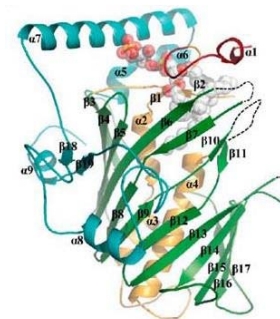
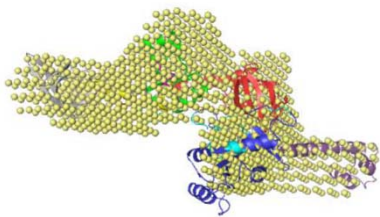


École Nationale de Biologie Structurale Intégrative

18 -25 Juin 2021, Ile d'Oléron, France





29 « students »

24 PhD students, 3 IE/IR, 1 AI, 1 Tech

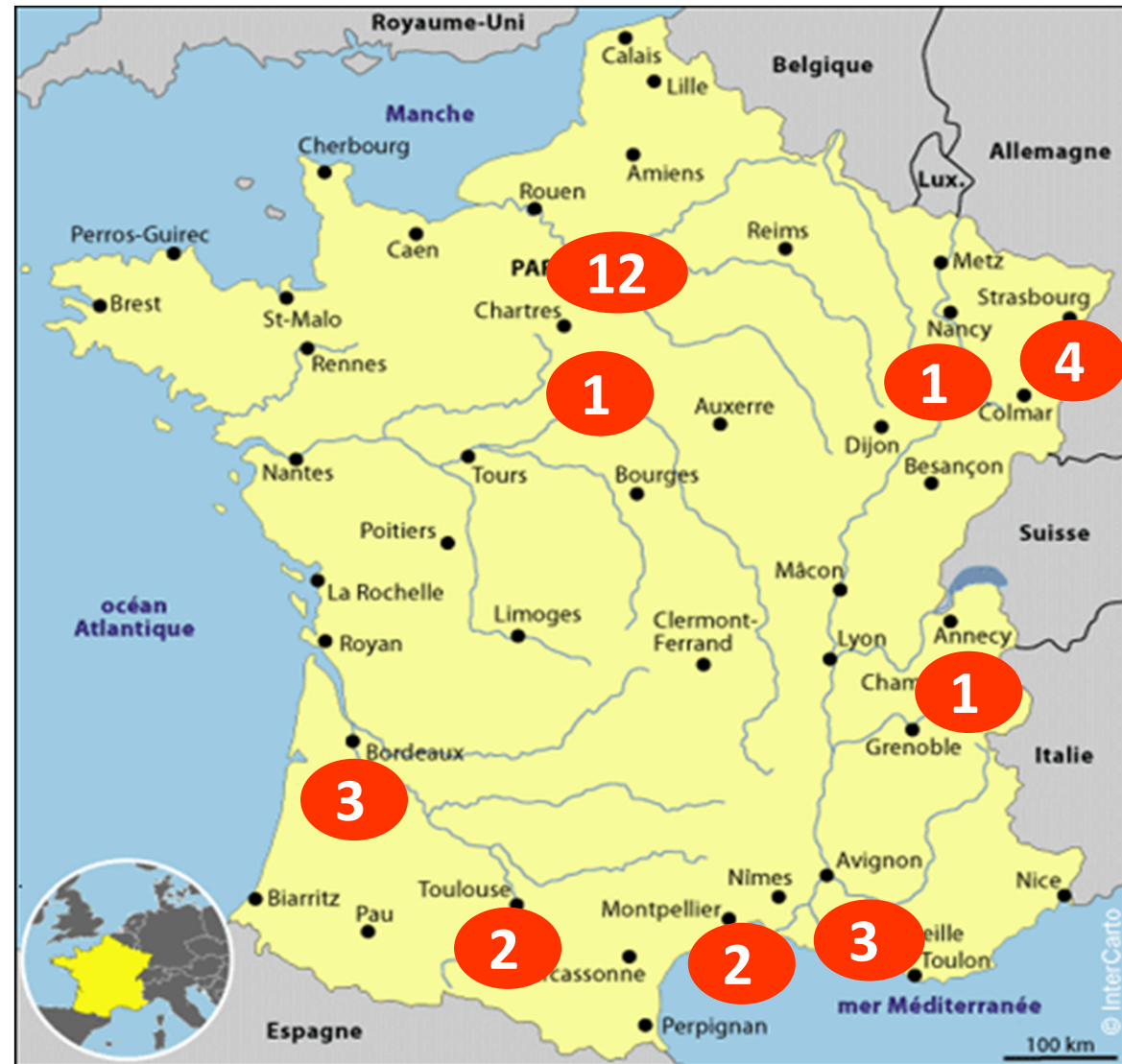
17 F, 12 M



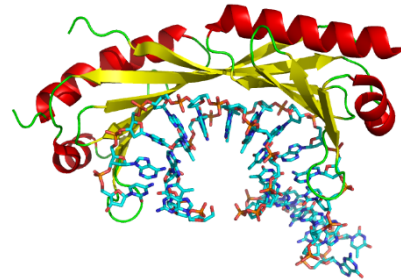
7 tutors « all week »

