology, and big data analysis to reveal protein function in genome regulation.

The quest to understand the human proteome

While the basics of the human genome, the DNA, was roughly mapped in 2001, the expression of the DNA in proteins – the human proteome – is still widely unexplored. With potentially millions of different protein variants in the human body, it is a huge challenge to find the key players relevant for disease diagnosis, prevention and treatment. CPR has taken up this challenge to lead the way for new treatments in the clinical world.

HOW PROTEINS ARE MADE IN A CELL



THE DNA HOLDS THE CODE

DNA is composed of a series of four alternating bases that define our genetic sequence. It contains around 20.000 genes that code for the expression of an unknown number - potentially more than a million - of protein variants, which regulate most functions in the human body.

→ THE mRNA TRANSPORTS THE CODE

The production of a specific protein begins when the DNA of a gene is copied into an mRNA molecule - a messenger RNA - which contains the code for the protein. The mRNA transports the protein code from the cell nucleus into the cytoplasm of the cell. It brings the code to the ribosome, the 'protein assembly line'.

→ THE RIBOSOME ASSEMBLES THE PROTEIN

The ribosome translates the code brought to it by the mRNA. Every sequence of three bases carries a signal for tRNAs – transfer-RNAs - to bring a specific amino acid to the ribosome and place it in an exact spot in the chain of acids that builds the protein like pearls on a string. Proteins are made out of a total of 20 different amino acids.

→ THE PROTEIN IS MODIFIED AND READY

In the final stage, the chain of amino acids is cut, folded and brought to a three dimensional shape. A variety of chemical groups are added by enzymes (other proteins) providing the new protein with its final distinctive structure, function and activity. These 'post-translational modifications' (PTMs) dramatically diversify the protein pool in the human body that contains potentially millions of different protein variants.

WHAT PROTEINS DO

Proteins run the human body in myriad ways. If you look into a medium-sized cell of a human, you find billions of proteins at work. All proteins perform a job of importance for human life and health. Sometimes errors occur and cause illness. In fact, most diseases manifest at the level of proteins, and most drugs target proteins or are proteins themselves.

Proteins take care of many different functions in the body.

They are:

- **enzymes** – or socalled biological catalysts - that speed up chemical processes – such as the addition of post-translation modifications to new proteins.
- **receptors** that bind to specific ligands in their environment and forward this signal to other molecules – such as the receptors in the nose that bind to odor molecules and convey this information to the brain.
- **transporters** that take molecules from one place to another – such as hemoglobin bringing oxygen from the lungs to the muscles.
- **structure builders** that hold together cells and tissue as a scaffold – such as collagen holding together the cells of the skin.
- **hormones** that travel the bloodstream to stimulate specific cells or tissues – such as insulin from the pancreas that promotes glucose uptake in liver, muscle and fat.
- **antibodies** that detect pathogenic bacteria and viruses in our body as part of the immune system.
- **contractile proteins** that allow biological structures to contract– such as myosin and actin that make up the majority of muscle tissue.
- **storage** that serves as biological reserves - such as ferritin that stores iron inside the cell.

Staying on mission to maximize impact of fundamental protein research

Generous funding from the Novo Nordisk Foundation enables CPR to recruit the best minds and maintain state-of-the-art technology. To acknowledge this privilege, we take utmost care to ensure that we continuously follow our mission to convert protein technology to discoveries with the strongest possible impact on society.

One of the most important tools CPR uses to maintain scientific excellence is quinquennial review of research group leaders and their group's scientific achievements and performance. At a one-day site visit, top international experts provide constructive feedback to the group leader towards developing the most successful research and leadership strategies. Based on this regular evaluation, CPR's management decides on the financial allocation to the group. In the last few years, six group leaders were evaluated and we are extremely proud that they were all rated with the highest score ('outstanding') as some of the most prominent scientists in their fields worldwide.

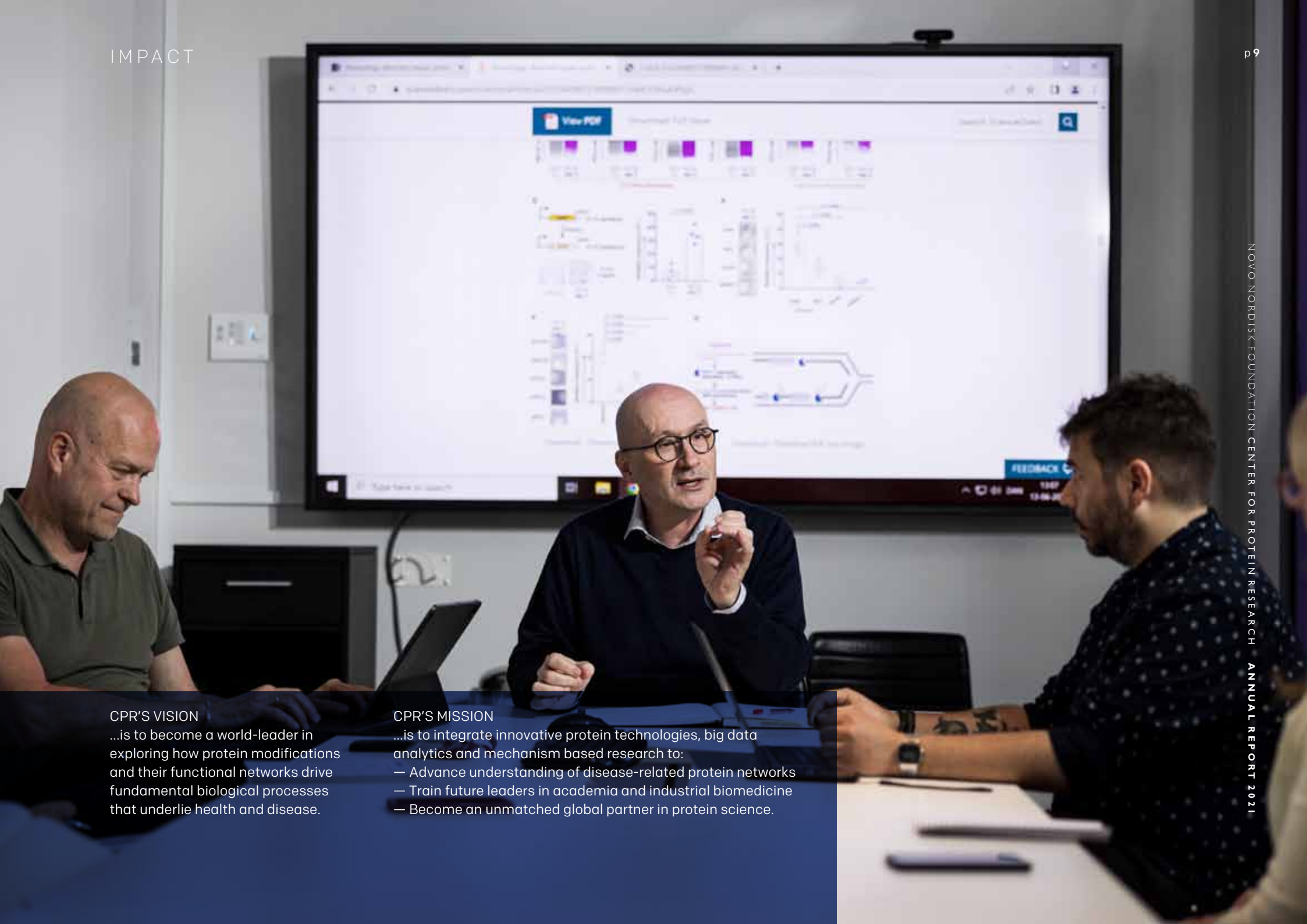
To strengthen scientific excellence in structural biology and epigenetics, CPR welcomed two new group leaders in 2021: Eva Kummer in the Protein Structure and Function Program (p. 36) and Nils Krietenstein in the Protein Memory Program (p. 30). To ensure best practice in these recruitments, CPR participated in a cross-university initiative to increase diversity in group leader recruitments and minimize the influence of unconscious bias (p. 22).

At CPR, we are strong advocates for the societal value of basic research in its own right. This year, the Choudhary Group published a study that fundamentally changes the understanding of how cell type-specific genes are activated and deactivated at the right times in either fetal development or in response to internal or external environmental factors. It is the cell-type specific genes - which constitute approximately half of all human genes - that allow complex organisms to produce completely different cell types such as liver, blood and brain cells, despite all these cells sharing identical genetic material. The study received a lot of attention in the global scientific community and now 'genetics textbooks need to be rewritten', to quote a news story by ScienceNews.dk.

We are proud that as a natural extension of our passion for basic research, CPR continues to be very successful in fostering translational medical research. An excellent example is a study by the Brunak Group that analyzed over one billion prescriptions issued by Danish general practitioners and identified common prescription trajectories of patients that shift between drugs prescribed for the same disease. This allowed them to compare survival statistics for different groups of patients, which could for example help identify suboptimal prescription patterns. The plan is to link the dataset to genetics to better predict which drug will likely be best to start with for a given patient, which can help Danish health personnel improve disease management of individual patients.

Guided by CPR's mission to train future leaders in academia and industrial biomedicine, we have a strong focus on building and strengthening a productive and inclusive leadership culture at CPR. In 2021, all managers attended leadership development workshops customized to CPR. The workshops created a common opportunity to share ideas and reflect on the center and its leadership culture. To leverage these efforts, CPR will from 2022 offer annual workshops in leadership and management skills for our senior postdocs and assistant professors.

Jiri Lukas
Executive Director and Group Leader
Novo Nordisk Foundation Center for Protein Research



CPR'S VISION
...is to become a world-leader in exploring how protein modifications and their functional networks drive fundamental biological processes that underlie health and disease.

CPR'S MISSION
...is to integrate innovative protein technologies, big data analytics and mechanism based research to:
— Advance understanding of disease-related protein networks
— Train future leaders in academia and industrial biomedicine
— Become an unmatched global partner in protein science.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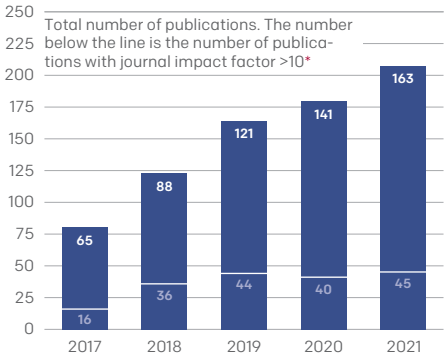
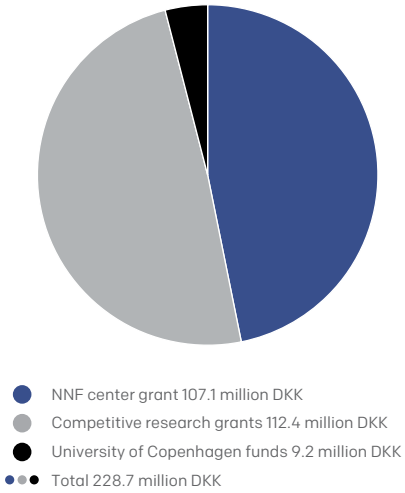
Selected numbers: CPR activities in 2021

No. of publications



* The journal impact factor (Web of Science) is an indicator calculated annually for peer-reviewed journals. The impact factor of a journal indicates the average yearly number of citations received per article published in that journal during the two preceding years.

