

EVALUATION REPORT OF THE UNIT  
LCQB - Laboratoire biologie computationnelle et  
quantitative

UNDER THE SUPERVISION OF THE  
FOLLOWING ESTABLISHMENTS AND  
ORGANISMS:

Sorbonne Université – Sorbonne U,  
Centre national de la recherche scientifique -  
CNRS

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**EVALUATION CAMPAIGN 2023-2024**  
GROUP D

Rapport publié le 14/03/2024



In the name of the expert committee :

Jean-Michel Jault, Chairman of the committee

For the Hcéres :

Stéphane Le Bouler, acting president

Pursuant to Articles R. 114-15 and R. 114-10 of the Research Code, the evaluation reports drawn up by the expert committees are signed by the chairmen of these committees and countersigned by the President of Hcéres

To make the document easier to read, the names used in this report to designate functions, professions or responsibilities (expert, researcher, teacher-researcher, professor, lecturer, engineer, technician, director, doctoral student, etc.) are used in a generic sense and have a neutral value.

This report is the result of the unit's evaluation by the expert committee, the composition of which is specified below. The appreciations it contains are the expression of the independent and collegial deliberation of this committee. The numbers in this report are the certified exact data extracted from the deposited files by the supervising body on behalf of the unit.

## MEMBERS OF THE EXPERT COMMITTEE

### Chairperson:

Mr Jean-Michel Jault, CNRS - Centre national de la recherche scientifique, Lyon

### Experts:

Mr Paolo De Los Rios, Ecole Polytechnique Fédérale de Lausanne - EPFL  
Mr Olivier Destaing, CNRS, La Tronche (representative of CSS Inserm)  
Ms Meriem El Karoui, University of Edinburgh, United-Kingdom  
Mr Gilles Kaczmarek, CNRS, Marseille  
Ms Cécile Raynaud, CNRS, Gif-sur-Yvette  
Ms Hélène Touzet, CNRS, Villeneuve d'Ascq  
Mr Patrick Wincker, CEA - Commissariat à l'énergie atomique et aux énergies alternatives, Evry  
Mr Gael Yvert, CNRS, Lyon

## HCÉRES REPRESENTATIVE

Ms Catherine Etchebest

## REPRESENTATIVES OF SUPERVISING INSTITUTIONS AND BODIES

Ms Cécile Bousquet-Antone , CNRS

Mr Stéphane Regnier, Sorbonne Université

## CHARACTERISATION OF THE UNIT

- Name: Laboratoire de Biologie Computationnelle et Quantitative
- Acronym: LCQB
- Label: UMR 7238
- Number of teams: 9
- Composition of the executive team: Director: Mrs. Alessandra Carbone; Deputy Directors: Mr. Gilles Fischer and Mr. Martin Weight

## SCIENTIFIC PANELS OF THE UNIT

SVE Sciences du vivant et environnement

SVE3 Molécules du vivant, biologie intégrative (des gènes et génomes aux systèmes), biologie cellulaire et du développement pour la science animale

## THEMES OF THE UNIT

This is an interdisciplinary laboratory which works at the interface between biology and quantitative sciences. It gathers presently nine teams (two additional teams will join the unit in 2025) made of theoreticians who develop notably bioinformatics predictive tools, model biological systems and biological physics, and experimentalists who make functional and comparative genomics, study evolution and make synthetic biology. The underlying questions asked by the different teams need some quantitative evaluations that are notably based on large-scale production of biological data.

## HISTORIC AND GEOGRAPHICAL LOCATION OF THE UNIT

Originally created in 2009 as a FRE (FRE3214 – Laboratory Genomics of Microorganisms), this laboratory became two years later an UMR (UMR7238). Initially the lab members were spread between different laboratories and were gathered on the same Campus (Cordelier campus, Univ. Pierre and Marie Curie, former name of Sorbonne University – SU) in Feb. 2010. The UMR changed its name in 2014 to become the 'Laboratoire de Biologie Computationnelle et Quantitative' (LCQB) and was integrated in a 'Fédération de Recherche', the Institut de Biologie Paris-Seine (IBPS).

## RESEARCH ENVIRONMENT OF THE UNIT

The unit belongs to the 'Institut de Biologie Paris Seine' (FR3631) that regroups five research units (LCQB; Biological Adaptation and Ageing-UMR8256; Neuroscience-UMR8246/U1130; Developmental Biology Laboratory-UMR7622; Laboratoire Jean Perrin-UMR8237) with a total of 48 research teams, and which hosts six core facilities to technically support the work of the teams (Aquatic Animal; Rodent Facility; Cellular Imaging; Electron Microscopy; Protein Engineering; Bioinformatics). The director of the LCQB is a member of the Steering Committee of this institute. The LCQB, like the IBPS, is part of the Sorbonne University (SU) and is primarily affiliated to the Engineering department (UFR919 'Ingénierie') but has a second affiliation to the Life Sciences department (UFR927 'Sciences de la vie'). Several Assistant Professors or Professors who are members of the unit are heavily involved with teaching duties including managerial tasks in Biology or in Computer Science: two unit members are co-directors of a Master Program in 'Bioinformatics and Modelling' and are coordinators of the European 4EU+ network of Master Programs in Bioinformatics and Modelling (including besides SU, the universities of Heidelberg, Warsaw, Milan, Prague). Another member of the unit was the head of the genetics department of the master of 'Biologie Moléculaire et Cellulaire' (until to 2021). He is now the Director of the doctoral school 'complexité du vivant' (since 2020) and is a member of the executive committee of the UFR Sciences de la vie (since 2018). Another lab member is the director of the i-Bio program which is an interdisciplinary initiative supported by the SU Alliance in the frame of the Idex program (including a PhD program, grants for interdisciplinary projects, starting packages, scientific symposia, postdoctoral fellowships...). He is also a member of the steering committee of the Campus Franco-Indien 'Life sciences for health' between SU and the Indian Institute of Technology of Delhi. Other lab members are involved in different tasks such as being the co-head of the interdisciplinary division in Bioinformatics, Mathematics, and Statistics for Biology, a member of the i-Bio work group for educational initiatives, an advisor for facilities at Sorbonne University (including coordinating shared service units, managing the call for facilities projects...), the Director of the 'Unité Mixte de Service' (PASS, 2019 to 2021), the Director of the UMS 'Omique' (2014 to 2018) and the co-manager of the Genomics platform at the 'École Normale Supérieure'. Also, some lab members are co-director of the 'Genome Analysis' course at the Pasteur Institute (until 2020), co-responsible for the Master 2 in Bioinformatics and Modelling for Biologists (BIM-BMC), president of the Scientific Council of the (until 2022), member of the executive committee of the i-Bio initiative.

The unit is affiliated to three different doctorate schools to attract and grant PhD students with fellowships from the French government: Edite (ED130- 'École Doctorale Informatique, Télécommunications et Electronique'), CdV

(ED515- 'École Doctorale Complexité du Vivant') and ED386 (« École Doctorale Sciences Mathématiques de Paris Centre).

Regarding the link with the CNRS, the unit is primarily affiliated to the INSB ('Institut National des Sciences Biologiques') but has also two secondary affiliations, the INSII ('Institut des Sciences de l'Information et de leur Interactions') and INP ('Institut de Physique'). The main section on which the LCQB depends on for the recruitment of young scientists is the interdisciplinary CID51 commission ('Modélisation mathématique, informatique et physique pour les sciences du vivant') but the thematic of the unit are also related to the scope of the sections 21 ('Organisation, expression, évolution des génomes'), 23 ('Biologie intégrative des organismes photosynthétiques et des microorganismes associés'), 41 ('Mathématiques et interactions des mathématiques'), two ('Théories physiques : méthodes, modèles et applications') and six ('Sciences de l'information : fondements de l'informatique, calculs, algorithmes, représentations, exploitations').

## UNIT WORKFORCE: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	5
Maîtres de conférences et assimilés	10
Directeurs de recherche et assimilés	4
Chargés de recherche et assimilés	1
Personnels d'appui à la recherche	14
<b>Sous-total personnels permanents en activité</b>	<b>34</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	1
Personnels d'appui non permanents	0
Post-doctorants	7
Doctorants	24
<b>Sous-total personnels non permanents en activité</b>	<b>32</b>
<b>Total personnels</b>	<b>66</b>

## DISTRIBUTION OF THE UNIT'S PERMANENTS BY EMPLOYER: in physical persons at 31/12/2022. Non-tutorship employers are grouped under the heading 'others'.

Nom de l'employeur	EC	C	PAR
AUTRE	15	0	5
CNRS	0	5	5
SORBONNE UNIVERSITÉ	0	0	1
<b>Total personnels</b>	<b>15</b>	<b>5</b>	<b>11</b>

## GLOBAL ASSESSMENT

This unit embodies the interdisciplinary in biology with research at the forefront of mathematics, biophysics and bioinformatics with strong links with biologists who used cutting-edge methodologies for large-scale data mining. The scientific objectives are very well defined and the newly set up biofoundry, created and now directed by one of the teams of the unit, will undoubtedly set the stage for future opportunities of collaborative works.

The scientific production is outstanding with more than 185 articles published in highly reputed journals, often in leading positions. This is quite a remarkable achievement for a unit where most of the scientists are teacher researchers with a heavy load of teaching and a strong implication in the management of the university and the educational programs. The fundraising has been extremely successful for most of the teams with, notably, the funds to support the biofoundry creation, one ATIP-Avenir and one ERC consolidator grant, with many additional grants such as ANR for all teams. The visibility of the Lab is recognised at an outstanding level, both

nationally and internationally, for their unique multidisciplinary expertise and this attracts many teams which seek to join this unit. This led to the recruitment of several new teams or group leaders over the last few years, including one ATIP-Avenir, and the senior team which managed the Biofoundry. In addition, two senior teams are expected to join the unit in 2025.