4 tutors « few days »

2 « remote » speakers



Objectives of Integrated Structural Biology

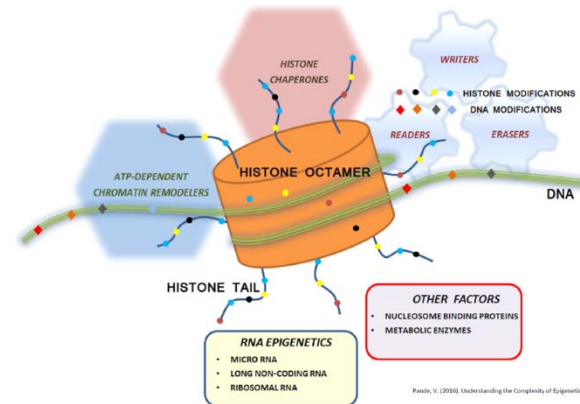


Understand the mechanisms of biological processes

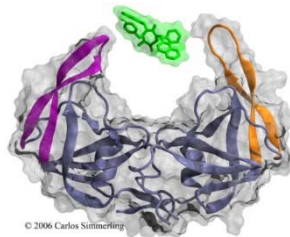
Explore the integration of biological functions in complex molecular and cellular systems.

Decipher pathways that lead to pathology

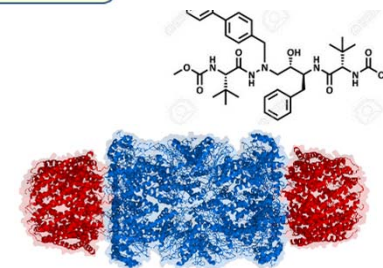
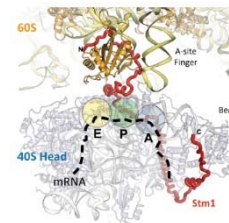
New routes for Drug discovery and Drug design



Pavlov, V. (2016). Understanding the Complexity of Epigenetic Target Space. J. Med. Chem. 59, 1299-1307.

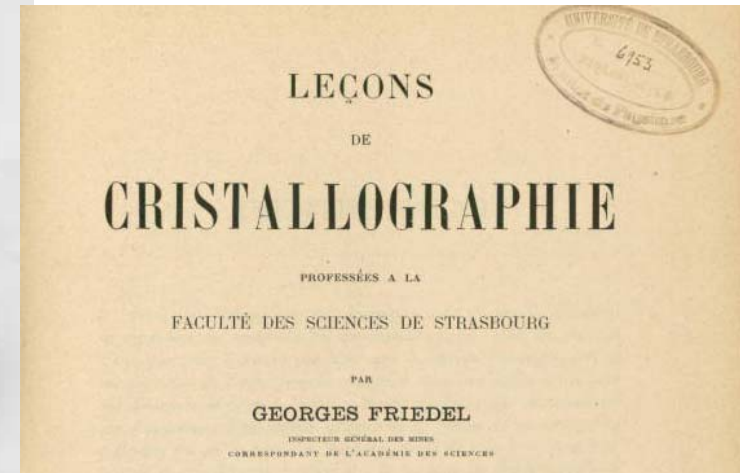


© 2006 Carlos Simmerling

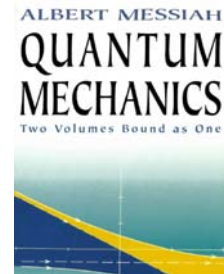
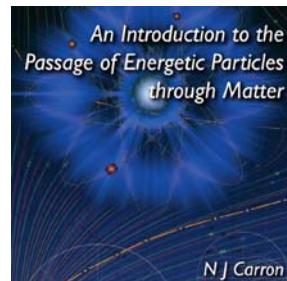
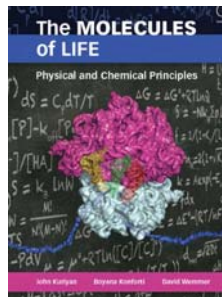
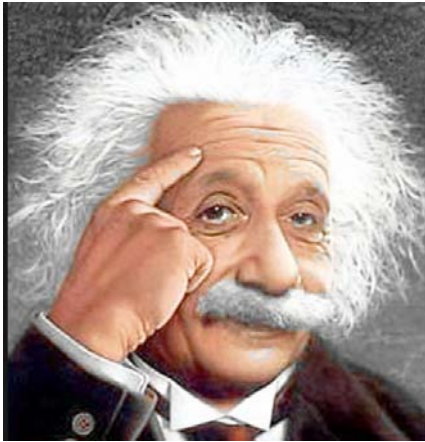