Annual funding and distribution



- NNF center grant 107.1 million DKK
- Competitive research grants 112.4 million DKK
- University of Copenhagen funds 9.2 million DKK
- Total 228.7 million DKK

No. of courses

No. of attendees

	Under graduates	PhD students	Post-docs	Mixed Audience**
CPR organized and co-organized	3 • *79*	2 • *42*	3 • *40*	2 • *60*
Faculty of Health and Medical Sciences at UCPH*	20 • *955*	6 • *264*	1 • *10*	3 • *90*
Outside Faculty of Health and Medical Sciences in DK and abroad*	8 • *285*	1 • *75*	1 • *20*	3 • *350*
Online resources organized by CPR	- • -	- • -	- • -	4 • ***
Total	31 • *1.319*	9 • *381*	5 • *70*	12 • *500*

* Excluding CPR organized courses.
** Mixed audience covers undergraduate students, PhD students, postdocs and academic staff.
*** Continuous uptake.

No. of outreach events

64

events in 2021

RESEARCH OUTPUT

In 2021, CPR researchers published 163 articles: 152 primary research articles reporting on original research and 11 review articles. Commentary and book chapters are not included in the diagram.

More than one in four of the articles (28%) were published in journals with a journal impact factor above 10.

FUNDING

In 2021, the total turnover of CPR was 228.7 million DKK.

- Just over half was attracted as competitive grants, supplementing the Novo Nordisk Foundation center grant of 107.1 million DKK.
- The competitive research grants (111.4 million DKK) stem from: 67% Danish private grants, 20% EU grants, 10% Danish public grants, and 3% other international grants.

TEACHING ACTIVITIES

Approximately xx persons attended xx courses taught by CPR researchers in 2021.

CPR's educational activities draw on the research excellence and unique opportunities associated with being a university-based research center. One example is a new course introduced in 2021: 'Data driven personal medicine - from epidemiology to patient' organized by the Brunak Group as part of a new professional master in personal medicine offered at the University of Copenhagen.

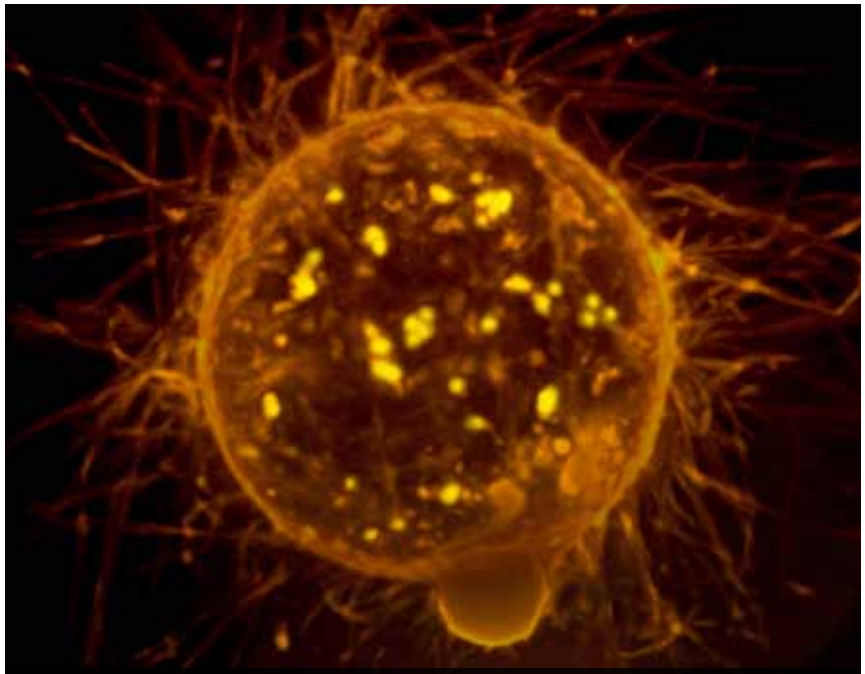
OUTREACH

CPR researchers want to share the knowledge on protein research. In 2021, they participated in 64 outreach events:

- **43** press and media interactions
- **3** broadcast e.g. TV/radio/podcast
- **14** talks
- **3** activities for high school students
- **1** website.

Discovery of molecular pathway reveals a possible 'Achilles heel' of cancer

For decades it has been a mystery how cancer cells adapt to and even benefit from an environment low on oxygen. Now, the Lukas Group and collaborators at CPR have uncovered the molecular mechanisms behind this growth advantage of cancer cells and reveal weak spots where pharmacological interventions could be fatal for cancer.



Stylized representation of insufficient blood supply arising in a solid tumor as it grows larger in size, creating regions with hypoxic conditions (bright areas).

The cells in our body depend on oxygen, so when deprived of oxygen, they die. When a solid tumor grows larger in size, the imbalanced growth can create areas with insufficient blood supply and thus hypoxic conditions. Hypoxia enables cancer cells to increase the number of mutations taking place in their DNA, which increases the tumor's chance of survival and further growth. This so-called hypoxia response has been known for decades. But it has remained unknown how the actual reprogramming takes place in cancer cells.

In 2021, a multi-disciplinary research collaboration involving the Lukas, Mann and Jensen groups at CPR provided some of the answers to this mystery. The researchers show that hypoxia initiates a three-step molecular pathway, as outlined in the graphic (next page).

ACHILLES HEAL OF CANCER

"Together, these findings provide us with thus far the most compelling mechanistic basis to understand accumulation of mutations in hypoxic tumors," says Professor and Group Leader Jiri Lukas.

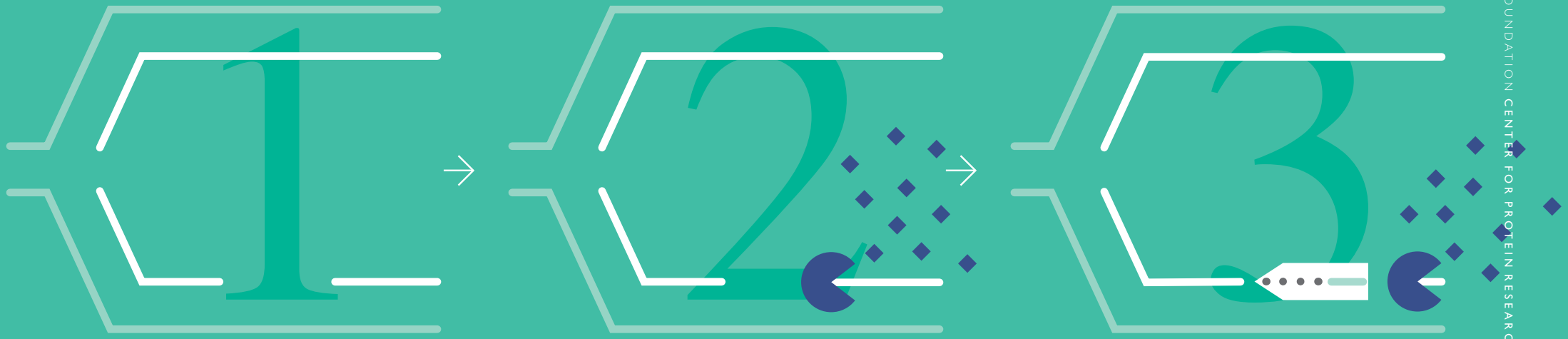
The discovery of this molecular pathway is important, because it reveals a situation that makes cancer susceptible to treatment.

"You can view the time between the first and the third step of the molecular pathway as an 'Achilles heel' of cancer. In that window of time, a new pharmacological intervention could stop the cancer from filling in the gaps using mutagenic DNA repair. That would be fatal for the incipient aggressive cancer," says Assistant Professor Kumar Somyajit, first-author and co-correspondent author of the study.

Read the study 'Homology-directed repair protects the replicating genome from metabolic assaults' in Developmental Cell.

A molecular pathway initiated by hypoxia

In 2021, researchers at CPR showed that hypoxia initiates a three-step molecular pathway in tumors that causes the accumulation of mutations:



1. COMPROMIZING DNA REPAIR:
During replication of DNA, replication errors occur, as represented here by a gap in the newly synthesized DNA daughter strand (white lines).

Facing hypoxia, cancer cells suppress important DNA repair proteins that would normally repair the gaps in an error-free manner. The result is that unrepaired gaps accumulate in the new daughter strands of DNA.

2. EXPANSION OF GAPS IN DNA DAUGHTER STRANDS:
The hypoxia also releases higher levels of reactive oxygen species (ROS) chemicals, which activate enzymes (blue sphere) that expand the unrepaired gaps

3. INCREASE OF THE MUTATION RATE
The expanded gaps are filled by highly mutagenic DNA polymerases (enzymes catalyzing the synthesis of DNA, represented as white bar), instead of the error-free repair used under normal oxygen levels. This leads to a rampant increase of the mutation rate of the cells.

New discovery could make life difficult for corona virus

Researchers at CPR have developed a molecule capable of curbing the spread of the SARS-CoV-2 corona virus. The method behind the discovery can be used to fight a potential future virus outbreak with medicine while waiting for a vaccine.

A virus has to copy itself in as many cells as possible to spread in the host body. To do so, it must "hijack" proteins from the infected body and use them to its own advantage.

This was known when the SARS-CoV-2 virus caused the COVID-19 pandemic in 2020. On this background, researchers at CPR and Uppsala University in Sweden asked themselves, if it would be possible to slow down the spreading of the virus by inhibiting the hijacking on the protein scale.

In 2021, they published the answer in the journal Nature Communications: The researchers had developed a molecule - a so-called peptide inhibitor - that slows down the SARS-CoV-2 virus spread at least ten times in a laboratory setup. If developed into a drug, the molecule may be able to limit the ability of coronavirus to spread in the body.

The study is based on a new method developed at Uppsala University in Sweden. The method enables the researchers to determine exactly how viruses interact with proteins in our cells via so-called SLiMs (short linear motifs) – stretches in the host and viral proteins that were until now somewhat ignored in the hunt for druggable virus-host protein interactions. In order to prevent the hijacking, you need to know how the virus actually does it, and which proteins it needs.

The SLiM-mediated interactions between SARS-CoV-2 and human host proteins that affect antiviral mechanisms are illustrated in the next page and were featured in The Scientist magazine (read the article here).