The functioning of the unit complies with all the rules regarding the safety and data protection. It is also in line with the principles of open access science and open-source data and software, thus respecting the FAIR recommendations. The young scientists in the unit are strongly encouraged to start their own lines of independent research and, at all the levels of the unit, there is a global feeling of well-being. This very good working atmosphere is conducive to harmonious development at work and is quite valued by all unit members. Nevertheless, unit members deplore the lack of a laboratory council, which is detrimental to formal dissemination of information between the different categories of staff.

Finally, the unit disseminates its discoveries to the society, in particular to the general public, and transfers them to the economic world, whenever it is possible. This criterium is considered excellent.

## DETAILED EVALUATION OF THE UNIT

### A – CONSIDERATION OF THE RECOMMENDATIONS IN THE PREVIOUS REPORT

The previous committee recommended to:

—‘Implement a procedure to temporarily alleviate the heavy teaching load of university members who look for funds or start new projects.’

SU has indeed launched such a program to reduce this problem during the preparation of competitive grants. One of the lab members benefitted from this program to apply to an ERC consolidator grant.

—‘Implement a mentoring system to improve the integration of small teams newly created.’

This has not been implemented *stricto sensus* but the three young team leaders are encouraged to get advice from other team leaders whenever needed.

—‘Submit grant proposals to two – three team Leaders from the unit, prior to the final submission to authorities, in order to improve the chance of success.’

This has been done only for ERC applications since for national grants (i.e. ANR), all the teams are involved in submitting applications at the same time.

—‘Create a “Conseil de Laboratoire”’.

This has been established but due to the sanitary crisis, this laboratory committee stop meeting quite prematurely. Clearly, this is a major issue that will need to be fixed for the next contract (see here below).

—‘Have a broader vision on how the computational approaches can be combined with experimental investigations to tackle major issues in Biology, notably to help raise international grants.’

A new scientific orientation has been initiated with the synthetic biology axis and the lab was quite successful in raising funds and was notably awarded an ERC consolidator; They were two additional applications to ERC this year.

—‘Create a “platform” to showcase the Bioinformatics tools and datasets produced by the unit, thereby promoting a larger utilisation by the scientific community and increasing the lab visibility.’

Although this is definitely a matter of concern for the unit, the paucity of engineers precludes such a recommendation, but all the tools, open software and databases developed by the LCQB are publicly available.

### B – EVALUATION AREAS

#### EVALUATION AREA 1: PROFILE, RESOURCES AND ORGANISATION OF THE UNIT

##### Assessment on the scientific objectives of the unit

The scientific objectives of this interdisciplinary unit are clearly defined with unique opportunities that build on the tight connection with the recent creation of the bio-foundry.

### Assessment on the unit's resources

There is a high ratio of 'teaching researcher'/'full-time researcher' in this unit with a lot of teaching duties and a paucity of Engineers/Technical staff. The ability of the unit/teams to raise funds is really outstanding.

### Assessment on the functioning of the unit

The functioning of the unit complies with all the rules regarding the safety and data protection. Despite a general feeling of well-being shared by all staff members, the lack of 'laboratory council' with written reports precludes for a formal dissemination of information.

*1/ The unit has set itself relevant scientific objectives.*

#### Strengths and possibilities linked to the context

The scientific themes developed in the LCQB is focusing on fundamental aspects of the research in Biology with a blend of unique expertise in large-scale data mining with computational methods as well as modelling using notably mathematical developments. The goals of the LCQB studies are to understand how the interactions among molecules shape the cells, allowing their adaptation to the environment from a molecular scale to a more integrative vision at the level of cells, tissues, organs or even within whole populations.

Since the creation of this unit, evolution and genomics have been the foundations of the research and they remain central to the development of the projects that are declined according to three axes: Computational, Quantitative and Synthetic Biology. This later axis was recently implemented in the unit and will be strongly supported by the late creation of the bio-foundry. This asset will undoubtedly foster new opportunities of projects leading potentially to grant applications such as European calls, with possibly translational applications linked to industrial developments.

#### Weaknesses and risks linked to the context

There is no weakness or risk identified.

*2/ The unit has resources adapted to its activity profile and research environment, and makes use of them.*

#### Strengths and possibilities linked to the context

As of January 2023, the unit is composed of 63 members including 27 permanent and 36 non-permanent members. Permanent members include fifteen Assistant Professors or Professors, five Researchers or Research Directors and seven Engineers or Technical Staff. Non-permanent staff is composed of eight postdoctoral students, 21 PhD students, plus seven Engineers and Technical Staff.

The unit has been extremely attractive to recruit PhD students and Postdoctoral students. In addition, without including the PhD scholarships or teaching fellowships, the unit has been very successful to finance their research as it secured more than 8.8 M€ during the 2017–2022 period, the large majority coming from the grants obtained by each team.

#### Weaknesses and risks linked to the context

The main risk is that the permanent members comprise many Assistant Professors/Professors, each of them having a heavy teaching load ( $\geq 192$  h/year) with an ever-increasing requirement for administrative tasks linked to it. This burden might put at stake the exceptional quality of the research performed up to now, but this is, unfortunately, very often the daily life of 'teacher researcher' in many French Universities. Some teams remain quite small with a single permanent researcher.

*3/ The unit's practices comply with the rules and directives laid down by its supervisory bodies in terms of human resources management, safety, the environment, ethical protocols and the protection of data and scientific heritage.*

#### Strengths and possibilities linked to the context

This unit complies with all the rules regarding the safety of the staff members, the environment and the protection of scientific assets. The unit director and deputy directors exchange on a regular basis with the team leaders, whenever a joint meeting is needed or via emails with copies to all PI. All major decisions (budget, research, general issues on personnel) are usually taken in a collegial way, usually by consensus from all team leaders. The main decisions regarding the unit practices and policy is well dispatched among the different staff categories but in a very informal manner (see the point below). The Hcéres committee acknowledges the very good atmosphere that prevails in this unit leading to a well-being of all staff members (students, postdoctoral students, technicians and engineers, administrative people, researchers, and PI) and the management of the unit by the director and deputy directors deserves strong credit for this overall feeling of contentment.

#### Weaknesses and risks linked to the context

The laboratory council has been stopped during the sanitary crisis and not resumed since then. This is clearly a weak point that prevents the diffusion of information in an official manner. The lack of engineer dedicated to computer installations and network access is a clear limitation for all staff members.

## EVALUATION AREA 2: ATTRACTIVENESS

### Assessment on the attractiveness of the unit

The unit has attracted many new group leaders, including one ATIP-Avenir, a senior team in the recent years, and two additional senior teams are expected to join the unit in 2025. One team created, and is now directing, the biofoundry. The young scientists are strongly supported to start independent lines of research. Overall, the unit has been extremely successful in fundraising. The attractiveness of the unit is therefore outstanding.

*1/ The unit has an attractive scientific reputation and is part of the European research area.*

*2/ The unit is attractive because for the quality of its staff support policy.*

*3/ The unit is attractive through its success in competitive calls for projects.*

*4/ The unit is attractive for the quality of its major equipment and technical skills.*

#### Strengths and possibilities linked to the context for the four references above

This unit is at the interface of several fields in science including biology (genetics and microbiology), formal sciences (mathematics, computer science, physics), and medical sciences (microbiology, parasitology, mycology and virology). It is a vivid example of interdisciplinarity with a unique position that complements the research themes otherwise present on the Jussieu Campus. As such, it plays a central role in teaching in different programs at SU (i.e. genetics, genomics, bioinformatics, modelling in biology) in particular in a joint Master in 'Bioinformatics and Modeling' originally created, and now operated, by team members.

The outstanding reputation of the unit led to the recruitment of three new scientists as three new PIs, one in 2018 (a biologist), one in 2022 (a biophysicist) who holds a competitive ATIP-Avenir grant, and a third one in 2022 (a



computer scientist). Moreover, a new DR CNRS from section 41 and coming from Lyon just join the lab in 2023. On top of that, the unit has integrated a senior team in 2019 which extended the scientific boundaries of the unit to empower the Synthetic Biology axis. This led notably to the creation of the biofoundry in April 2023. This Synthetic Biology axis will be reinforced in 2025 with the arrival of another senior team. In addition, a second senior team, today at B2A, will join the lab in 2025.

The high reputation of the unit members is also reflected by their strong involvement in the science at the University level, e.g. being part of the steering committee of the Labex Calsimlab (SU 2012–2019), director of the i-Bio program, official advisor for many facilities at SU or coordinators of the European 4EU+ network of Master Programs (see the research environment section), or different evaluation committees (e.g. president of the SAB of the LBMC (ENS de Lyon, 2017 and 2019) or members of Hcéres committees. Members of the unit received several awards such as senior IUF (2013–2018) for the unit director, or the prizes Thierry Célérier–Femmes & Sciences and Prix Jeunes Talents France 2022 L'Oréal-Unesco pour les Femmes et la Science, for a PhD student, and the research prize of the Academy of Sciences of Cuba to one of the deputy directors (2022). One PI is a deputy director of INSB-CNRS, responsible for the Genetics and Genomics field.

The attractiveness of the unit is also demonstrated by a large number of national and international collaborations with top research centers.