Naissance	19 juillet 1865 Mulhouse (France)
Décès	11 décembre 1933 (à 68 ans) Strasbourg (France)
Nationalité	 français
Domaines	Minéralogie
Institutions	École nationale supérieure des mines de Saint-Étienne Université de Strasbourg
Diplôme	École polytechnique (1885)
Renommé pour	Étude des cristaux liquides



« le but de l'enseignement, et surtout celui de l'enseignement supérieur, doit être moins d'**instruire** que d'**éduquer** et de faire **réfléchir** ; moins d'entasser des connaissances que d'apprendre à en digérer quelques-unes ; moins de glisser sur **les difficultés** que de les **mettre en lumière** ; moins de laisser croire à l'infailibilité des méthodes en usage et à la certitude des résultats que d'en montrer les points faibles et de **cultiver** ainsi **l'esprit de critique** et de **libre examen**, base nécessaire de l'esprit de recherche »



Quarterly Reviews of Biophysics 28, 2 (1995), pp. 171–193
 Printed in Great Britain

171

The potential and limitations of neutrons,
 electrons and X-rays for atomic resolution
 microscopy of unstained biological molecules

RICHARD HENDERSON
 MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH, UK



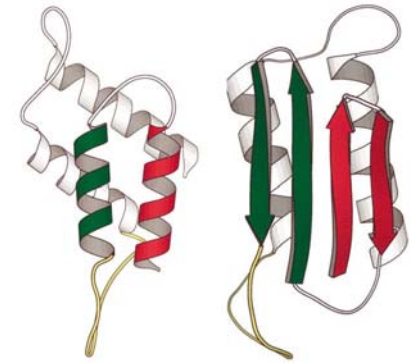
There's Plenty of Room at the Bottom

An Invitation to Enter a New Field of Physics



by Richard P. Feynman Nobel Prize in Physics 1965

Lecture on December 29th 1959



What are the most central and fundamental problems of biology today ?

They are questions like:

What is the sequence of bases in the DNA? What happens when you have a mutation ? How is the base order in the DNA connected to the order of amino acids in the protein ? What is the structure of the RNA; is it single-chain or double-chain, and how is it related in its order of bases to the DNA ? How are proteins synthesized ? Where does the RNA go ? How does it sit ? Where do the proteins sit ? Where do the amino acids go in ? In photosynthesis, where is the chlorophyll; how is it arranged; where are the carotenoids involved in this thing? What is the system of the conversion of light into chemical energy ?

It is very easy to answer many of these fundamental biological questions



You just look at the thing!



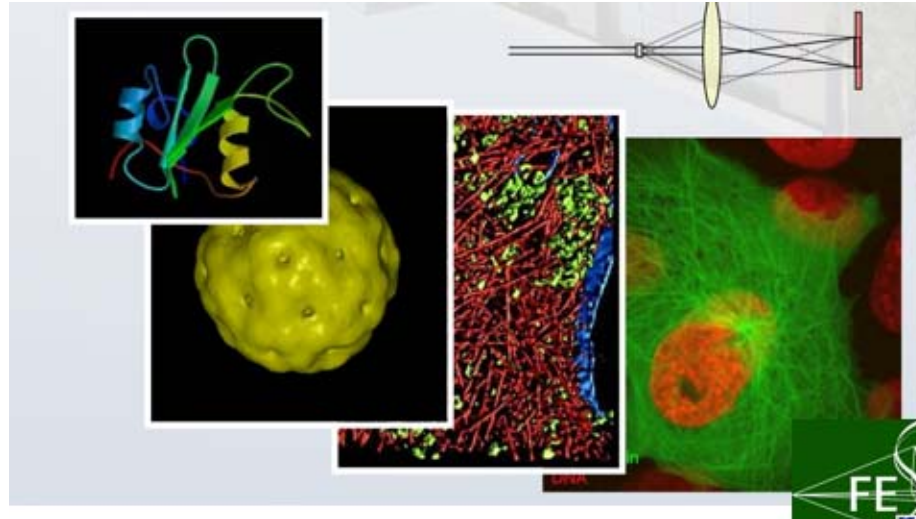
Make the microscope one hundred times more powerful, and many problems of biology would be made very much easier.