PAVING THE WAY FOR NEW VIRUS CONTROL

The discovery can prove important in case of a future virus outbreak, says Professor Jakob Nilsson from CPR.

"We hope our results can pave the way for a new virus control tool, which we can put to use in case we get a new virus outbreak at a time when there is no available vaccine," says Jakob Nilsson.

"If we should see an outbreak of a brand new virus 10 years from now, for example, this should enable us to fight it with medicine while we wait for a vaccine."

The Danish-Swedish collaboration has mapped potential SLiM-mediated interactions with human proteins for 23 different corona viruses.

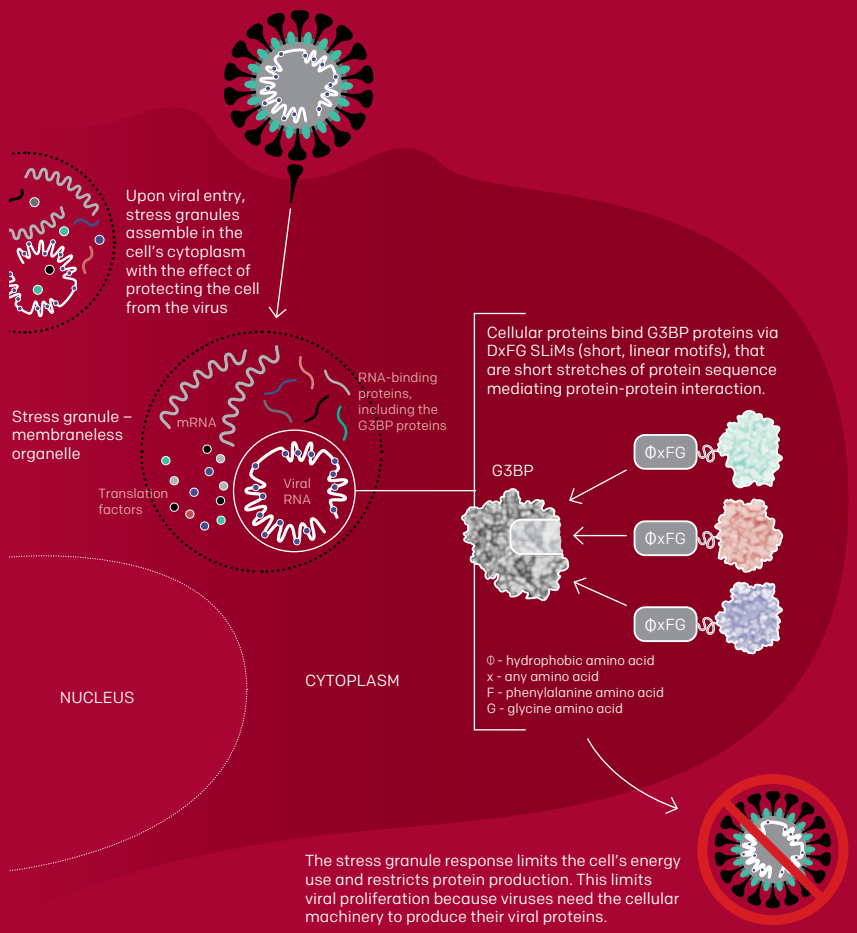
"Aside from SARS-CoV-2 - the coronavirus causing the current pandemic - we have screened 22 other coronaviruses for interaction with the proteins in our cells. The fact that we now have a relatively large database of knowledge of how these viruses operate, enables us to compare potential new coronaviruses and determine how we can fight them," says Jakob Nilsson.

Researchers from the Mann group at CPR also contributed to the study 'Large scale discovery of coronavirus-host factor protein interaction motifs reveals SARS-CoV-2 specific mechanisms and vulnerabilities', which was published in Nature Communications.

Targeting stress granule formation during SARS-CoV-2 infection

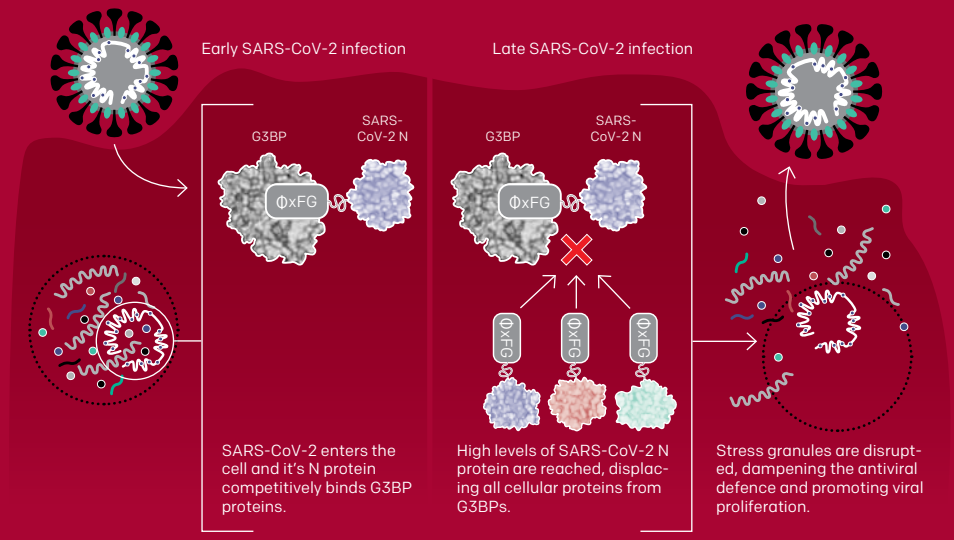
The research team screened the ability of a large number of viral proteins to interact with human proteins via so-called SLiM binding motifs that mediate protein–protein interactions. Focusing their attention on the SARS-CoV-2 virus, they noticed that the N protein had a potential SLiM-interacting motif for the human G3BP proteins. This was of great interest, as G3BP is known to have an important role in protecting the host cell against various stresses and viral infections. In addition, several viruses are known to target G3BP proteins.

NORMAL ANTIVIRAL DEFENSE MECHANISM

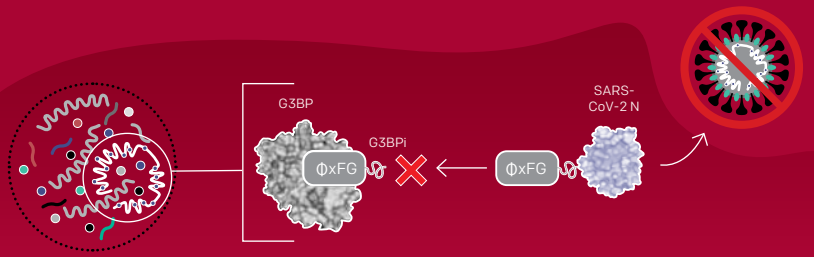


The stress granule response limits the cell's energy use and restricts protein production. This limits viral proliferation because viruses need the cellular machinery to produce their viral proteins.

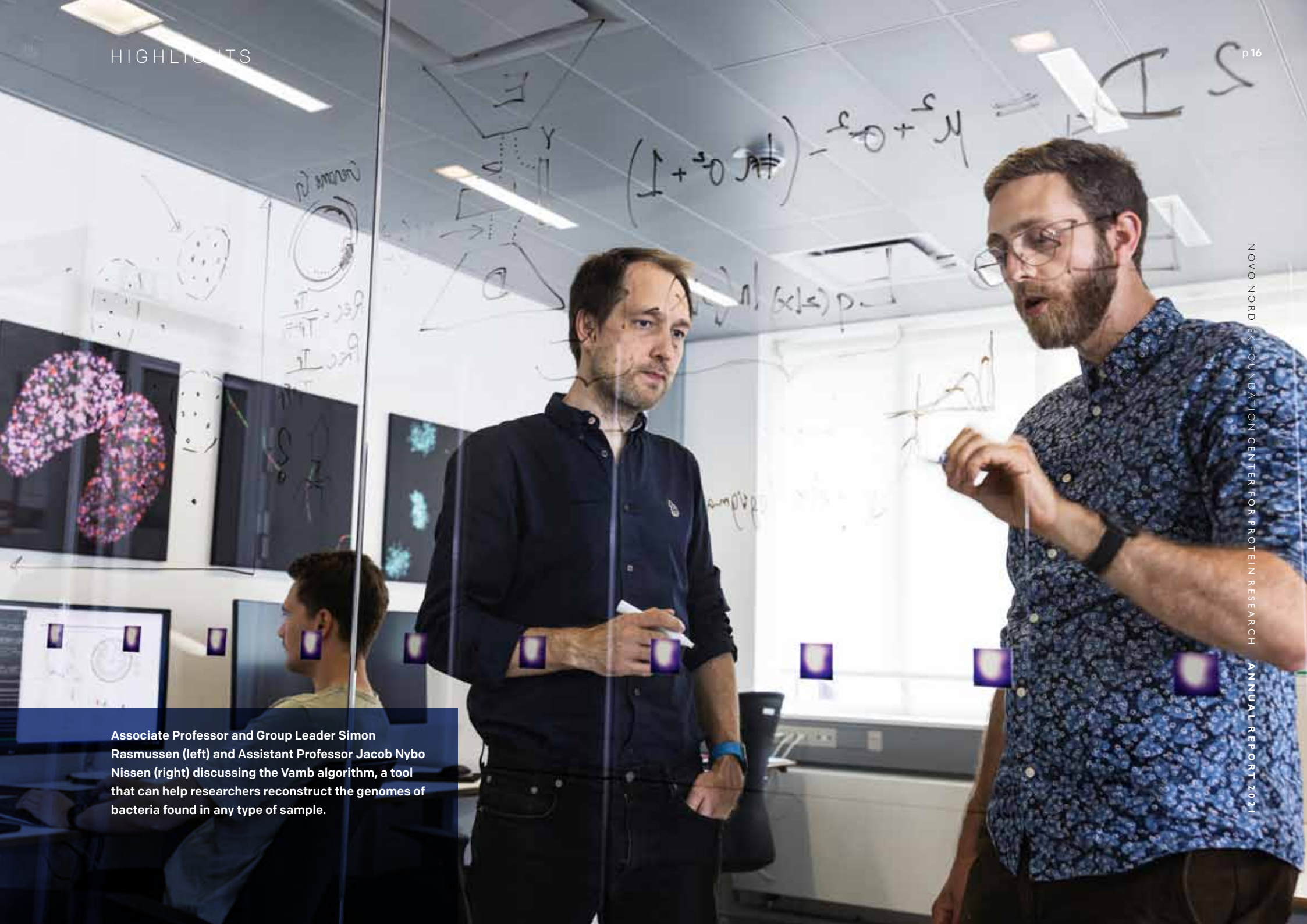
SARS-COV-2 INFECTION DISRUPTS ANTIVIRAL DEFENSE



NEW INHIBITOR PREVENTS SARS-COV-2 FROM DISRUPTING THE DEFENCE



Researchers have designed a G3BP inhibitor termed G3BPi, which binds to the G3BP protein and displaces the SARS-CoV-2 N protein. This slows down the viral proliferation, although the mechanism is not clear.