To facilitate the integration of young team leaders, they receive 10 k€ from the unit to help their installation. The unit encourages the young permanent members to submit grant proposals and become independent in their research activities, and the unit fosters collaboration with Post-Docs and supervision of PhD students. This appears quite successful as all assistant professors succeeded in getting grants and thus they can lead independently their own lines of research. Young researchers are financially helped to organise a one-day conference to increase their visibility and promote their network.

To ease the integration of new PhD students or postdoctoral fellows, there is a working group in the unit where they present their work to each other. They are encouraged to participate in national and international meetings and the unit can contribute to the cost of these conferences.

At IBPS, the PhD and Post-Docs Association (IDPA) organises activities that facilitate the integration of newcomers.

The unit has been extremely successful to secure grants during the last five years among which it obtains a total of seventeen ANR including three ANR JCJC (plus some ANRS, Ligue contre le cancer, CNRS MITI grants...). Thanks to these grants, the unit recruits many PhDs and Postdoctoral students (half of the personnel of the unit) in addition to some PhDs that obtained some fellowships from the University. The unit was also strongly involved in two 'Investments for the Future Program' of the French Government, one PIA – 'Programme d'Investissement d'Avenir' –, in Bioinformatics (2017–2020) and the labex CALSIMLAB dedicated to Bioinformatics and Theoretical Chemistry (2013–2018). One PI got a competitive ATIP-Avenir grant. On top of that, one PI of the unit created the Biofoundry.

At the European level, one unit member got an ERC consolidator grant in 2022 and another member was involved in two European grants (Eurostars and MSCA-RISE programs).

Without PhD fellowships from doctoral schools or teaching fellowships from the university (ATER), the funds raised by the unit totalise 8.8 M€.

One of the major strengths is the Biofoundry hosted by the unit and this unique new structure will undoubtedly be quite appealing for many scientists involved in Synthetic Biology, thereby promoting new opportunities for collaborations. In line with this, the team in charge of this structure was involved in a European collaborative project to develop a cloning toolkit (MoClo) for Chlamydomonas. MoClo has generated a strong interest from the scientific community and is now widely used worldwide (>150 citations in 4 years).

Moreover, the exceptional expertise developed over the years by the LCQB in Computational and Quantitative Biology and Mathematical Modelling puts it at the forefront internationally.

## Weaknesses and risks linked to the context for the four references above

One team which will join the lab in 2025 is presently hosted by Inserm and it will apply to be an ERL – 'Équipe de Recherche Labelisée' – from Inserm, but this configuration is still under discussion with the funding bodies and this will need to be clarified as soon as possible.

## EVALUATION AREA 3: SCIENTIFIC PRODUCTION

### Assessment on the scientific production of the unit

With more than 185 articles published in highly reputed journals, and very often in leading positions, the scientific production of the LCQB is outstanding. The unit also releases many open-source softwares and adheres to open access science and the FAIR principles.

- 1/ The scientific production of the unit meets quality criteria.*
- 2/ The unit's scientific production is proportionate to its research potential and properly shared out between its personnel.*
- 3/ The scientific production of the unit complies with the principles of research integrity, ethics and open science. It complies with the directives applicable in this field.*

### Strengths and possibilities linked to the context for the three references above

The unit has produced > 185 articles during the period under evaluation, many of which are being published in top-quality journal (e.g. Science, Nat. Genetics., Proc. Natl. Acad. Sci. U.S.A., Nucleic Acids Res., PLoS Comput. Biol. ...), and very often the researchers of the unit are in a leading position in these articles. The work issued from the computational biology has been accompanied by the release of new softwares (14), web servers (4), or databases (3) and they are all freely available to the scientific community. Given the high number of teachers/researchers in the unit and their strong implication in teaching duties, this scientific production is outstanding both in terms of quality and quantity.

As mentioned above, many scientists in the unit have heavy loads of teaching but they nevertheless maintain at the same time an exceptional level of scientific production, and this quality of production is shared among all the teams. All PhD students and postdocs publish at least two papers during their stay in the lab. The technical staff is associated to the publications and the young researchers have the opportunity to develop their own projects.

The LCQB is committed to open science and is ranked above the other research units of SU for this criterion. It also uses preprint servers (Arxiv, BioRxiv, HAL) and shares many codes and softwares directly accessible from the unit website or from public repositories. The unit also adheres to the FAIR (Findability, Accessibility, Interoperability and Reusability) principles.

### Weaknesses and risks linked to the context for the three references above

No weakness was noted

## EVALUATION AREA 4: CONTRIBUTION OF RESEARCH ACTIVITIES TO SOCIETY

### Assessment on the inclusion of the unit's research in society

The unit has developed strong ties with the society and tries to transfer its discoveries to the economic world, or share them with the general public, whenever possible. This criterion is considered as excellent.

- 1/ The unit stands out for the quality and the amount of its interactions with the non-academic world.*

*2/ The unit develops products for the cultural, economic and social world.*

*3/ The unit shares its knowledge with the general public and takes part in debates in society.*

Strengths and possibilities linked to the context for the three references above

The unit director is a member of the scientific committee of the IHEST – 'Institut des Hautes Études pour la Science et la Technologie' – since 2017 that helps decision-makers to take action on economic and societal issues, based on scientific knowledge. The DNA data storage technology was developed by one team in close partnership with the 'Archives Nationales' and the proof of concept was used to encode two historical texts: the 'Declaration of the rights of man and of the citizen' (in 1789) and the 'Declaration of the rights of women and the female citizen' (in 1791). This led to a press conference and had an important impact in different media (e.g. TV news and radio broadcasts...).

The unit director is a member of the Tremplin Carnot Smiles, to strengthen the interaction between academia and industry on the possible application of mathematics (2017–2019). One patent was submitted by a member of the unit to treat hepatitis B and D infection. One team which develops Synthetic Biology got a grant with an industrial group (Pierre Fabre) and a Cifre was also obtained from this company to develop new microalgae strains. This team was awarded a CNRS innovation fund, a prematuration fund from SU and the SATT Lutec and its work on DNA storage technology led to the creation of the start-up company, Biomemory. This start-up was a laureate of the i-Lab competition (2021) and raised 5 M€ of seed funding (2022). One member of the unit developed new modules for microscope in collaboration with a private company (Errol Laser). Other collaborations with private companies were developed (cLecta in Germany, Innophore in Austria) in the context of a European funding (Eureka Eurostars). One unit member is in charge of the organisation of the meeting MABI – 'Matinée sur les applications de la bio-informatique' – at SU to bring together master students, biotech start-ups, and industrial groups.

As indicated above, the DNA storage technology was widely advertised in many media and thus made publicly available to a large audience. The unit has overall many outreach activities to promote science to a large public. In addition, many articles from the unit are published in open access journals.

Weaknesses and risks linked to the context for the three references above

No weakness was noted.

## ANALYSIS OF THE UNIT'S TRAJECTORY

The Unit name will be changed from LCQB to LCSQSB to acknowledge the new scientific direction of the lab by including the Synthetic Biology axis. This is quite appropriate, especially with the creation of the Biofoundry. The unit has been actively looking for a new director for the next contract by launching a call in 2022 but, unfortunately, this quest has been unsuccessful so far. If the perfect candidate cannot be found, the only option chosen by the unit would be that one of the two deputy directors will take over the lead for the next contract. The committee is aware that this may be the only possible solution and greets the deputy director's dedication for the sake of the unit.

## RECOMMENDATIONS TO THE UNIT

### Recommendations regarding the Evaluation Area 1: Profile, Resources and Organisation of the Unit

Although the well-being of all staff members have been deeply appreciated by the Hcéres committee members, and the availability of the director and deputy directors acknowledged by all unit members, the direction of the unit needs to rejuvenate the laboratory council with new elections. This council must meet at least twice per year to allow an efficient flow of information in a very formal way, with a written report to be shared with everyone in the unit.

The relationship between the IPBS and the LCQB does not appear to be optimal at the moment but the two parties should find a way to restore an efficient collaboration between them.

There is an urgent need to find a dedicated person for the informatic resources of the unit.

### Recommendations regarding the Evaluation Area 2: Attractiveness

The scientific relevance for the integration of the two new teams, particularly for the bio-foundry, was well appreciated by the committee.

The smaller team needs to be strengthened in terms of recruitment, so strategic choices will have to be made.

If new experimentalist teams are to be recruited in the future, one has to think about attributing some technical help for these teams. If necessary, some money could be withdrawn from all the grants to help support these new teams (e.g. some temporary contracts be paid by the unit).

The LCQB was particularly successful for fundraising but due to the exceptional visibility of this unit, notably at the international level, this could lead to an increase in getting European funds.

### Recommendations regarding Evaluation Area 3: Scientific Production

The unit should maintain the exceptional quality performed in the unit together with the excellent working conditions for the staff members.

### Recommendations regarding Evaluation Area 4: Contribution of Research Activities to Society

There is no specific recommendation regarding this particular point.

## TEAM-BY-TEAM OR THEME ASSESSMENT

**Team 1:** Analytical Genomics  
 Name of the supervisor: Mrs. Alessandra Carbone

### THEMES OF THE TEAM

The team's federating theme is computational biology, which encompasses several specific areas, including gene and protein analysis, protein conformations, protein-protein interactions, genotype-phenotype relationships, genome architecture, and evolutionary studies. The methods employed across these application domains draw upon theoretical models incorporating algorithms, statistics, and deep learning.

### CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

In the preceding evaluation, the committee made several recommendations:

—The collaboration with biological teams within the IBPS should be strengthened:  
 There is no clear change in this direction. A point worth noting: collaborations with other teams from LCQB are still active, with several joint publications during the period (namely with Synthetic and Systems Biology of Microalgae and Biology of Genomes teams).