You know the reason you fellows are making so little progress :

You should use more mathematics



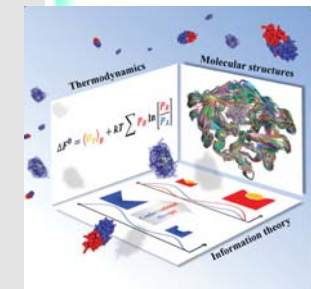
Make the microscope one hundred times more powerful, and many problems of biology would be made very much easier. (1959)

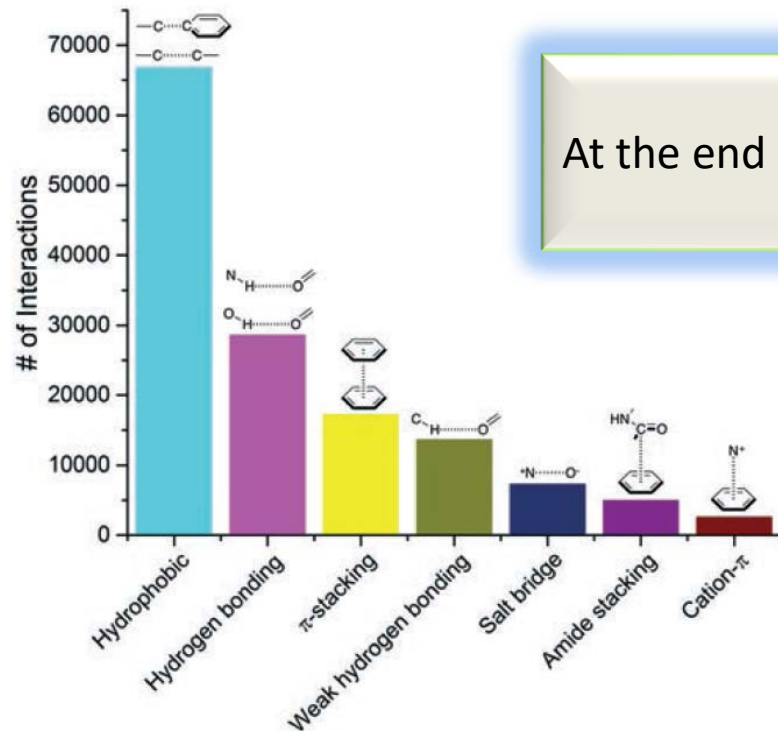


- Develop techniques and methods to see more and more
 - challenges for structural cell biology
- Understand, explain what you see, predict
- A “new” way of thinking in biology.

All field of Life Sciences

At the end of the day, Biology is just Chemistry

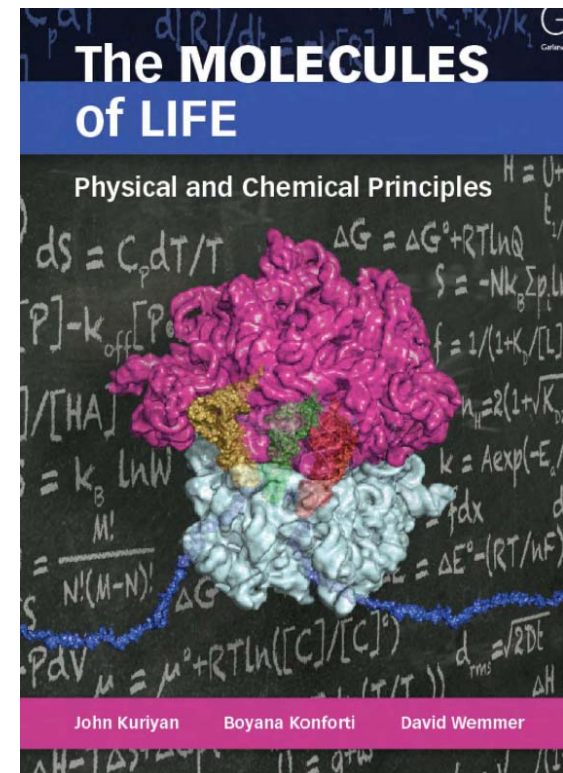




At the end of the day, Biology is Chemistry

Fig. 1 Frequency distribution of the most common non-covalent interactions observed in protein-ligands extracted from the PDB.

Chemistry is not only Thermodynamics but Kinetics



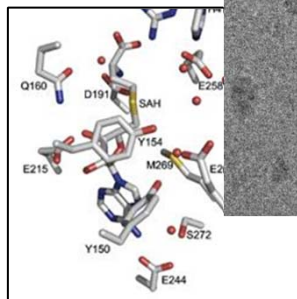
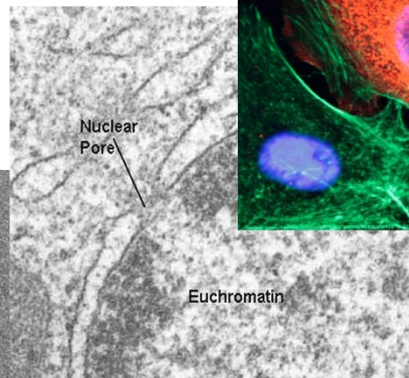
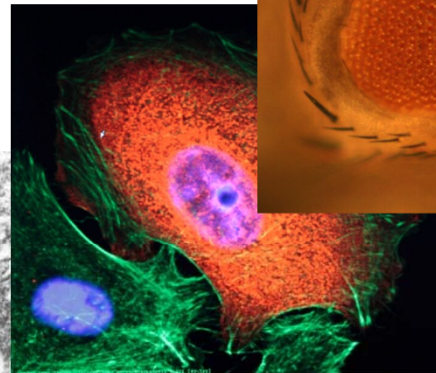
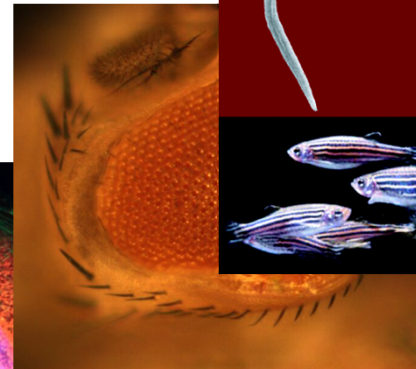
Macromolecular interactions (life) are a compromise between affinity and specificity