Associate Professor and Group Leader Simon Rasmussen (left) and Assistant Professor Jacob Nybo Nissen (right) discussing the Vamb algorithm, a tool that can help researchers reconstruct the genomes of bacteria found in any type of sample.

Feces and algorithms

Artificial Intelligence to map our intestinal bacteria. Researchers from the Rasmussen Group at CPR have developed a method that uses artificial intelligence to map intestinal bacteria based on feces.

The presence of bacteria is vital to the health of humans. This is true not least of intestinal bacteria where present-day studies focus on their role in diseases such as diabetes, overweight, autism, schizophrenia and depression.

This is why scientists are keen to study the approximately 100 billion active bacteria in our intestines representing 500-1000 different species. However, researchers have difficulties studying the bacteria in their natural environment, on which bacteria deeply depend to survive. The main method of studying them is by sequencing their genomes, however this is challenging and leads to gigantic DNA puzzles that are impossible to solve using current computational techniques.

In 2021, researchers at CPR found a promising solution to this challenge. They developed a groundbreaking computational technique that is able to complete the DNA puzzles and reconstruct the genomes of bacteria found in faeces.

DNA COMPLETED BY ARTIFICIAL INTELLIGENCE

"In recent years we have discovered that bacteria have a great impact on the body. Knowledge of the bacteria is vital if we are to understand what is going on. Although a lot of research is being done within this field, we have still not identified all the bacteria found in and on the human body.

"That is where our technique can make a difference," says Associate Professor Simon Rasmussen, who together with his team of researchers at CPR was responsible for the study published in Nature Biotechnology.

The new technique is an algorithm that uses artificial intelligence to complete the DNA strings of bacteria. The algorithm, named 'Vamb', is available to other researchers and free to use, giving researchers from all over the world a tool to help map the full human gut microbiome.

A TECHNIQUE FOR MULTIPLE PURPOSES

The method can be used to analyze the bacterial content of very small samples from any place. As Simon Rasmussen points out:

"If there are bacteria present, they can now be identified. For example, you could use the new method to analyze the effect of pollution in a soil sample and learn how the microorganisms are affected. The same applies to investigations of the biological water quality of lakes and watercourses located close to a factory or similar activity."

The team has several studies in the pipeline demonstrating the use of the new method. One example is the identification of hundreds of different types of bactericidal viruses, so-called phages, some of which help maintain a healthy bacterial balance in the intestines. This might lead the way for new treatments of infections caused by bacteria resistant to antibiotics. Another example is the study of the microbiome of healthy individuals older than 100 years. Here, the aim is to identify bacteria and viruses that support a healthy life.

Read the study, 'Improved metagenome binning and assembly using deep variational autoencoders' in Nature Biotechnology.

Protein can release trapped histones in the cell

A study lead by the Groth Group has added a piece to the puzzle of how cells organize their DNA to maintain healthy genome function. The heat-shock protein DNAJC9 has a surprising dual histone chaperone functionality, a new study in Molecular Cell shows.

In the cell nucleus, histones play a crucial role packaging DNA into chromatin. Histone proteins wrap DNA into structures called nucleosomes, which makes it possible to fit approximately two meters of DNA into the cell nucleus. The positioning and composition of nucleosomes governs the access of cellular machinery to DNA, thereby affecting all aspects of genome function, including gene expression.

Histones are very sticky molecules that easily bind to both DNA and RNA, so to ensure they are transported to the cell nucleus after synthesis and bind to the right portion of DNA to organize the chromatin, they are guarded by complexes of histone chaperones. Histone chaperones are proteins that bind to histones to help protect them from non-specific binding events until they reach their goal. This process fails sometimes and histones get stuck during their supply to chromatin without any purpose.

In a study published in Molecular Cell, assistant professor Colin Hammond and colleagues have shown that the protein DNAJC9 holds an important role in safeguarding histones and thereby chromatin.

ACTIVE FIXER JOINS PASSIVE BYSTANDERS

"Until now researchers have assumed that histone chaperones only act to passively shield histones without the need for the consumption of cellular energy resources (ATP). We have found out that DNAJC9 actively engages the cellular protein folding machinery – which means it recruits enzymes (molecular chaperones) that consume ATP to redeploy histones that have been trapped," says lead author Colin Hammond.

Once released from their trapped condition, DNAJC9 bound histones can re-engage with other histone chaperones like MCM2 and others, which assemble nucleosomes on chromatin. When the protein DNAJC9 is mutated to lose its ability to recr uit the protein folding machinery, the histones stay trapped and are thereby lost for proper chromatin deposition.

"This means that traditional histone chaperones cannot fully protect histone proteins from spurious interactions. Rather, the cell is dependent on the combined action of protein folding molecular chaperones and histone chaperones to safeguard these fundamentally important proteins during their dynamic lives," Colin Hammond underlines.

RELEVANT INSIGHTS FOR CANCER RESEARCH

DNAJC9 is an essential protein in many cancer cell types and the levels of the protein correlate with the rates at which cancer cells proliferate. Chromatin in cancer cells may be more reliant on DNAJC9 compared to regular cells, and if this is the case DNAJC9 could be a target for the development of future cancer treatments.

"Although it's still early days, we hope this fundamental advance in our understanding of DNAJC9 biology helps to pinpoint a function essential for cancer cell viability with therapeutic potential," Colin Hammond says.

The study is based on a strong collaboration with international partners in China and US. The functional analysis was spear-headed by Colin Hammond in close collaboration with colleagues from the Nielsen Group at CPR, to dissect the function of the protein through in-depth proteomic assays.

The project was funded in part by Anja Groth's ERC consolidator grant. Read the study "DNAJC9 Integrates Heat Shock Molecular Chaperones into the Histone Chaperone Network" in Molecular Cell.

The Groth Group at their 2021 retreat in Esbjerg. The DNAJC9 study in Molecular Cell was spearheaded by Colin Hammond (far left) and Anja Groth (third from the right in green)

PHOTO: ROBERT ATTERMAN / RED STAR

STRING helps researchers make sense of protein–protein interactions

How do human proteins interact with each other? This question is key in disease research and drug target discovery. The Jensen Group helps researchers all over the world analyze thousands of known protein–protein interactions with the STRING database.

When the COVID-19 pandemic struck in 2020, there was an immediate need to understand how the virus spreads in the human body. Which viral proteins interact with human proteins and what are the consequences?

One tool that can assist such analysis of virus-host protein interactions is the STRING database, a scientific tool built and maintained with the help of Professor and Group Leader Lars Juhl Jensen and his team at CPR. The STRING database integrates all known data of how proteins in thousands of organisms interact with each other (see box).

NEW FUNCTIONALITY ALLOWS USERS TO UPLOAD EXPERIMENTAL DATA

In 2021, the researchers behind STRING published an updated version of the database, increasing the number of integrated organisms from around 5,000 to 14,000 and adding several new functionalities.

One of the most interesting new features, according to Lars Juhl Jensen, is the possibility for users to easily upload their own experimental data and combine it with data retrieved by STRING.

To demonstrate this function, the research team decided to integrate all current knowledge about how SARS-Cov-2 infects human cells (see illustration). They achieved this by combining three things:

1. All existing knowledge about how human proteins interact, as retrieved by STRING
2. All currently available data about which SARS-CoV-2 proteins bind to human proteins
3. Data from a study identifying human proteins that affect the ability of SARS-CoV-2 to enter cells

With this input, STRING can visualize human proteins that either aid or prevent entry of virus particles into human host cells, as well as proteins that are indirectly involved in the process (visualized in the illustration by red, green and white circles, respectively).

"In itself, STRING is a powerful tool to help researchers uncover a new pathway or drug target. Combining this with user-uploaded data really expands the possibilities to visualize protein–protein interactions between different organisms and even integrate it with experimental data. This provides researchers with additional means to analyze complex processes such as COVID-19 infection," says Lars Juhl Jensen.

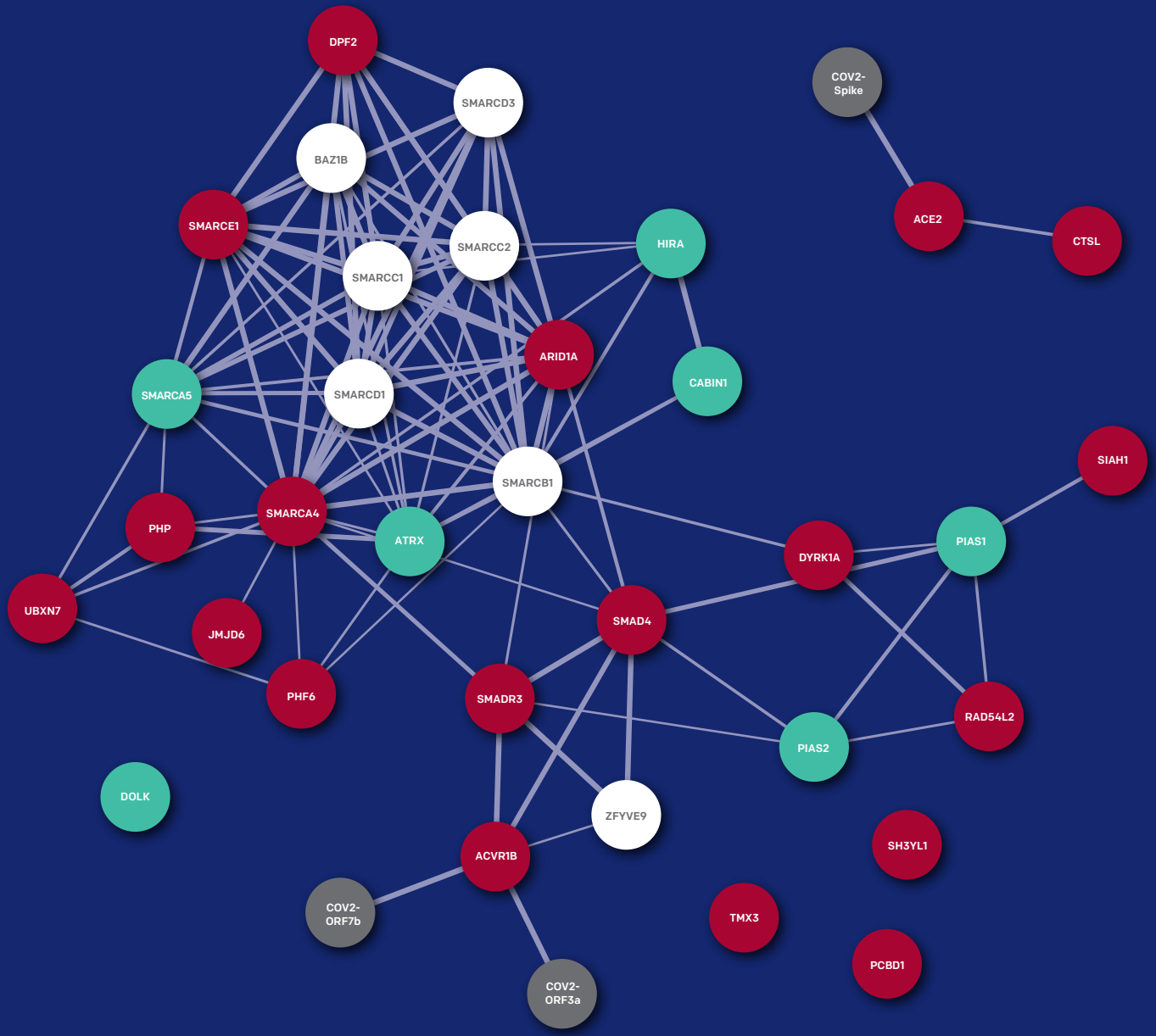
Read the article 'The STRING database in 2021: customizable protein–protein networks, and functional characterization of user-uploaded gene/measurement sets' in Nucleic Acids Research.