—The team should consider having a third faculty member applying to the HDR to efficiently supervise the PhD students:  
 All permanent members of the team now hold an HDR.

—The team should prioritise the projects to avoid losing a clear focus in their research topics:  
 The team continued on its path without any adverse effects.

### WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	1
Maîtres de conférences et assimilés	1
Directeurs de recherche et assimilés	0
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	0
<b>Sous-total personnels permanents en activité</b>	<b>2</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	2
Doctorants	6
<b>Sous-total personnels non permanents en activité</b>	<b>8</b>
<b>Total personnels</b>	<b>10</b>

## EVALUATION

### Overall assessment of the team

The team conducts outstanding research with a strong national and international presence. It also maintains a rich and well-balanced portfolio of activities for all aspects under consideration (teaching, training, software development, animation of the community...).

### Strengths and possibilities linked to the context

The team is highly dynamic, producing a substantial body of scientific work published in outstanding journals well suited to disseminating its interdisciplinary research to the community (more than 30 publications over the period). The team's scientific contributions are also reflected in the development of open-source software, which is distributed to the user community and widely cited.

The team has consistently developed its research themes coherently since the last evaluation, aligning them with the contemporary challenges in biology and bioinformatics, such as a growing role of deep learning and new applications to genomics. All of these strengths are accompanied by a high level of contractual activity (5 ANR projects, 2 ANRS and 2 PIA during the period, and an ERC grant in 2023), strong national visibility (both current permanent members are members of IUF), and international visibility through participation in European networks and consortia (CAPRI, Elixir, two cost action, European Reference Genome Atlas), multiple invited talks in international conferences (more than 40 for the period), presence in program committees of major conferences in the field (including WABI – co-chair in 2021 and ISMB/ECCB co-chair in 2023).

The team has an ambitious training policy for young researchers (PhD students and postdocs), resulting in the recruitment of four former team members by EPSTs during the assessment period. Additionally, the team actively engages in academic teaching, offering bioinformatics courses, co-heading the interdisciplinary division in Bioinformatics, Mathematics, and Statistics for Biology, Life Sciences Department of the University, coordinating the 4EU+ European network of Bioinformatics Programs (with the universities of Heidelberg, Warsaw, Prague, Milan) and contributing to the Meet-U experience. Furthermore, it is involved in community outreach through the GDR BIM working group, and it extends its scientific outreach through the creation of videos and articles for the general press.

Finally, the addition of a new CNRS researcher in 2023 will strengthen the team's human resources and further enrich its methodology.

### Weaknesses and risks linked to the context

As previously mentioned in the preceding report, the topics addressed by the team are quite diverse, and there is a risk of dispersion, even though the team members appear to handle this diversity well (and perhaps even draw inspiration from it).

Another concern is the limited number of permanent researchers and the team's reliance on temporary contract resources. The addition of more permanent staff members could assist the team in both reinforcing their interactions with other groups within the unit and consolidating their position in the laboratory.

### Analysis of the team's trajectory

The team has an ambitious and timely research project, further enriched by the arrival of a new CNRS research director. Key features include an increased emphasis on deep learning in the methods employed and developed. The applications build upon the team's existing work on protein-protein interactions, protein conformation and evolution, with an added focus on health. In addition, new research themes are introduced such as antimicrobial resistance, bacterial genome-wide association studies, phylogeny, and phylodynamics. It's worth noting that the antimicrobial resistance research could potentially lead to new collaborations within the laboratory.

The proposed project aligns well with the team's existing skill set, collaborations and resources. One challenge in the coming years will be to foster synergy, ensuring that the individual research themes and skills serve as sources of creativity and inspiration for the team as a whole.

## RECOMMENDATIONS TO THE TEAM

The committee recommends continuing the excellent work, with a specific emphasis on maintaining close connections with the ongoing theoretical research conducted in the mathematical and computer science community.

**Team 2:** Genetic Networks  
 Name of the supervisor: Mr. Frederic Devaux

## THEMES OF THE TEAM

The general theme of the group is the evolution of gene expression, using yeast as a resource for experimental genetics and comparative genomics/transcriptomics. One axis, led by the PI, covers the structure and evolution of transcriptional networks, searching for specificities of transcriptional regulations in evolutionary branches; a second axis, led by another teacher researcher, covers translationally regulated protein fates, and in particular the role of N-ter signals to target proteins to the mitochondria, and how this regulation evolves across yeast species.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

In the previous evaluation, the committee recommended to:

- increase collaborations. This has not been achieved yet. Nonetheless, the team has worked on this point: a comparative transcriptomics project on sexual identity and cycles in the *Nakaseomyces* group of yeasts is planned and will involve Université Paris Saclay and McGill University. This work has not started yet but a collaborative ANR grant application was submitted last year and will be resubmitted this year. In addition, an upcoming collaboration with team 1 is mentioned and discussions recently started with external specialists of co-translational protein regulations (Univ. Paris Saclay and IJM Paris).
- consider innovation projects with potential medical applications. This was not achieved. Nonetheless, the team is considering working on questions related to mitochondrial import defects in diseases.
- increase team size and especially recruit PhD students. This was achieved: the team was of 3 permanent staff, two non-permanent support and one PhD student. It is now of five permanent staff, one non-permanent support and three PhD. Students.
- keep focused and avoid working on too many research problems. This recommendation was followed.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	2
Maîtres de conférences et assimilés	2
Directeurs de recherche et assimilés	0
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	1
<b>Sous-total personnels permanents en activité</b>	<b>5</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	0
Doctorants	1
<b>Sous-total personnels non permanents en activité</b>	<b>1</b>
<b>Total personnels</b>	<b>6</b>



## EVALUATION

### Overall assessment of the team

Given its heavy load in teaching and management, the team has made very good scientific achievements with three core studies published in international journals, and by contributing to other publications. The team's involvement in teaching programs and technological facilities contributes to the implication of the unit in the local community. No funding is already obtained beyond 2024 but the team is actively applying for grants. The research is in line with the computational and quantitative biology nature of the unit and with several other units' teams working on evolutionary processes.

### Strengths and possibilities linked to the context

The team discovered, in the yeast *S. cerevisiae*, the conserved role of position 2 amino-acid in driving the co-translational modification of proteins that address them to the mitochondria. These results were published in a recent PLoS Genetics publication (first and last authors from the team) and will therefore reach the international community interested in such regulations. The publication describes a rigorous and abundant work, which started from bioinformatic predictions and followed up with innovative experimental validations and robust findings. This position 2 rule seems fundamental and exploring its evolutionary origin and history is a promising route to make discoveries.

The overall productivity of the team (8 research articles, 2 review articles and 1 book) is not outstanding but very good given the heavy teaching load of all permanent researchers. These productions indicate an ability to stay focused on specific projects and get them finalised.

The team has a long-time expertise in functional genomics and comparative transcriptomics as well as yeast molecular genetics. This, and the data already gathered on a new project on iron starvation in non-model yeast, is a strength for the proposed work.

The team is deeply involved in teaching. This provides possibilities for the recruitment of students.

The team is also involved in management beyond its own perimeter (the PI is director of a graduate school, a team member is an advisor of ~150 technological facilities at Sorbonne University). This offers networking with many other laboratories and possibilities for exchanges and collaborations.

The research themes and approaches are in adequacy with the interdisciplinary context of the unit and with several other teams working on evolutionary genomics/proteomics (teams 1, 3, 8). This offers possibilities for scientific interactions such as shared lab meetings and journal clubs for example.

### Weaknesses and risks linked to the context

The major weakness of the team is the very heavy teaching load and duty load of all permanent scientists, leaving a limited amount of the time for research projects.

Another weakness is the very limited secured funding of the team, with no financial support beyond 2024. This (unfortunately) happens and the team seems prepared to re-applying to national sources. Partnering with other laboratories on possible medical applications (strategies against fungal infections or against mitochondrial diseases) could open opportunities to apply to additional, health-related, programs.

The results on comparative transcriptomics were published in 'Frontiers in' journals. These are peer-reviewed and open-access media, but their readership is much specialised and this limits the international visibility of work.

Finally, the team does not meet regularly to discuss science collectively. Team members rarely confront their scientific interpretations and hypotheses to the views of their immediate colleagues and this may slow the progress of their research. The lack of regular lab meetings may also generate communication issues among team members.

### Analysis of the team's trajectory

The work achieved on fungal transcriptomics led to descriptions of whole-genome transcriptional regulations in the pathogen *C. glabrata* and to the identification of species-specific transcriptional signatures. In project 1, the team will apply their comparative approaches to study i) the regulation of sexual identity and sexual cycles in another group of yeasts (*Nakaseomyces*) and ii) iron-starvation stress in twelve non-model yeast species. The first study is planned with external collaborators and will start after funding is obtained. The second study was initiated with starting grants from CNRS (a first dataset was produced). Given the funding uncertainty and the specificity of the topics addressed, the committee is not convinced that these studies will produce results of high

impact and international visibility. Nonetheless, given the teaching and management load of the PI, it is a good choice to seek collaborations where the team's expertise is valuable, such as envisioned in study (i).

Regarding project 2, the trajectory initiated with the discovery of the 'position 2' rule of protein Nter co-translational modification is promising: the team will study the evolutionary origin and history of this regulation, and the committee considers this strategy as novel, of importance (because fundamental in the understanding of protein regulations in eukaryotes), focused-enough given the team workforce and in good synergy with the activities of other teams of the unit.