French Infrastructure for Integrated Structural Biology

***Integrated Structural Biology -
from the atomic to the cellular level***

Developments of Cutting-edge technologies
at the interfaces of biology,
physics, chemistry, computer
science and mathematics



3D structure & function

***Get continuum of information:
scales / resolution / dynamics / function***

leading scientific projects with key biological questions such as gene regulation or signalling cascade, especially those connected with infectious and neurodegenerative diseases or immunity in order to integrate the molecular and cellular complexity of functional systems in healthy and pathological cases.

Fine details in complex environments: the power of cryo-electron tomography

Joshua Hutchings and Giulia Zanetti

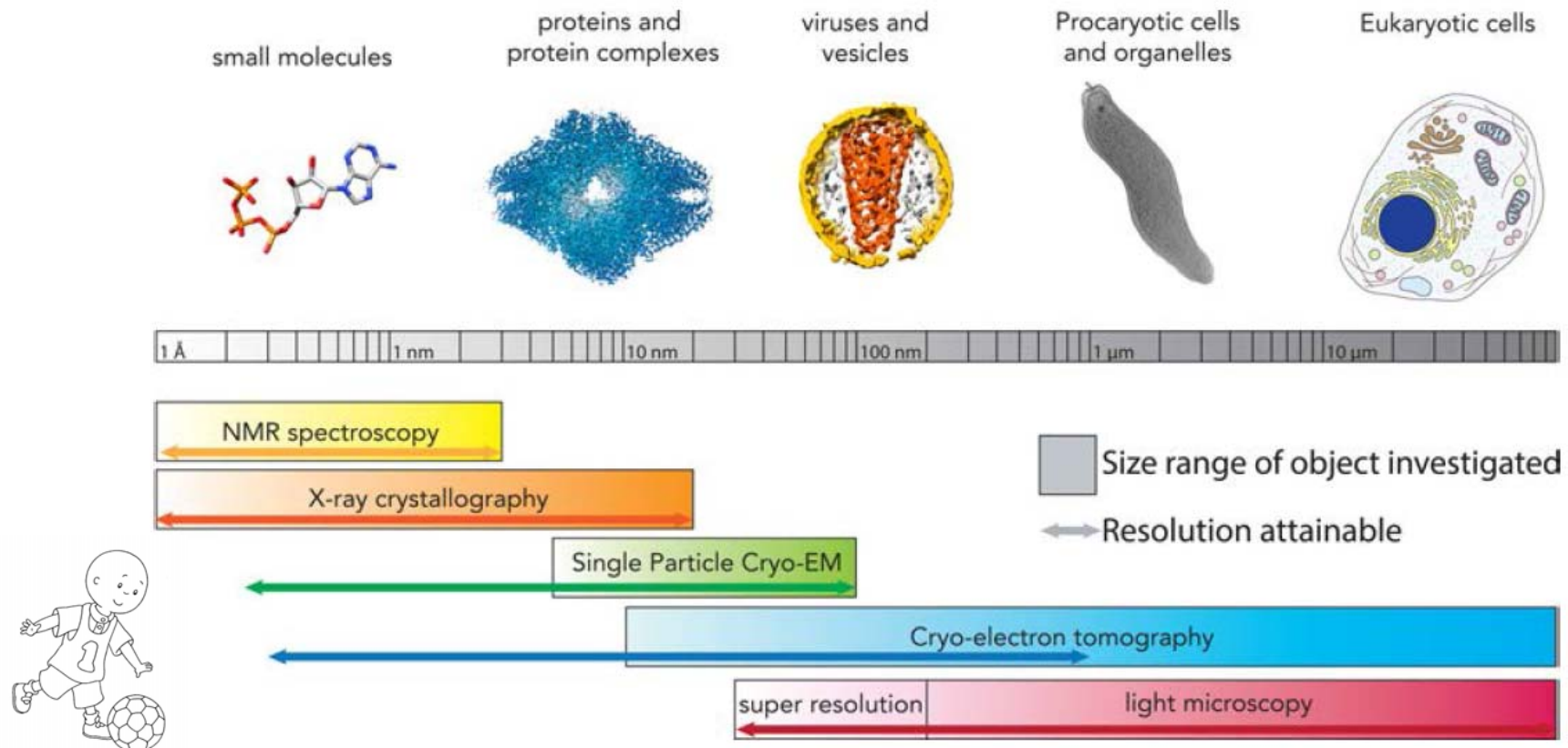


Figure 1. An overview of structural biology techniques and the biological objects they investigate.