LARS JUHL JENSEN GROUP

- Lars Juhl Jensen's group contributes to STRING with protein data gained from automated text mining of scientific literature, searching through all open access publications in full-text and abstracts from the PubMed database of biomedical and life sciences literature.
- Text mining enriches the network analysis with interactions and knowledge about pathways or diseases where a protein may play a role.
- If a publication mentions a protein in relation to a disease or another protein that it binds to, that relation is made available in STRING.

Professor and Group Leader Lars Juhl Jensen.

Visualizing host genes that regulate SARS-CoV-2 infection



THE STRING OVERVIEW

When the COVID-19 pandemic hit, network biology provided a tool to visualize how the SARS-CoV-2 virus' proteins interact with proteins in human cells (host proteins). This example demonstrates how STRING can be used to provide an overview of existing knowledge about the complex interactions between virus and host proteins.

GREY: SARS-CoV-2 proteins that are known to interact with host proteins based on experimental laboratory evidence.

RED and **GREEN**: Host proteins whose level of expression appears to control entry of SARS-CoV-2 virus into cells, as determined in laboratory experiments. Red illustrates proteins whose removal causes a drop in virus entry efficiency. Green indicates proteins whose removal enhances virus entry.

WHITE: Proteins that are known to be functionally associated with the red and green proteins and therefore indirectly affect SARS-CoV-2 infection.

For more information about the data, see original research article in Nucleic Acids Research

STRING: SEARCH TOOL FOR RETRIEVAL OF INTERACTING GENES/PROTEINS

- The STRING database aims to integrate all known and predicted associations between proteins in organisms from Homo sapiens to fungi, fish, bacteria and many more.
- The database collects and scores evidence from a number of sources, such as databases and the scientific literature.
- In 2021, STRING served more than 5,000 distinct users per day.
- STRING is built in collaboration between researchers at University of Zurich, European Molecular Biology Laboratory and CPR.

New process ensures diversity in recruitments

A dedicated effort has transformed the recruitment process of group leaders at CPR in order to promote diversity. Mitigation of unconscious biases is now an integral part of the process in candidate shortlisting, interviews and assessments.

Even though diversity and equality is a priority at CPR, the center has had difficulties attracting female group leaders. That is why CPR in 2019 joined the University of Copenhagen project Equality and diversity in recruitment, retention and attraction of scientific personnel to get the tools and knowledge to systematically work with diversity in recruitment and reduce unconscious biases.

To facilitate the process, CPR established a diverse working group with broad representation from the center and strong support from the management, including Research Directors Anja Groth and Guillermo Montoya.

THE BENEFIT OF DIVERSITY IN RESEARCH PROJECTS AND TEAM COLLABORATION

Research Director and Professor Anja Groth highlights the advantages diversity brings to research:

"When you need to find new solutions and creative ideas to solve complex problems, it is an advantage to have a diverse group of people both with respect to scientific background, culture and gender as they bring different ways of thinking. It is also important to have diverse role models in a center like ours," says Anja Groth.

The new procedure was created in parallel with the recruitment of several group leaders from 2019-2021.

As a result, the candidates were assessed on a range of criteria in addition to the impact factor of their publication list. Other factors were also important to evaluate, including management skills, innovative research programs and contributions to the center's other research and teaching activities.

DIVERSITY AT CPR

The new process ensures that CPR can vouch for its group leader recruitment process, knowing that diversity has been taken into consideration regardless of who gets the job.

"We have not compromized on quality in any way. Diversity is not the deciding factor. Diversity comes into play when you have a group of candidates who are comparable across key academic parameters" explains Anja Groth.

In the coming years, CPR will work to actively promote and create inclusive team cultures. To create a common language for inclusion and diversity in the center, all staff will be offered bias training and the management will be trained in inclusive leadership. Inclusion surveys will be used as a tool to decide further actions.

New process ensures diversity in recruitments of group leaders

Diversity, equity and inclusion is a high priority at CPR. The new procedure for recruitment of group leaders was created with direct involvement of Executive Director Jiri Lukas and Research Directors Anja Groth and Guillermo Montoya.

HIGHLIGHTS OF THE NEW RECRUITMENT PROCEDURE FOR GROUP LEADERS

Written procedure
A written procedure for recruitment promotes compliance and makes it easier for CPR to evaluate and improve the procedure.

Broad announcement
CPR uses various international networks and targeted campaigns on social media to ensure the broadest possible reach of job adverts. The approach may vary between different research fields.

Gender balance among candidates and reviewers
The candidates shortlisted and interviewed for the positions include an equal number of men and women to avoid having one candidate deviate from the rest. The composition of the reviewing panel is also gender balanced.

Set program for panel interviews
Job interviews are conducted as panel interviews and a set program for interviews is used with all candidates to avoid unintentional bias in questions posed to the different candidates.

Evaluation criteria
When assessing candidates, a broad range of criteria is in play in addition to the impact factor of their publication list: How innovative is their research program? How does it fit with the center's research and teaching activities? Will the candidate be able to interact with the other researchers in the center and the Danish research environment in general? Does the candidate have good management skills and an interest in research management?

Evaluation form
An evaluation form allows the reviewers to form independent opinions about the candidates before discussing them with the other reviewers. The intention is to avoid conformity among reviewers.

2021 Brief Highlights

NEW GROUP LEADERS

Two group leaders joined CPR in 2021: Associate Professor Eva Kummer leads a group in the Protein Structure and Function Program, exploring the biology of human mitochondria with a specific focus on how they maintain DNA and produce functional RNA. Associate Professor Nils Krietenstein leads a group in the Protein Memory Program, using novel methodologies to investigate the mechanisms driving the three-dimensional organization of the genome.

GROUP LEADER REVIEWS

The groups of Professors Chuna Ram Choudhary and Jakob Nilsson underwent their second quinquennial peer reviews of scientific achievements, while Associate Professor Julien Duxin's group was evaluated for the first time in 2021. All received the most successful rating on CPR's scale, recognizing them as some of the most prominent scientists in their fields worldwide.

TRAINING JUNIOR RESEARCHERS FOR SUCCESS

As part of the EU project ENABLECARES (Enabling Careers), CPR primes talents among PhD students and postdocs for success in biomedicine. In 2021, expert trainers from Radboud University in The Netherlands trained CPR research coordinators, who then developed and held courses in open access and research data management. A course in entrepreneurship is scheduled for 2022. The courses will be offered to CPR researchers annually.

SUCCESS IN ATTRACTING FUNDING

CPR researchers maintained competitiveness by securing a total of 71 million DKK in external funding in 2021. Professor Guillermo Montoya and Associate Professor Nicholas Taylor received research project grants from Independent Research Fund Denmark, while several group leaders attracted funds from Novo Nordisk Foundation: Distinguished Investigator, Professor Anja Groth (10 million DKK); Hallas-Møller Emerging Investigator, Associate Professor Eva Kummer (10 million DKK); Exploratory Interdisciplinary Synergy, Professor Jesper V. Olsen (5 million DKK); Data Science Collaborative Research, Associate Professor Simon Rasmussen (5.5 million DKK); and Pioneer Innovator, Professor Jakob Nilsson (1 million DKK). COVID-19 related research was supported by Sygeforsikringen "danmark": Professors Jakob Nilsson and Mathias Mann were awarded 2.6 million DKK, and Prof. Søren Brunak 0.7 million DKK.

SUSTAINABLE LABORATORY PILOT AND WASTE SORTING

In 2021, CPR started a pilot project in selected wet labs and was instrumental in recruiting other Faculty departments to the project. With the assistance of a sustainability expert and in close interaction with the faculty campus service, CPR will increase waste sorting and recycling, implement sustainable purchasing solutions, and more via the LEAF green lab certification scheme (LEAF: Laboratory Efficiency Assessment Framework). Outside the labs, CPR continues to integrate green initiatives by the 'CPR Goes Green' association, including extensive waste sorting. In May 2021, CPR Goes Green co-organized the first iteration of 'Sustainable Research Symposium' (SuReSymp), which gathered 700 online attendees to promote the integration of sustainability in science. SuReSymp will be a traveling symposium with a new group of organizers every year.

BIOSCIENCE AND ENABLE CONFERENCES

In 2021, CPR co-organized the 20th NNF Copenhagen Bioscience Conference, 'Protein Signaling – from mechanism to cellular function' that had been postponed from 2020 due to COVID-19. Via a hybrid set-up, conference managers presented a strong list of world-leading scientists. The fourth ENABLE conference, originally planned to take place in Milan in 2020, took place virtually in May, including scientific symposium, career day, job fair and pub talks. Public outreach activities to schools took place in Milan.

ALUMNI OVERVIEW

An important part of CPR's mission is to train future leaders in academia and industrial biomedicine. On average, young researchers train with us for a 4-year period as a PhD student or postdoc before moving on to the next step of their career outside CPR. Since the opening of CPR in 2009, CPR alumni have established 22 academic research groups outside CPR, around one third at University of Copenhagen. In 2021, nine PhD students received their degree. Six PhDs, seven postdocs, four assistant professors and two associate professors left CPR for new positions.