## RECOMMENDATIONS TO THE TEAM

The committee recommends prioritising the team's efforts on project 2. Success on the transcription network front (project 1) will depend on the collaborative project on sexual identity and life cycle in *Nakaseomyces* yeasts which requires funding; the committee recommends pursuing fundraising efforts (ANR resubmission or other sources) and to look for alternative collaboration opportunities (within and outside the unit) where the transcriptomics expertise can be exploited. The committee also strongly recommends to (re-)establish regular scientific exchanges within the team and with other teams of the unit, by scheduling lab meetings and journal clubs where science is presented and discussed collectively.

**Team 3:** Biology of Genomes  
 Name of the supervisor: Mr. Gilles Fischer

## THEMES OF THE TEAM

The group has two main research axes. Axis 1 focuses on genome functioning. Using *E. coli* as a model, they study how the regulation of gene expression allows cells to coordinate essential processes such as DNA replication, cell division and cell growth, and how this allows adaptation to unfavourable conditions, notably exposure to sub-lethal antibiotics doses. Axis 2 studies genome evolution in yeast. Both axes use an elegant combination of experimental data and mathematical modelling.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

After the previous evaluation, recommendations were to (i) strengthen their interactions with other groups at IBPS and other yeast genomics group at the international level, (ii) trying to attract postdocs and more female members, (iii) to take into account 3D genome organisation in their studies, and to add some expertise in bioinformatics to the group.

Most of these suggestions have been met. The team as obtained funding to support a collaboration with two research groups in Chile, which has allowed exchanges of PIs and PhDs between the two labs. This collaboration has already led to two joint publications. They also have fruitful interactions with other groups at LCQB, with whom they published articles in excellent journals. Since the previous evaluation, one person has joined the team, which meets the advice to try and attract female members. The group has also attracted two postdocs. Only the last point does not seem to have been taken into account, or at least this does not stand out based on the report.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	1
Directeurs de recherche et assimilés	2
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	1
<b>Sous-total personnels permanents en activité</b>	<b>4</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	1
Doctorants	1
<b>Sous-total personnels non permanents en activité</b>	<b>2</b>
<b>Total personnels</b>	<b>6</b>

## EVALUATION

### Overall assessment of the team

This research group is outstanding with a strong publication record, novel and seminal results on both research axes developed in the team, high success in grant application and strong activity in training through research. Over the last five years, the number of permanent staff has increased, allowing the team to diversify its strengths, with the development of new collaborations, and more outreach activities.

### Strengths and possibilities linked to the context

The team has an outstanding publication record, with 24 publications during the evaluated period (6 as senior authors) in internationally recognised journals such as Nature Comm, PLoS Genet or mSystems. The team has made very significant advances in both research axes. Regarding the functioning of the bacterial genome, they have discovered that sub-lethal doses of antibiotics that act by inhibiting translation result in an unexpected decrease in transcription due to a limitation of free RNA polymerase activity. This original result published in mSystems in 2020 provides a novel framework to understand the appearance of antibiotic resistance. Regarding genome evolution, the group has notably studied the evolution of temporal replication programs in yeast (Nat Comm 2018), showing that replication origins are permanently gained and lost during evolution. Importantly, they also show that origin loss and gain occur in close proximity, suggesting that natural selection acts to keep origins regularly spaced along chromosomes, or that constant loss of origins prevents the maintenance of origin-rich regions in the genome. In parallel, they have generated a CRISPR/Cas-based system to be induced controlled genome rearrangements in yeast (PLoS Genetics 2019). They thus have a very powerful tool in hand to elucidate how genome architecture impacts cellular phenotypes. Very recently, the group has characterised the genome of over 140 yeast isolates, unravelling the unexpected complexity of yeast genomes in the wild (Nat. Genetics. 2023). This yeast pangenome sets the ground for the team's research project.

**Attractiveness:** Attractiveness of the team is outstanding. The group has been very successful in its funding application, securing over 600k€ during the last five years. One ANR project is still ongoing. They have attracted two postdoctoral students during the evaluated period, which illustrates their international recognition. In addition, both GF and BS have been invited to give several seminars in Europe and in South America. The outreach activities of the group have increased, and have reached an excellent level. The PI has many institutional responsibilities, notably as deputy director of the research unit and director of the I-Bio initiative.

### Weaknesses and risks linked to the context

The group has attracted new members during the past five years, which increases their potential to obtain funding, expands their collaborations and brings together two complementary research topics. As mentioned above, the publication record of the group is excellent. On possible point that could be improved is that not all PhD students and postdocs that worked in the groups during the evaluated period have published a first-author paper at this stage. However, some of them defended their PhD quite recently. Another point is that the two research axes, although complementary, appear to be completely independent. However, beyond the research topics that can appear very different, the team members share approaches and expertise that can benefit to both projects. The group's interactions with the private sector remain very limited, but their focus on basic research questions gives excellent results.

### Analysis of the team's trajectory

The group proposes two very original research lines that are well supported by preliminary data, and will make the most of the team's expertise and of the tools they have generated in the past few years. Regarding the part on genome functioning, they wish to follow up on their finding that adaptation of cells to sub-lethal doses of antibiotics can go through global reprogramming of gene expression. They are planning to combine wet-lab and computational approaches to test their hypotheses. Regarding the part on genome evolution, the group hopes to revisit the life cycle of *S. cerevisiae*. This project stems from the recent intriguing discovery that polyploidy and heterozygosity are much higher in natural populations than would be expected if the yeast life-cycle fitted the commonly accepted view. This project is timely as studies in a number of unicellular organisms are beginning to reveal that genetic diversity is much higher than anticipated, and we now need to understand the molecular and cellular mechanisms that explain

this diversity. Like the first research axis, this project will combine computational biology (bioinformatics and mathematical modelling) with experimental approaches (genome editing and experimental evolution). These two projects are based on recent and very interesting novel findings, and the team has all the required expertise to conduct them successfully. In addition, both fit nicely with the global objectives of the Unit, notably by combining theoretical and experimental approaches.

## RECOMMENDATIONS TO THE TEAM

The panel recommends that the team continues taking care that PhD and postdoctoral students obtain first-authors papers as soon as possible after the completion of their projects.

Given the considerable progress that has been made recently in the analysis of 3D genome architecture, the group could consider it in their project. Notably, the group has generated unique tools to manipulate the yeast genome, and now has all tools in hand to address long-standing questions regarding the determinants of 3D genome organisation.

The team lacks permanent staff dedicated to computational biology and modelling. The panel suggests that they may try to attract candidates to recruit a CNRS researcher who could bring this expertise to the team.

**Team 4:** Synthetic and Systems Biology of Microalgae  
 Name of the supervisor: Mr. Stephane Lemaire/Mr. Julien Henri

## THEMES OF THE TEAM

Team 4 is developing new tools and methods to understand photosynthetic carbon fixation, adaptation to environmental stresses, and the redox signalling network in green microalgae (*Chlamydomonas reinhardtii*) and cyanobacteria (*Synechocystis PCC6803*). In the long term, they are aiming to use the photosynthetic organisms' inherent ability to fix CO<sub>2</sub> to produce organic molecules in a sustainable and sunlight-dependent process. This is addressed using a synthetic biology approach combining fundamental understanding and practical applications. There are five research areas: DNA Data Storage, Synthetic Biology of Microalgae, Structure and Interactions of Calvin-Benson Enzymes, Redox Signalling Network, and Environmental Stress Responses.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The team was not evaluated in the previous report

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	3
Directeurs de recherche et assimilés	1
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	6
<b>Sous-total personnels permanents en activité</b>	<b>10</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	0
Doctorants	2
<b>Sous-total personnels non permanents en activité</b>	<b>2</b>
<b>Total personnels</b>	<b>12</b>

## EVALUATION

### Overall assessment of the team

The team is assessed as outstanding. Their achievements are impressive and their trajectory is coherent and ambitious whilst simultaneously realistic. It has an excellent publication track record and has secured significant funding for the future. Despite a hefty teaching load, it is very productive and fully engaged in training through research.

### Strengths and possibilities linked to the context

Team 4 has made a major strategic choice to steer their scientific expertise towards synthetic biology since 2015. They are poised to become the reference group in France (and likely in Europe) for synthetic biology of photosynthetic organisms. Indeed, they are combining deep expertise in photosynthetic processes with novel

technical development from synthetic biology such as a MoClo system for *Chlamydomonas* (they were coordinators of an EU project to develop the toolkit) or DNA digital storage (with a start-up founded in 2021). The team is now taking this commitment to the next level by creating the Biofoundry Sorbonne University (BFSU) co-led by two team members.

The team has an outstanding publication track record (45 publications in 5 years) and has obtained an impressive amount of external funding. The team is fully engaged in training through research, having trained three postdoctoral researchers and five PhD students. The three PhD students who have already defended their PhD published very nice papers, which will set the base for their future scientific career. Two permanent researchers have obtained their HDR and all participate actively and successfully in gaining external funding.

The attractiveness of the team is outstanding. They are extremely efficiently organized, each scientist in charge of a research axis secured funding to support his research. The PI of the group is extremely well recognised at the international level, and all group members are well-recognised experts who get invited to give seminars and to present their work at international conferences.

The inclusion of the group in society is outstanding. Through the creation of a company and the biofoundry, they have taken an important step towards the exploitation of their findings. On the one hand, they are moving rapidly towards the development of an effective data storage method that will have a very low carbon impact and has the potential to solve crucial issues for a variety of end users. On the other hand, the biofoundry is expected to have a major impact both for the scientific community and for the development of partnerships with the industry.

The involvement of the team in LCQB will ensure continued interaction with other synthetic biologists (e.g. team 11) as well as theoreticians. There is an excellent opportunity to integrate more AI/ML approaches to the synthetic biology design-built-test concept.