The size range of biological objects that can be studied is represented with thick bars, while arrows of corresponding colours indicate the resolution ranges that can be targeted. CET is ideally placed to resolve biological molecules at subnanometer resolutions, while studying large and complex assemblies such as eukaryotic cells. ATP is used as an example of small molecules, EMD-2984 was used as representative protein, a segmented tomogram from Mattei et al. [6] was used as representative of virus, EMD-2754 was used to extract a *Campylobacter jejuni* cell to represent bacteria.

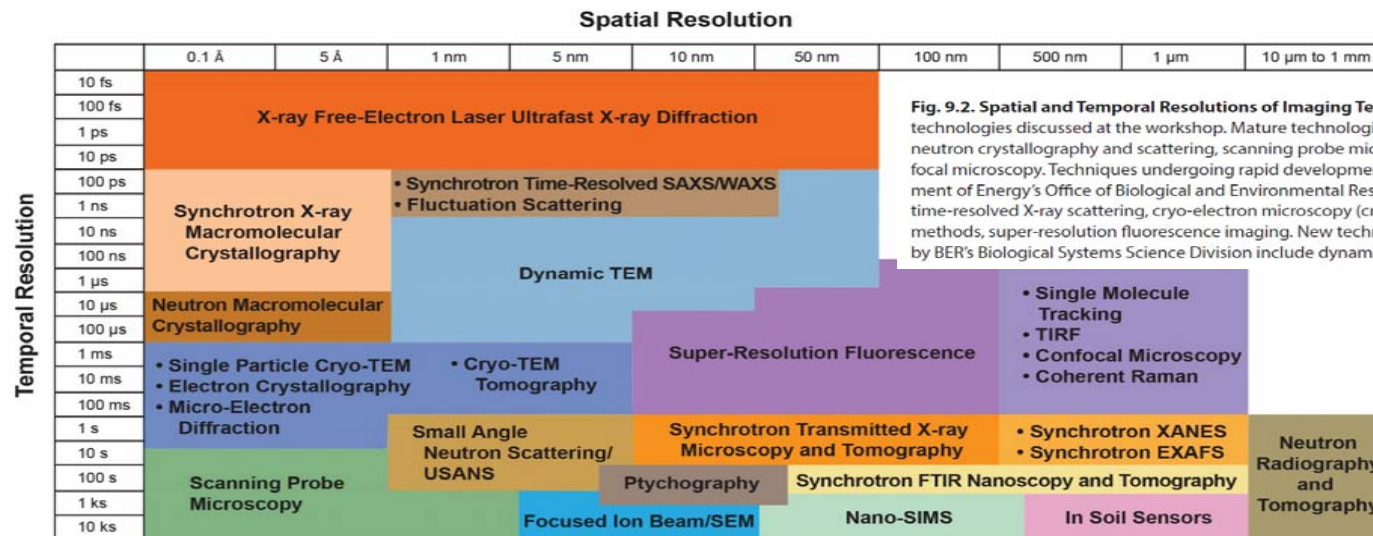
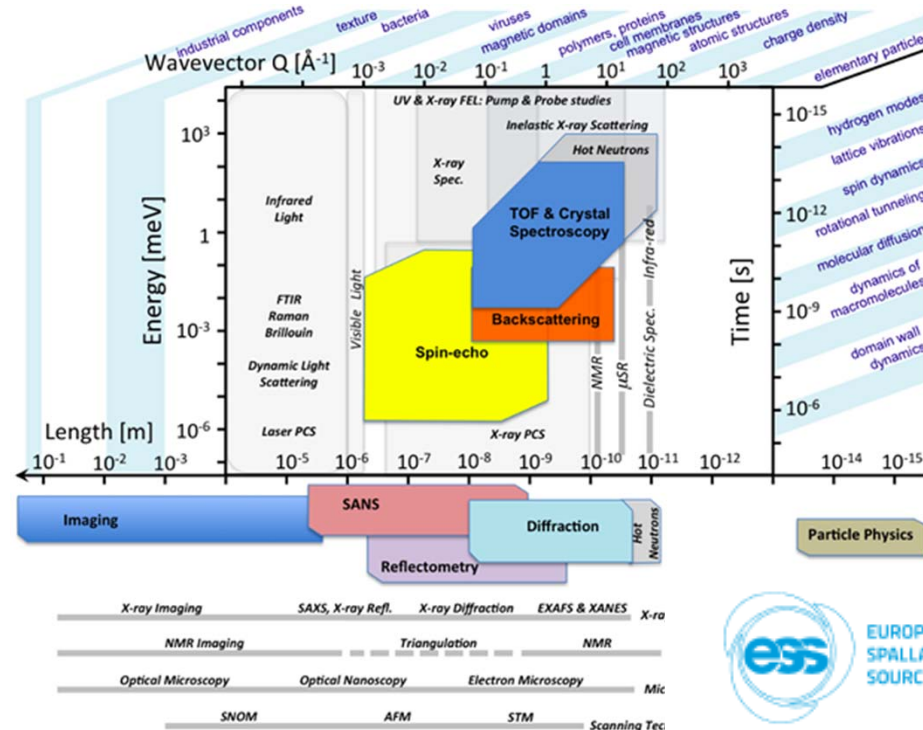
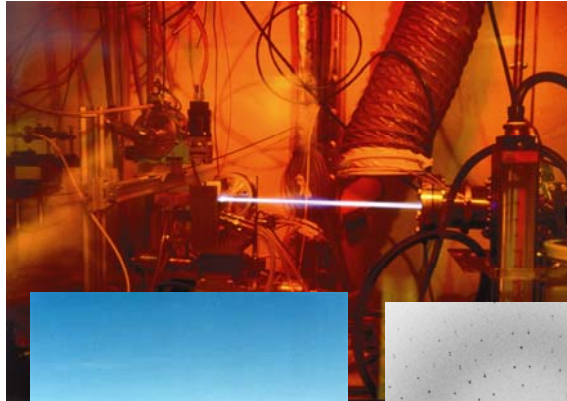