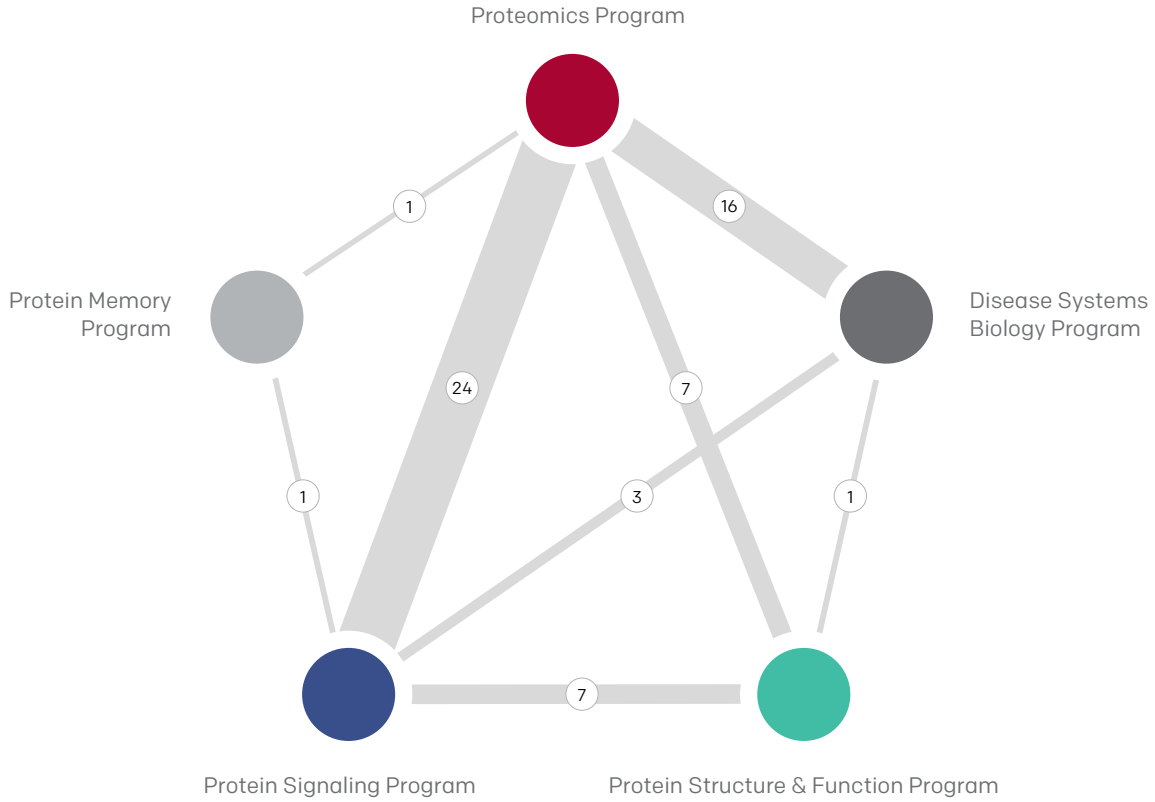
Researchers leaving CPR in 2021		→	To these sectors		→	In these regions	
PhD	6	→	Academia	7	→	Denmark	10
Postdoc	7	→	Industry	9	→	EU	5
Assistant Professor	4	→	Other*	3	→	Outside EU	4
Associate Professor	12	→			→		
Total	19	→	Total	19	→	Total	19

* The category 'Other sector' covers hospitals and research foundations

Internal and external synergy

Collaboration and exchange of ideas is a high priority at CPR, since an open-minded and curious attitude among researchers increases the chance of generating frontier research. This applies to CPR internally as well as in collaboration with hospitals, universities and the biomedical industry in Denmark and abroad.

CPR is a highly integrated research center. With all research, knowledge and technology located closely together, CPR has been able to establish an inter-disciplinary environment where research programs complement each other and collaborate extensively.



SYNERGY BETWEEN CPR RESEARCH PROGRAMS

Synergies illustrated by the number of program-to-program shared research publications in 2017-2021. The number of collaborations is represented by the thickness of lines (1-24).

Network created with Cytoscape 3.9.1.

Internal and external synergy

CPR actively interacts with the Faculty of Health and Medical Sciences at University of Copenhagen, hospitals in the region and scientific partners from around the world. The global reach of CPR is evident in the large number of collaborations that the center has established around the world.

SYNERGY BETWEEN CPR AND EXTERNAL COLLABORATORS

Synergies illustrated by the number of published collaborations with external partners in 2018-2021. The 60 most frequent partners across five different categories are shown. The number of collaborations is represented by the thickness of lines (2-101).

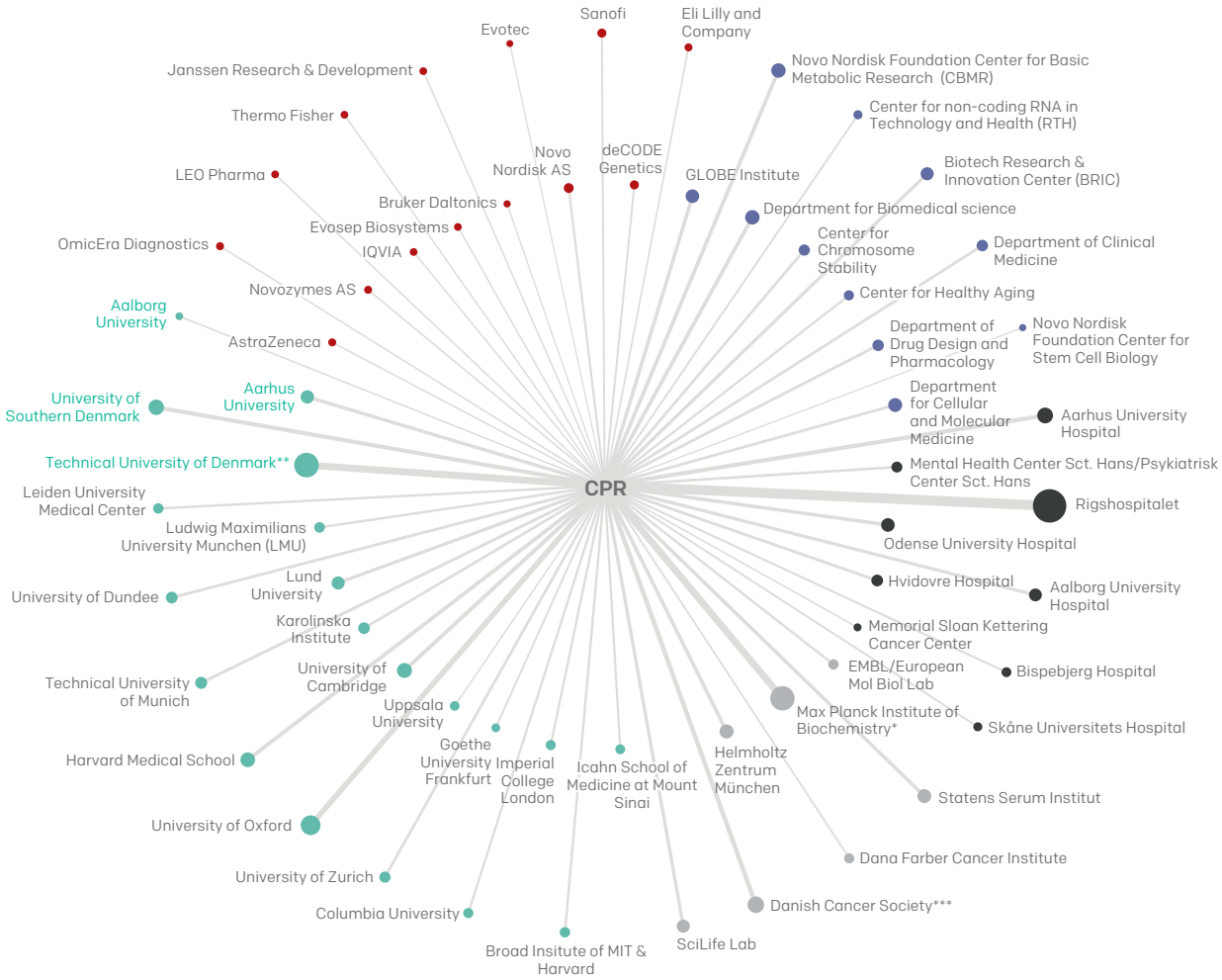
Network created with Cytoscape 3.9.1.

- Faculty of Health and Medical Sciences, University of Copenhagen
- Hospital
- Research Institution
- University
- Corporation

* 44 of 67 collaborations with Max Planck Institute of Biochemistry (MPI) are related to Matthias Mann's appointment as Director of Department of Proteomics and Signal Transduction, MPI.

** 36 of 68 collaborations with Technical University of Denmark (DTU) are related to Søren Brunak's appointment as Professor of Bioinformatics, Department of Health Technology, DTU.

*** 22 of 38 collaborations with Danish Cancer Society (DCS) are related to Elena Papaleo's appointment as Group Leader of Computational Biology Laboratory at DCS.




400
300

Research programs and technologies in 2021

The research groups at CPR are organized into five research programs. Each program is dedicated to run a technological platform that provides state-of-the-art research resources and interdisciplinary support to fellow researchers in the center.

Professor Anja Groth
Research Director
and Group Leader

Protein Memory Program

The program investigates how proteins control cellular identity via epigenetic mechanisms that govern the expression of the genetic information encoded in DNA. How cell identity is copied to new cells is essential to understand how we maintain healthy life, delay aging and avoid disease.

THE GROTH GROUP

... elucidates how chromatin organization is copied and epigenetic information passed on during cell division to maintain cellular function. The group develops innovative genomics and proteomics technologies to understand chromatin replication and epigenome maintenance.

2021 landmark

“ We uncovered a mechanism that safeguards histones – vital proteins in the cellular nucleus that wrap DNA into the compact chromatin fiber that constitutes the basic construction of our genomes. When histones get trapped in spurious binding to DNA or RNA, the histone chaperone DNAJC9 actively recruits the protein folding machinery to fold and release histones, directing them back to their job of organizing chromatin. ”

- Professor, Research Director and Group Leader
  Anja Groth

THE KRIETENSTEIN GROUP

... studies 3D folding of human chromatin – the fundamental organization of DNA and its associated proteins inside the cell – to understand how this folding helps establish and maintain cell-type-specific gene expression patterns.