## Weaknesses and risks linked to the context

International funding has so far been somewhat less than could be expected, given the team position. Whilst this is not a weakness *per se*, there is an opportunity that could probably be further developed and could contribute to increasing further the international standing of the team. The very heavy teaching load of some of the team members is noted and likely limits some of the potential developments, including applying to large projects (i.e. ERC).

The setting up of BFSU will be a time-consuming process but the team has identified an additional team leader, which mitigates the risk.

## Analysis of the team's trajectory

The team will continue to develop their research program and will benefit from already secured robust external funding (already 431k€ for 2023-26) as well as a large amount of lab space as part of BFSU. The five themes are coherent and well connected and will benefit from additional experimental capacity from the BFSU (e. g. for the study of CBBC enzymes). They are based on outstanding recent results, are very exciting and are very likely to lead to important novel discoveries.

Whilst the team has already engaged with two other teams for LCQB, it would be interesting to explore further collaborations, especially around synthetic design of proteins.

## RECOMMENDATIONS TO THE TEAM

The team could consider the possibility of developing additional collaborations within LCQB, which is likely to require deliberate engagement as there will be a large commitment linked to the BFSU.

As mentioned above, they could also consider applying to larger international grant funding mechanisms (and may explore whether they could benefit from support mechanisms from the University to free up time for such applications).

**Team 5:** Functional Imaging of Nuclear Architecture

Name of the supervisor: Mrs. Judith Mine-Hattab

## THEMES OF THE TEAM

The team studies the spatial organisation of chromosomes in the nucleus, with a particular focus on how this organisation is dynamically modified during DNA repair. The team expertise is live microscopy, enabling them to track the spatio-temporal dynamics of biomolecular objects, such as nucleoprotein DNA-repair filaments, in the nuclear space. The experimental system of the team is the budding yeast and they collaborate with external teams working on human cells. The team leader has a long-standing experience of interdisciplinary collaborations with biophysicists (especially polymer physicists) and she has been studying the implication of liquid-liquid phase separation in the dynamic remodelling of repairing chromatin foci.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The team is very young (created in 2022) and was not among those previously evaluated.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	0
Chargés de recherche et assimilés	1
Personnels d'appui à la recherche	0
<b>Sous-total personnels permanents en activité</b>	<b>1</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	0
Doctorants	0
<b>Sous-total personnels non permanents en activité</b>	<b>0</b>
<b>Total personnels</b>	<b>1</b>

## EVALUATION

### Overall assessment of the team

This is a very promising young team: it benefits from a young-investigator ATIP-Avenir grant, the PI has an excellent track record and specialised expertise in live microscopy and perfect knowledge of the biological process investigated (DNA repair). The team's activities and interests, which are at the intersection of biology and physics, nicely match the interdisciplinary nature of the unit.

### Strengths and possibilities linked to the context

As this is a very young team, the strengths and possibilities mostly rely on the team leader herself. Following her activities in the lab at Institut Curie, she obtained an ATIP-Avenir young-investigator grant, which is highly competitive. Her track record testifies an excellent international visibility and competitiveness, with 5 publications



as first or second author in top-ranked international journals (eLife, NatSMB, MBoC, NatCB). She received eight invitations to international meetings, seven of which were in France, including an EMBO conference.

Publication in eLife, 2021 describes an outstanding achievement of the PI: with her colleagues at Institut Curie and physicists collaborators, she was able to describe multiple types of motions of a repair factor (yeast Rad52, homologous to BRCA2) which, during repairs, has a fast and confined motion within repair foci, this motion being faster than the motion of the filament itself. This illustrates that the expertise of the team has the power to compare motions of subcomponents of intracellular machinery, in vivo. The fact that the PI is a co-corresponding author of the study indicates that she is herself a leader in the field.

Her excellent expertise in live-microscopy and single-particle tracking is demonstrated (6 articles) and rare. She has set up a home-made microscope dedicated to this, which is a plus for the unit and she trains users on this system. This expertise and set up offers many possibilities for collaborations. Some are already initiated to study DNA repair in human cells, with laboratories in Rennes and Toulouse. Her expertise can also provide high added value in collaborations on other topics in the future. For example, when the team reaches a larger size in the future, they may have the opportunity to apply image-based tracking to processes other than DNA repair. Collaborations of the team leader with physicists, and her interests in quantitative spatiotemporal dynamics, will likely generate fruitful intellectual and methodological interactions with other teams of the unit who also use data analysis, biophysics and model-based inferences in their studies. This is already noticeable by the collaborative development of an innovative single-particle tracking method with team 7.

The PI defended her 'Habilitation à Diriger des Recherches' and is therefore ready to supervise students in total independence.

Overall, the team presents all possible factors of success.

### Weaknesses and risks linked to the context

As a small and recently created team, its main weakness and source of risks is its small size. This is judiciously partially compensated by collaborating with external laboratories. The team will need to produce last-author publications showing its creativity and independence, which will be needed when applying to future fundings.

Given the potential and power of the live-microscopy single-molecule imaging expertise of the team, one risk could be to get involved in too-many collaborations before the team size expands. A good strategy to avoid this could be to stay focused on DNA repair first, and then extend the activities to other topics.

### Analysis of the team's trajectory

The team will build on its expertise in live-cell single-molecule imaging, yeast genetics and DNA repair to further characterise the biophysical changes of nuclear dynamic processes participating to DNA repair. They will also extend their conclusions from yeast to human cells. Two other themes are mentioned, 'dynamic organisation of the nucleus in cells under pressure' and 'phase separation as a nuclear organiser' but the scientific program on these themes is less mature.

The team is currently very small but has the financial possibility to grow in the next two years.

## RECOMMENDATIONS TO THE TEAM

It will be important to secure a first publication where the PI is the last author. The committee recommends avoiding dispersing in multiple projects too early. For example, the collaboration with team 7 on the development of a novel SPT method is ambitious, novel and therefore very promising; the committee recommends considering giving this project a higher priority than the high-pressure related stress project.

The committee also recommends keeping interacting with the previous PI's lab (A. Taddei) which has a larger size and long-time international connections. This will allow the team to avoid working in competition with this lab and to benefit from additional information on the international activities that are ongoing or planned in the field.

Opportunities to connect with foreign laboratories can probably be found after group size reaches ~ five people. This will open possibilities to apply to network grants (EU, HFSP or others) in the future.

**Team 6:** Mathematical modelling in biology  
 Name of the supervisor: Mrs. Delphine Salort

## THEMES OF THE TEAM

The team's research blends rigorous mathematical research on the foundations of understanding of Partial Differential Equations used to describe biological systems with more applied work in collaboration with several experimental groups. Applications range from neurosciences, to cell heterogeneity in cancers to adipose tissues. The team is also engaged in raising interest for their work and for research in high schools.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The previous report raised two issues:

- 1) Whether it was wise for the team, which at the time only consisted of the team leader, it was wise to be dispersed over two quite different directions, suggesting instead that the biological applications one could be more impactful. In this regard, the team has instead kept its strategy of still working on its two main approaches.
- 2) International visibility: the team leader was still lacking some more visibility. The team has recently acted on this (although, of course, the Covid pandemic has not helped), by participating to and organising an increased number of international meetings.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	1
Maîtres de conférences et assimilés	1
Directeurs de recherche et assimilés	0
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	0
<b>Sous-total personnels permanents en activité</b>	<b>2</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	1
Doctorants	1
<b>Sous-total personnels non permanents en activité</b>	<b>2</b>
<b>Total personnels</b>	<b>4</b>

## EVALUATION

### Overall assessment of the team

This excellent team is presently composed by two permanent members, which allows for a more even sharing of the administrative load. Research is diverse and of high quality. The funding is very good and improving as well as international visibility. The applications may represent a great opportunity to inspire the more fundamental mathematical work, and vice versa.

## Strengths and possibilities linked to the context

The new directions at the LQCB, in particular in the direction of synthetic biology, might offer novel opportunities for the team where to apply their methods. Indeed, in many instances, the language of PDEs is the most appropriate to describe systems at the cellular level. Given the very recent and increasing relevance of synthetic biology, it might also provide novel funding opportunities.

## Weaknesses and risks linked to the context

While the team's work is excellent, the attitude toward data-linked research perceived as risky might represent a risk. This is so if the role of the modeller is seen as a consequent to the data. Instead, modelling should be seen as a great opportunity to interact with experimentalists and down the line being involved in the design of the experiments themselves.

## Analysis of the team's trajectory

Compared to the previous assessment, the team has at least partially accepted the advice and has engaged more in applied research in collaboration with experimentalists. This is positive and shows a certain degree of maturation of the permanent members.

Funding is very good and improving, as well as visibility.

Overall, the trajectory is excellent.

## RECOMMENDATIONS TO THE TEAM

While the academic independence of the team must be respected, and for sure they are in the best position to judge and decide, it should be called to their attention that investment in the more impactful part of their research, such as the applied one, can bring more funding that can be used to free resources (even time is a resource) to work on the more fundamental part that, because of its lesser visibility, might struggle more finding third-party funding.

The team should also be bolder in its interactions with experimentalists, thinking better at what the role of a theorist should be.

Otherwise, the team seems to have clearly improved along most directions with respect to the previous evaluation.