Fig. 9.2. Spatial and Temporal Resolutions of Imaging Technologies. Summary of imaging and other selected measurement technologies discussed at the workshop. Mature technologies that will benefit from further development include X-ray and neutron crystallography and scattering, scanning probe microscopies, X-ray tomography, synchrotron spectroscopy, and confocal microscopy. Techniques undergoing rapid development and with potential application to the mission of the U.S. Department of Energy's Office of Biological and Environmental Research include time-resolved X-ray scattering, cryo-electron microscopy (cryo-EM), super-resolution fluorescence imaging. New techniques by BER's Biological Systems Science Division include dynamic

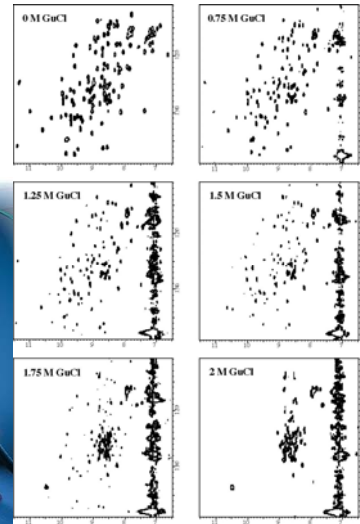
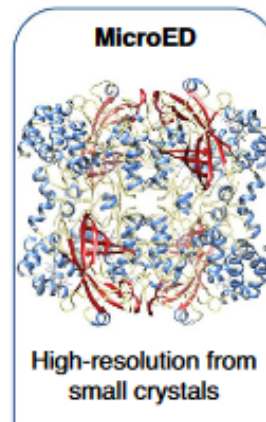
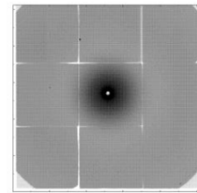
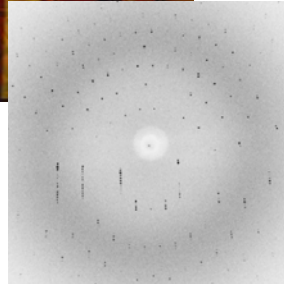


Key: Å, Angstrom; EXAFS, extended X-ray absorption fine structure; fs, femtosecond; ks, kilosecond; µm, micrometer; µs, microsecond; mm, millimeter; ms, millisecond; nm, nanometer; ns, nanosecond; ps, picosecond; s, second; SAXS, small-angle X-ray scattering; SEM, scanning electron microscopy; TEM, transmission electron microscopy; TIRF, total internal reflection fluorescence; USANS, ultrasmall-angle neutron scattering; WAXS, wide-angle X-ray scattering; XANES, X-ray absorption near edge structure.