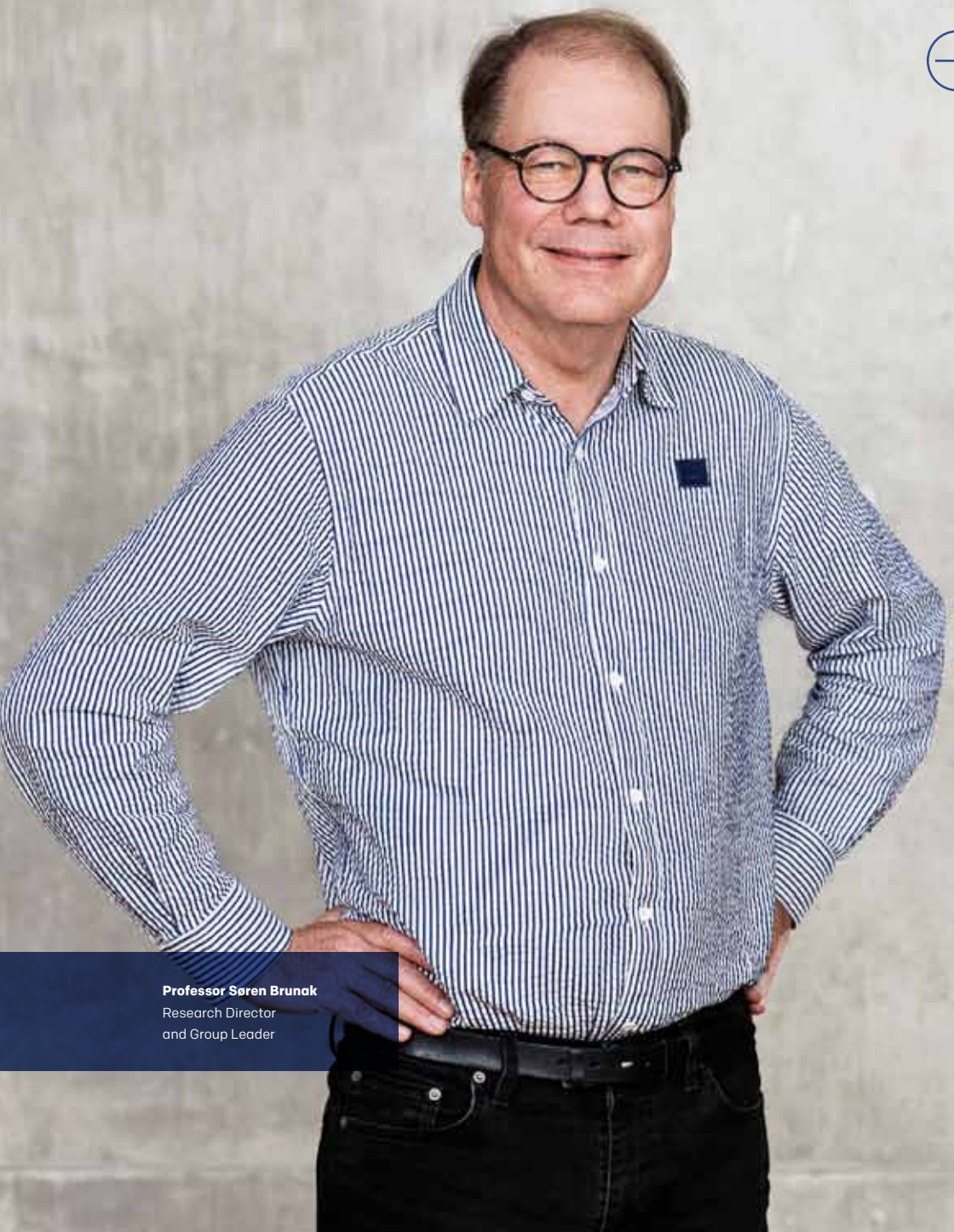
2021 landmark

“ We have successfully initiated a new group and laboratory that will develop novel spatial genomic approaches to investigate the structure and function of the 3D genome in health and disease. The aim is to study how non-coding mutations can contribute to the development of e.g. neurological disorders and cancer by changing the 3D organization of genomes. ”

- Associate Professor and Group Leader
  Nils Krietenstein

PLATFORM RUN BY THE PROTEIN MEMORY PROGRAM

The Genomics Platform provides high-throughput DNA and RNA sequencing and covers applications from classical genomics to single-cell transcriptomics. The platform offers support from project planning to downstream analyses to all researchers at CPR.



Professor Søren Brunak
Research Director
and Group Leader

Disease Systems Biology Program

The program is leading in developing innovative tools to analyze and interpret big biomedical data effectively to better understand disease development and improve treatment options. The program combines multi-omics molecular network biology data and clinical data from the healthcare sector.

THE BRUNAK GROUP

... combines population-wide molecular and clinical data in novel ways in order to understand disease progression patterns in multi-morbidity patients. Understanding diseases in a lifelong perspective gives valuable insights for better treatment of diseases and complications.

2021 landmark

“ We analyzed over one billion prescriptions issued by Danish general practitioners and identified common prescription trajectories of patients that shift between drugs prescribed for the same disease. This allowed us to compare survival statistics for different groups of patients, which could for example help identify suboptimal prescription patterns. We plan to link the dataset to genetics to better predict which drug will likely be best to start with for a given patient. ”

– Professor, Research Director and Group Leader
Søren Brunak

THE JENSEN GROUP)

... develops state-of-the-art tools for generation and analysis of molecular interaction networks from proteomics data and text mining. The tools are made freely available to the scientific community.

2021 landmark

“ We published an updated version of the widely used STRING database (>5000 users/day) which integrates all known and predicted associations between proteins in 14,000 organisms (5,000 in the previous version). The new version allows users to upload their own data, e.g. experimental data, and combine it with data retrieved by STRING. The Jensen group contributes to STRING with protein data gained from automated text mining of scientific literature. ”

– Professor and Group Leader
Lars Juhl Jensen

THE RASMUSSEN GROUP

... focuses on computational analysis of variation in the human proteome, genome and microbiome. By developing deep learning algorithms for massive amounts of omics data, they aim to increase the understanding of human diseases for more precise diagnostics and treatments.

2021 landmark

“ We published an algorithm that uses artificial intelligence to map bacteria found in various samples. The study used the algorithm to reconstruct the genomes of bacteria found in fecal samples in order to map the human gut microbiome, which is vital to the health of humans. The algorithm, named ‘Vamb’, is freely available to use for other researchers. ”

– Associate Professor and Group Leader
Simon Rasmussen

PLATFORM RUN BY THE DISEASE SYSTEMS BIOLOGY PROGRAM
The Big Data Management Platform provides a shared, scalable computational infrastructure to handle the vast amounts of data produced by the various technology platforms at CPR, such as raw mass spectrometry and imaging data.

Professor Niels Mailand
Research Director
and Group Leader

Protein Signaling Program

The Program uses cutting-edge methodologies to illuminate how proteins communicate and work together in time and space to protect cellular DNA from harmful changes. This enables a detailed molecular understanding of the molecular basis of many human diseases and paves the way for improved treatment of patients.

THE MAILAND GROUP

... employs CRISPR/Cas9- and proteomics-based screening approaches to obtain detailed molecular insights into the signaling processes promoting cellular stress management, which is critical in many disease contexts. This knowledge provides opportunities for the development of novel targeted treatment strategies.

2021 landmark

“ Together with collaborators at CPR, we discovered the mechanism by which cells repair highly toxic DNA-protein crosslinks (DPCs) via the SUMO pathway. These findings reveal how failure to remove DPCs undermine genetic stability and provide opportunities for more targeted deployment of DPC-inducing chemotherapeutics. ”

- Professor, Research Director and Group Leader
  Niels Mailand

THE NILSSON GROUP

... investigates the function of essential enzymes called protein phosphatases in signaling processes in human cells and the role of binding motifs in virus-host protein interactions. Understanding how they each function may advance rational drug design for a range of diseases.

2021 landmark

“ In collaboration with the Mann group, we mapped the interaction of SARS-CoV-2 and 29 other corona viruses with the cellular host factor proteins that viruses need in order to replicate in human cells. This type of screen can pinpoint therapeutically relevant interactions, as demonstrated with a small peptide-inhibitor drug that slowed down SARS-CoV-2 replication by a factor 10 in infected cells. ”

- Professor and Group Leader
  Jakob Nilsson

THE LUKAS GROUP

... explores how proteins that guard the integrity of the human genome assemble into functional pathways, how they organize themselves in the cell nucleus, and how they communicate with the external environment and cellular metabolism to shield DNA against heritable and disease-predisposing mutations.

2021 landmark

“ Together with collaborators at CPR, we solved the mystery of how cancer cells adapt to and even benefit from an environment low on oxygen, a condition they encounter when tumors grow larger in size. We uncovered the molecular mechanisms behind this growth advantage of cancer cells and revealed weak spots where pharmacological interventions could be fatal for cancer. ”

- Professor, Executive Director and Group Leader
  Jiri Lukas

THE DUXIN GROUP

... uses protein extracts from frog eggs to study fundamental mechanisms of DNA repair and DNA replication. They primarily focus on how cells repair DNA lesions known as DNA-protein crosslinks, which can cause cancer and accelerated aging if left unrepaired.

2021 landmark

“ Together with collaborators at CPR, we discovered the mechanism by which cells repair highly toxic DNA-protein crosslinks (DPCs) via the SUMO pathway. These findings reveal how failure to remove DPCs undermine genetic stability and provide opportunities for more targeted deployment of DPC-inducing chemotherapeutics. ”

- Associate Professor and Group Leader
  Julien Duxin

PLATFORM RUN BY THE PROTEIN SIGNALING PROGRAM

The Protein Imaging Platform provides cutting-edge technology and support to all researchers at CPR that use microscopy to investigate the behavior of proteins in the cell, such as protein localization, activity and interactions, either as a snapshot or over time.

Professor Guillermo Montoya
Research Director
and Group Leader

Protein Structure and Function Program

The program visualizes the 3D structure of individual proteins and their assemblies to understand key biological processes. Understanding how these molecules function improves the understanding of biological mechanisms and disease development and facilitates drug development.

THE MONTOYA GROUP

... visualizes the functional details of protein complexes involved in cell cycle progression and genome editing and integrity. Deciphering the mechanisms behind these important processes provides the basis for understanding disease and the possible development of treatments.

2021 landmark

“ We determined and published the structure of CRISPR-Cas12j3, also known as Cas-phi3, which may be a new and better genome editing technology than the existing CRISPR-Cas9 due to its smaller size, which means it should be possible to include longer sequences to facilitate editing than for its larger cousins. ”

- Professor, Research Director and Group Leader **Guillermo Montoya**

THE TAYLOR GROUP

... uncovers the structure and function of the complex molecular machines involved in transporting molecules across cell membranes. By understanding their biological role, it will ultimately be possible to adapt or modulate these systems for biomedical purposes.

2021 landmark

“ We published a review article about the structural basis of bacterial movement. We also contributed to a study that reveals how endolysin enzymes from phages (virus that attack bacteria) specifically recognize their targets in the bacterial wall. Endolysins are a potential alternative to the use of antibiotics against multidrug-resistant bacteria by their exogenous application to degrade the bacterial cell wall. ”

- Associate Professor and Group Leader **Nicholas MI Taylor**

THE KUMMER GROUP

... investigates the biology of human mitochondria, which are energy-producing cell compartments, to understand how they maintain their DNA and how they produce functional RNA species. Their work can shed light on the molecular triggers of mitochondrial disorders that are frequently caused by mutations in the involved protein factors.