**Team 7:** Computational medicine  
 Name of the supervisor: Mrs. Natalya Sokolovska

## THEMES OF THE TEAM

The team is active in both fundamental research and biological and medical applications in machine learning. It proposes to address the problem of the understandability of ML which when relying on Black Box concepts may lead to low acceptance in some fields like medical diagnostics. The team proposes to optimise interpretable models for these applications. The main topics covered over the last few years was the development of a scoring system for type 2 diabetes remission prediction. On a more fundamental basis, the team developed a partially observable Markov decision process-based framework to learn cost-sensitive heterogeneous cascading systems.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The team joined the LCQB in 2022. It was previously hosted by the NutriOmics unit at SU for 10 years. It was not evaluated in the previous LCQB Hcéres evaluation.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	1
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	0
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	0
<b>Sous-total personnels permanents en activité</b>	<b>1</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	0
Doctorants	0
<b>Sous-total personnels non permanents en activité</b>	<b>0</b>
<b>Total personnels</b>	<b>1</b>

## EVALUATION

### Overall assessment of the team

The team consists of a single professor, with four PhD students. The team leader is a well-established researcher in the field of machine learning applications for bioclinical research. The research production is excellent. The team leader has strong publication record in specialised journals. Many invitations to workshops and conferences have been obtained. The orientation towards biomedical applications may have an important impact in the field.

### Strengths and possibilities linked to the context

The team seems well positioned in the unit, as its capabilities in computational science creates strong opportunities for interactions with other computationally oriented teams as well as with the experimentalists.

## Weaknesses and risks linked to the context

The small size of the team and the heavy teaching duties of the leader appear as the main risks for the integration in the LCQB.

## Analysis of the team's trajectory

Most of the research topics that are emphasised in the document are follow-up of the previous projects of the team leader in her previous lab. They are mostly focused on AI applications to specific medical problems, including exploration of heterogeneous data to understand complex diseases. It remains to be shown how these interests would allow collaborations with other teams at LCQB. The prospects are rather broad and would need some focusing on taking into account the small size of the team.

## RECOMMENDATIONS TO THE TEAM

The team should find a way to attract postdoctoral students, and possibly to increase the number of permanent positions over the next years.

The targeted projects may gain in searching for interactions with other members and thematics of the unit.

**Team 8:** Statistical Genomics and Biological Physics

Name of the supervisor: Mr. Martin Weigt

## THEMES OF THE TEAM

The team aims at characterising and designing proteins based on the large-scale statistical analysis of their genomic sequences, an approach that they have pioneered since the early 2010s and that has paved the way for the creation of AlphaFold. Their methods have been historically grounded on statistical physics and, in more recent years on new Machine Learning (including Deep Learning) techniques.

Over the years, their work has been noticed and also appreciated for its application potential, as testified by several collaborations with the industry.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

While the previous report highly praised the group's quality, it also pointed to a few, albeit not critical, actions that the group could have undertaken to improve.

1) Funding: given the extraordinary expertise in statistical modelling of genomic data, ERC-style funding should be within reach. There has been no clear action in this direction.

2) Outreach: there was, and still there is, limited presentation to a broader public of the group's research. Given that the methods originating from the PI are at the basis of the structural revolution brought about by AlphaFold, it is not difficult to see how this could have been made.

3) Keep focus: overall, the core of the group's activities is coherent, so that there is no lack of focus. Possibly, the limited size of the group, and the heavy teaching and administrative duties, might represent a problem in further expansion. This though ties with point 1) above, about funding.

4) Industrial partnerships: the previous report mentioned its lack as something to be expected, but by now there are a few industrial collaborations, showing that the group has taken action in this direction.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	1
Maîtres de conférences et assimilés	1
Directeurs de recherche et assimilés	0
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	0
<b>Sous-total personnels permanents en activité</b>	<b>2</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	2
Doctorants	6
<b>Sous-total personnels non permanents en activité</b>	<b>8</b>
<b>Total personnels</b>	<b>10</b>

## EVALUATION

### Overall assessment of the team

The team is clearly a world leader in its field, and the research projects and output are impressive. While limited in size (many PhD students are co-directed with other labs) and with the permanent personnel highly engaged by teaching and administration, the team manages excellently at keeping up with research and doctoral training.

It has recently also expanded in industrial collaborations, which is not a given for purely theoretical researchers.

The methodological expansion from only statistical physics inspired approaches to ML and DL techniques is important and correct, since the field is moving fast and competitiveness must be preserved. This action also shows that the team has a broad view of the field.

As a remedy for the time constraints on the permanent personnel, further funding might help, as long as it does not come at the price of losing focus.

Overall the future is bright for this team.

### Strengths and possibilities linked to the context

DL approaches, while extremely powerful, are based on supervised techniques, where data are learned by the algorithm so to extract the signals relevant for a specific task. This limits their exploration potential because they might have a harder time at finding 'any' signal. Unsupervised approaches, pioneered in the field of protein sequence analysis by the PI, have instead a great potential in this direction, which should be exploited, and emphasised, by the team, to distinguish themselves from the growing DL crowd. In this respect, there is a great potential to establish their research as more fundamental in nature than what most other people in the field do. They have built a special niche for themselves and they should exploit it to the max.

### Weaknesses and risks linked to the context

The flip side of 'not being DL' is that there is an inherent risk of being progressively neglected by the community in favour of practically more effective DL approaches.

The limited group size (both in number and ability to be directly engaged in research) might constitute a problem in trying to also address all the important differences between their approach and the incoming wave of ML/DL ones.

### Analysis of the team's trajectory

The evolution of the team's research over the years has been appropriate, and the permanent members, who guarantee the continuity, have always shown a clear view of the field and of what problems to address. The addition of more ML/DL-based approaches, besides the physics-inspired ones, also shows the team far-sightedness.

The future of the team is surely bright.

## RECOMMENDATIONS TO THE TEAM

While the evaluation of the team is strongly positive, there are a few actions that the team might consider undertaking.

1) Funding: as already stressed by the previous report, there is space for expansion. While it is reasonable for the team not to look to grow more than it can manage, the heavy duties of the permanent staff, the great collaboration opportunities and the growing competition might require some extra effort that is not presently compatible with the group's size.

2) Research: given the advent of very powerful novel DL techniques, also on the generative side, it is risky for the team not to do more to emphasise the difference between their goals and the meaning of their research with respect to the growing offer in the literature.

Apart from this, citing the previous report, 'keep up the good work'!

**Team 9:** Telomere and Genome Stability

Name of the supervisor: Mr. Zhou Xu

## THEMES OF THE TEAM

The team studies genome instability in relation to DNA damage responses and telomere dysfunction. It uses two different model organisms, *Sacharomyces cerevisiae* and *Chlamydomonas reinhardtii*. It develops original approaches to these questions, using in particular single-cell analyses to detect population heterogeneity and temporal differentiation during the senescence process.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The team was created in 2019, and therefore not evaluated in the previous report.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	1
Chargés de recherche et assimilés	0
Personnels d'appui à la recherche	2
<b>Sous-total personnels permanents en activité</b>	<b>3</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	1
Doctorants	1
<b>Sous-total personnels non permanents en activité</b>	<b>2</b>
<b>Total personnels</b>	<b>5</b>

## EVALUATION

### Overall assessment of the team

This is a young team, recently created by a CNRS DR2 researcher. It uses a mix of molecular biology, microfluidics and mathematical modelling to study genome instability at the cell level. They publish very first interesting data on *S. cerevisiae* genome instability in telomere-deficient cells, as well as first characterisations of *C. reinhardtii* sub-telomeres, at an excellent to outstanding level. Due to the originality of their approach, the future outputs of these research lines very appear promising.

### Strengths and possibilities linked to the context

The team leader has an excellent track record related to the main themes of the team, and there is room for collaborations internal to LBCQ and with external collaborators. Indeed, the team has recently received a collaborative award (as partner) on mathematical modelling. It has an excellent funding track record (approximately 600k€ since 2019) both as coordinator and partner. The interest of the team for modelling trajectories of individual cells in the processes of repair or telomere shortening may meet other computational



capabilities in the unit. Additionally, the work on *C. reinhardtii* is likely to bring additional collaboration with team 4 as understanding of telomere biology is critical to synthetic genomes. The team is very attractive, having trained three PhD students and two postdoctoral students. The team leader has gained international recognition and is regularly invited to conferences as well as to review papers. He is also engaged in teaching, having contributed to the Biotechnology major at the Ecole des Mines. The team is involved in outreach and has contributed to a patent that has led to the creation of a start-up company.

### Weaknesses and risks linked to the context

The team seems small to pursue three different lines of research. It is to be noted, however, that all depends on collaborative works which are ongoing. While funding has been secured for collaborative work with mathematical modellers addition funding will probably be required for the experimental work. This risk is mitigated by the active engagement of the team leader in applying for funding.

### Analysis of the team's trajectory

The team proposes three projects for the next mandate. The study on chromosome instability in *C. reinhardtii* appears well engaged, it remained to be seen how novel findings on this topics can be found with this new model. A recent publication of the team shows that these promises are taking excellent shape. Moreover, these findings are very likely to have important impact for synthetic biology tools in *C. reinhardtii*. The adaptation mechanisms in *S. cerevisiae* project may lead to important new results and has already led to a very elegant modelling paper. The third project using a circular chromosome appears more dependent on external collaborations. Together, these three projects are well structured around common themes or methodologies.

## RECOMMENDATIONS TO THE TEAM

The algal and yeast projects are more related by methods than by thematics and it will be useful to delineate their respective importance in the future depending on the outcomes of the current projects.

**Team 10:** Epigenetics and RNA Metabolism in Human Diseases

Name of the supervisor: Mr. Christian Muchardt

## THEMES OF THE TEAM

The team investigates the synthesis, the fate, and the function of RNA byproducts related to gene expression, forming collectively the dark transcriptome. This encompasses promoter- and enhancer-RNAs, splicing products, and gene extensions. To achieve this, the team employs wet-lab omics techniques (RNA-seq and ChIP-seq, and more) in combination with bioinformatics approaches. The primary objective is to comprehend the initial regulatory mechanisms responsible for the accumulation of these RNAs, which may have pro-inflammatory properties.