2021 landmark

“ We have successfully established a highly qualified group of five members and integrated advanced experimental pipelines for insect and mammalian protein production as well as cryo-electron microscopy, which will form the basis of our research in the coming years. We also published an exhaustive review article on mitochondrial gene expression and RNA maturation as well as two research papers based on work in the Ban lab. ”

- Associate Professor and Group Leader **Eva Kummer**

PLATFORM RUN BY THE PROTEIN STRUCTURE AND FUNCTION PROGRAM

The Protein Production and Characterization Platform provides CPR with purified proteins and protein complexes of the highest quality and characterizes proteins using biophysical methods. The platform is an important asset as entry point for the cryo-EM facility.

Professor Matthias Mann
Research Director
and Group Leader

Proteomics Program

Innovative use of mass spectrometry technology allows the program to map all proteins in a cell (the proteome) to gain a deep biological understanding of cellular processes in health and disease. They can also identify proteins involved in disease and disease biomarkers.

THE NIELSEN GROUP

... develops novel proteomic strategies and combines this with other protein technologies and bioinformatics to understand how underexplored post-translational modifications (PTMs)* of proteins affect mammalian cell biology.

* Post-translational modifications (PTMs) are chemical groups added to proteins after they are synthesized, affecting protein structure and function.

2021 landmark

“ We published several studies that furthers current understanding of ADP-ribosylation (ADPr) – a PTM involved in fundamental biological processes, such as the DNA damage response – and which is still poorly understood. We additionally contributed to several cross-disciplinary studies within CPR with the Groth, Mailand and Duxin groups, where our proteomics analysis provided essential insights into the function of the proteins being studied. ”

- Professor
  and Group Leader
  Michael Lund Nielsen

THE MANN GROUP

... develops innovative methods for rapid quantification of proteins in body fluids and tissue. By profiling patient samples, they aim to identify novel biomarkers that can be used for patient diagnosis and possibly for prevention and treatment of metabolic diseases, such as diabetes and cancer.

2021 landmark

“ We published a preprint paper on Deep Visual Proteomics (DVP), a ground breaking method to identify the disease-specific protein signatures of cells in a tissue sample and then study their protein landscape in depth. DVP can provide doctors with an in-depth understanding of various diseases and possibly identify new drug targets. We also contributed to several cross-disciplinary studies within CPR with the Rasmussen, Nilsson and Lukas groups. ”

- Professor, Research Director
  and Group Leader
  Matthias Mann

THE OLSEN GROUP

... develops mass spectrometry technology towards increased speed and sensitivity while applying it to biological questions such as mapping cellular signalling via growth factor receptors on the cell surface and the study of ancient proteins (palaeoproteomics).

2021 landmark

“ We identified a combination treatment, which could potentially benefit patients with T-cell acute lymphoblastic leukemia (T-ALL), an aggressive cancer mostly affecting children, where about one in four do not respond to or develop resistance against the standard chemotherapeutic treatment. The study demonstrates the potential of proteomics to dissect alterations in cellular signaling and identify druggable pathways in cancer. ”

- Professor, Vice Director
  and Group Leader
  Jesper Velgaard Olsen

THE CHOUDHARY GROUP

... deciphers the regulatory effects of post-translational modifications in cell signalling by subjecting engineered mammalian cell line models to state-of-the-art quantitative proteomics

2021 landmark

“ We published a study that changes the understanding of how cell type-specific genes are activated and deactivated at the right times in either fetal development or in response to internal or external environmental factors. We also contributed to a study with the Groth group that provides a new framework to understand how cells orchestrate repair of DNA strand breaks that arise when DNA is replicated during cell division. ”

- Professor
  and Group Leader
  Chuna Ram Choudhary

PLATFORM RUN BY THE PROTEOMICS PROGRAM

he Mass Spectrometry Platform provides technical support and maintenance for research groups in the Proteomics Program to ensure that CPR retains state-of-the-art mass spectrometry technology. Additionally, the Platform provides analytical proteomics support for CPR researchers.

CPR organization and leadership

The research groups at CPR are organized into five programs. Each program is dedicated to run a technological platform that provides state-of-the-art research resources and interdisciplinary support to fellow researchers in the center.

The governance model incorporates all leaders and principal investigators with top-down advice from the Scientific Advisory Board and bottom-up perspectives from the center's Collaboration, Health and Safety Committee as well as the Student and Postdoc Association.

All key decisions are made by the executive management headed by the Executive Director, who answers directly to the Dean of the Faculty. The CPR executive management team consists of the Faculty Dean, the CPR management, and the Research Directors. The team interacts frequently and on different levels to discuss strategic matters, scientific strategy, finances, and to streamline the day-to-day management

CPR MANAGEMENT
Executive Director: **Jiri Lukas**
Deputy Director and Director of Education: **Jesper Velgaard Olsen**
Head of Administration and Finance: **Peter Dyrsting**

CPR SCIENTIFIC ADVISORY BOARD
Once a year, the Scientific Advisory Board evaluates the center's performance, productivity, innovation, synergy and education. The board consists of some of the most influential scientists of our time, covering world-leading expertise in all of CPR's major research fields.
Angus Lamond (Chair), Wellcome Trust Centre for Gene Regulation and Expression, Dundee University (UK). Expert in proteomics and advanced imaging.
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Christoph Müller, Structural and Computational Unit at EMBL, Heidelberg (Germany). Expert in cryo-EM, X-ray crystallography and advanced biophysical and biochemical approaches.
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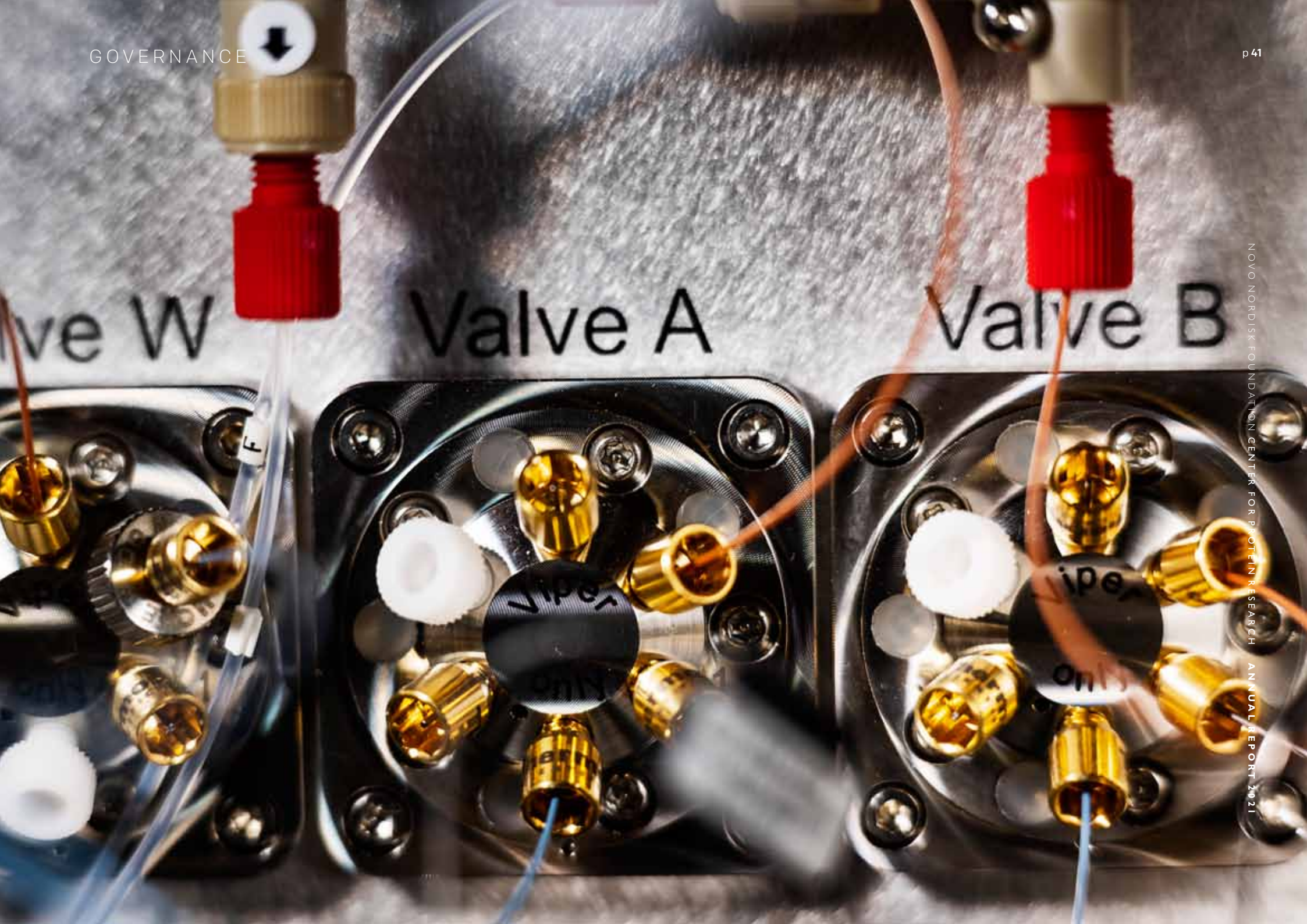
Naama Barkai, Department of Molecular Genetics, Weizmann Institute of Science (Israel). Expert in systems biology and design principles of biological circuits.
Steve Henikoff, Fred Hutchinson Cancer Research Center (USA). Expert in chromatin conformation and epigenetic inheritance.

COLLABORATION, HEALTH AND SAFETY COMMITTEE
A dialogue forum where decisions and new ideas are discussed and developed between management and employee representatives. Topics include personnel policy, work/life balance, trust, cooperation, well-being, safety, competence development and finances.

STUDENT AND POSTDOC ASSOCIATION
A bottom-up initiative created by students and postdocs to promote internal center synergy. Not a governing body per se, but the association has a direct and positive impact on the strategic decisions made by the management, and its representatives have a regular slot at group leader meetings.

CPR GOES GREEN
A bottom-up initiative promoting sustainability in the center's daily activities. Works to reduce the carbon footprint of CPR by implementing green initiatives related to waste, energy, water, lab reagents, consumables and daily habits.


Valve A
Valve B

Publications 2021

The list includes primary research papers, reviews, commentary and book chapters published in 2021 (print and online ahead of print). CPR authors are highlighted in bold.

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Front page: In 2021, Associate Professor and Group Leader Simon Rasmussen (left) and Assistant Professor Jacob Nybo Nissen (right) published a research article describing the Vamb algorithm and how it was used to map bacteria found in the human gut.

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