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

The team should join the unite for the next mandate, in 2025.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	1
Chargés de recherche et assimilés	2
Personnels d'appui à la recherche	0
<b>Sous-total personnels permanents en activité</b>	<b>3</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	0
Post-doctorants	0
Doctorants	1
<b>Sous-total personnels non permanents en activité</b>	<b>1</b>
<b>Total personnels</b>	<b>4</b>

## EVALUATION

### Overall assessment of the team

The team's scientific positioning, coupled with the recent expansion into bioinformatics analyses, is promising. Looking ahead, the goal for the next mandate is to strengthen the team through new collaborations and contractual support. Overall, the team maintains an excellent standard.

### Strengths and possibilities linked to the context

The team is currently part of the IBPS, previously affiliated with the Institut Pasteur until 2020. Throughout this period, it has maintained a good level of productivity despite two relocations and the administrative duties of its leader (deputy director of INSB-CNRS, responsible for the Genetics and Genomics field).

The team relies on a long-term partnership between three full-time researchers, sharing research topics and technical expertise, thus creating a stable core. Two PhD theses were successfully defended (in 2019) and one is ongoing. The team also welcomed a postdoctoral researcher, until 2021.

The work has been recognised in publications such as 'Nucleic Acids Research' (2022), 'EMBO Reports' (2021), and 'Life Science Alliance' (2021). A notable aspect during the period is the increasing diversification of

techniques used for data analysis, with a growing emphasis on bioinformatics analysis, thanks to dedicated support. The team's transition to the LCQB is expected to foster mutual growth, strengthen the unit's quantitative biology focus, and further solidify the *in silico* activities of the team.'

## Weaknesses and risks linked to the context

The transition from Institut Pasteur to IBPS resulted in a staff reduction, notably affecting the technical personnel in molecular biology. This shift has also had implications for the animal facility, specifically concerning mouse strains of the team. Consequently, adjustments and adaptations within the new environment at LCQB will be necessary.

The current contract funding is at a low level, and the collaboration network is fragile.

## Analysis of the team's trajectory

The team presents a project structured around two core axes that align with its existing themes and available resources, while being very timely:

- the role of subproducts RNA in cancer and cellular senescence
- virus-induced transcription and particularly the role of non-coding RNAs in inflammatory phenotypes focusing on Covid 19 patients

## RECOMMENDATIONS TO THE TEAM

The team is in position to expand its scientific network and international visibility, to gain more fundings and attract more temporary staff (PhD students and postdoc researchers).

**Team 11:** Engaged Life Science  
 Name of the supervisor: Mr. Ariel Lindner & Mr. Vincent Libis

## THEMES OF THE TEAM

Team 11's project is organised around five axes: (1) building RNA based synthetic organelles (called Tears) in bacteria through Liquid Liquid phase separation (2) identifying new antimicrobials using a combination of bioinformatics mining of soil microbe genomes and reconstitution of biosynthetic pathways using Tears (3) design and production of new antimicrobial peptides (4) antiphage systems and (5) age modulated mortality in *E. coli*

## CONSIDERATION OF THE RECOMMENDATIONS OF THE PREVIOUS REPORT

Information not available as this is a new team.

## WORKFORCE OF THE TEAM: in physical persons at 31/12/2022

Catégories de personnel	Effectifs
Professeurs et assimilés	0
Maîtres de conférences et assimilés	0
Directeurs de recherche et assimilés	1
Chargés de recherche et assimilés	1
Personnels d'appui à la recherche	2
<b>Sous-total personnels permanents en activité</b>	<b>4</b>
Enseignants-chercheurs et chercheurs non permanents et assimilés	0
Personnels d'appui non permanents	8
Post-doctorants	3
Doctorants	3
<b>Sous-total personnels non permanents en activité</b>	<b>14</b>
<b>Total personnels</b>	<b>18</b>

## EVALUATION

### Overall assessment of the team

This is an outstanding team which is bringing exciting new capabilities to LCQB. The team's project will add to the overall strategy of LCQB, with enough overlap of interest to trigger new collaborations but also distinct expertise so there is no risk of duplication. The team is operating at the highest international level and given the quality of the proposed research it is clear that it will continue to do so in the future.

### Strengths and possibilities linked to the context

The team has an outstanding track record in terms of publications (95 as first, last or corresponding author in the last 5 years) and securing funding (approximately 2.6M€/year in the last five years). They have exceptional expertise in synthetic biology (at the highest international level), which will underlie all Team 11 research projects and will additionally reinforce the expertise in team 4.

The team has multiple exciting projects that will benefit from the proximity of BFSU (e. g. large-scale identification of new biosynthetic pathways, or Tears synthesis). It uses a combination of cutting-edge techniques (e. g. microfluidics, quantitative microscopy) as well as theoretical approaches (bioinformatics, mathematical

modelling), which will allow interactions with many other teams in LCQB, that are either primarily theoretical or experimental. There is therefore a strong potential for this team to act as a catalyst for even more collaborative projects within LCQB.

The team has an exceptional track record in open and citizen science which is much beyond what is usually achieved. They are leading the way in creating true partnerships between scientists and citizen scientists.

### Weaknesses and risks linked to the context

Team 11 is moving from the Learning Planet Institute, where it relied in part on philanthropic funding from the Bettencourt Schuller Foundation, to LCQB and there is a risk that several collaborations/pieces of equipment/non-permanent staff will not be sustained/present after the move. However, this risk is mitigated by the positioning of the team close to the BFSU and the fact that the team has secured 1.9M€ funding for 2025 and beyond.

### Analysis of the team's trajectory

The team will continue their exciting projects, which are well positioned to address significant problems such as the antimicrobial crisis as well as develop truly novel technologies (e. g. RNA organelles). As excellent recent scientific achievements underpin this, there is no doubt that they will be highly successful.

## RECOMMENDATIONS TO THE TEAM

It would be helpful to clarify what kind of support the team will have access to in LCQB.

## CONDUCT OF THE INTERVIEWS

### Dates

**Start:** 30 octobre 2023 à 9 h

**End:** 31 octobre 2023 à 17 h

**Interview conducted: hybrid mode: on-site for all except one member.**

### INTERVIEW SCHEDULE

#### DAY 1, 30<sup>th</sup> October

<b>8:30 – 8:45</b>	Preliminary meeting of the expert committee (closed hearing)
<b>8:45 – 9:00</b>	Presentation of the Hcéres evaluation to the unit
<b>9:00 – 10:00</b>	Presentation of the research unit by the Director (40' +20' questions)
<b>10:00-10:30</b>	Martin Weigt
<b>10:30-11:00</b>	Stéphane Lemaire/Julien Henri
<b>11:00-11:20</b>	Break
<b>11:20-11:50</b>	Alessandra Carbone
<b>11:50-12:20</b>	Judith Miné-Hattab
<b>12:20-12 : 50</b>	Nataliya Sokolovska
<b>12:50-14:00</b>	<b>Lunch</b>
<b>2 p.m.-3 p.m.</b>	Platforms (20' +5')/Visit of the lab
<b>3 p.m.-3:30 p.m.</b>	Delphine Salort
<b>3:30 p.m.-4 p.m.</b>	Ariel Lindner
<b>4 p.m.-4:30 p.m.</b>	Christian Muchardt
<b>4:30 p.m.-5 p.m.</b>	Frédéric Devaux
<b>5 p.m.-5:15 p.m.</b>	break
<b>5:15 p.m. – 5:45 p.m.</b>	Gilles Fischer
<b>5:45 p.m.-18:15</b>	Zhou Xu
<b>6:15 p.m.-7:15 p.m.</b>	Committee debrief

#### DAY 2: 31<sup>st</sup> October

<b>8:30-9:10</b>	Meeting with technical and administrative staff (in French)
<b>9:10-9:50</b>	Meeting with thesis students and postdoctoral students
<b>9:50-10:30</b>	Meeting with researchers and professors
<b>10:30-10:45:</b>	<b>Break</b>
<b>10:45-11:15</b>	<b>Meeting committee and supervising bodies</b>
<b>11:15-12:00</b>	Meeting with the head of the unit/deputy directors
<b>12:00-1 p.m.</b>	<b>Lunch</b>
<b>1 p.m.-2:30 p.m.</b>	committee meeting/final debrief: overview of all teams

### PARTICULAR POINT TO BE MENTIONED

N/A

Marie-Aude Vitrani  
Vice-Présidente Vie institutionnelle et démarche  
participative  
Sorbonne Université

à

Monsieur Eric Saint-Aman  
Directeur du Département d'évaluation de la recherche  
HCERES – Haut conseil de l'évaluation de la recherche  
et de l'enseignement supérieur  
2 rue Albert Einstein  
75013 Paris

Paris, le 19 février 2024

Objet : Rapport d'évaluation LCQB - Laboratoire biologie computationnelle et quantitative

Cher Collègue,

Sorbonne Université vous remercie ainsi que tous les membres du comité HCERES pour le travail d'expertise réalisé sur l'unité de recherche « LCQB ».

Sorbonne Université n'a aucune observation de portée générale à formuler sur le rapport d'évaluation transmis.

Je vous prie d'agréer, Cher Collègue, l'expression de mes cordiales salutations

**Marie-Aude Vitrani**  
Vice-Présidente Vie institutionnelle  
et démarche participative



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