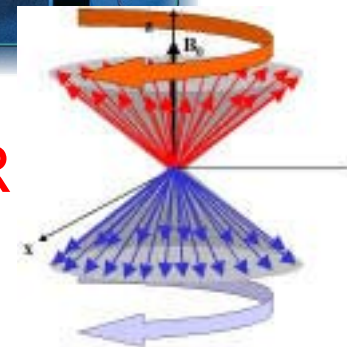




X-ray



NMR



Electron microscopy



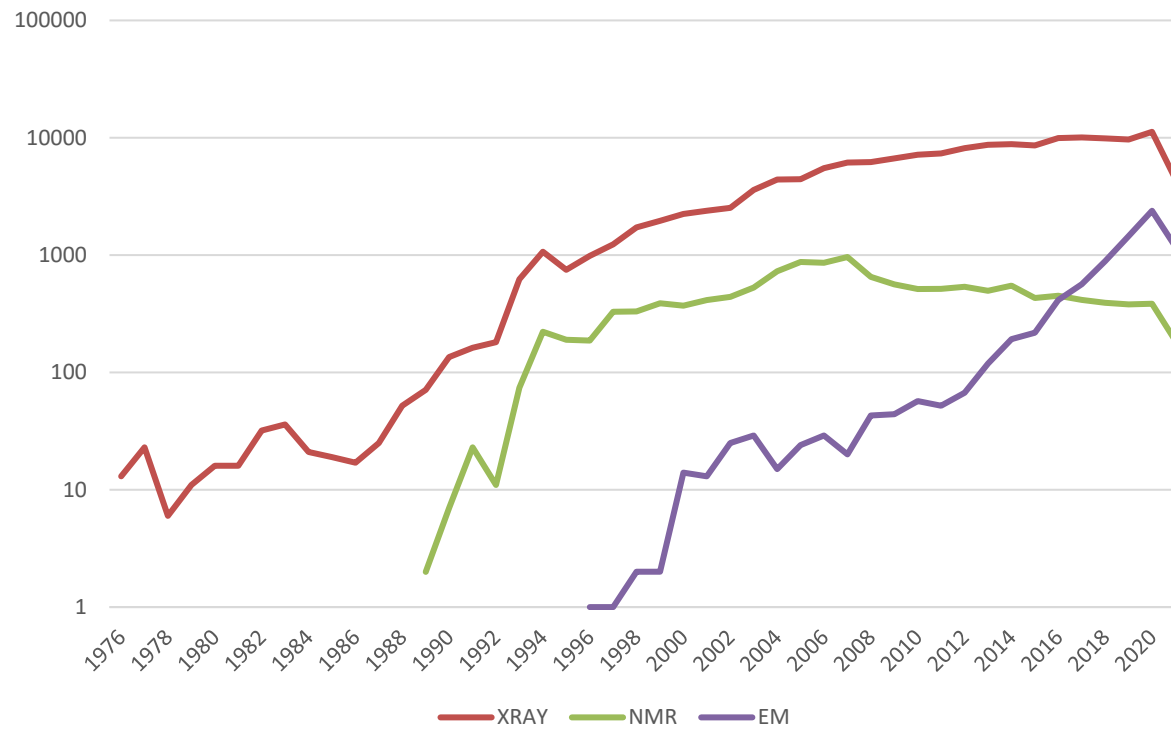
Current Opinion in Structural Biology 2020, 64:1-8

CryoEM Technique	Tomography	Single-Particle Analysis	2D Electron Crystallography	MicroED
Advantages	Samples in near native states	High-resolution	Samples in lipid-bilayer	High-resolution from small crystals
Challenges	Typically low (~10 Å) resolution	Molecular weight limit >40 kDa	Requires 2D crystal growth	Requires 3D crystal growth

Current Opinion in Structural Biology



Data RCSB



Oléron
2021

**Monday
SPA Cryo-
EM**

**Tuesday
Interactions**



**Sunday
MX**

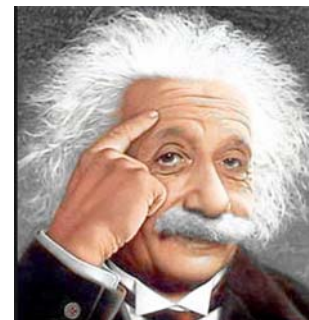
NMR

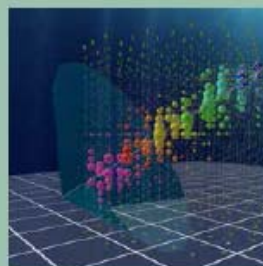
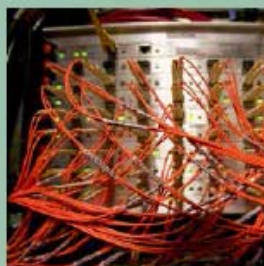


**Saturday
BSI 101**

**EM and
Brothers**

TPs: TM - BLI





STRATÉGIE NATIONALE DES INFRASTRUCTURES DE RECHERCHE ÉDITION 2018 - N°2



herche.gouv.fr



TGIR	ESRF	Source Européenne de Rayonnement Synchrotron/ European Synchrotron Radiation Facility
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TGIR	SOLEIL	Source Optimisée de Lumière d'Energie Intermédiaire du LURE
------	--------	--

TGIR	XFEL	European X-ray Free Electron Laser
------	------	------------------------------------



IR	RMN-THC	Résonance Magnétique Nucléaire à Très Hauts Champs
----	---------	---



ProFI
PROTEOMICS

IR	PROFI	Infrastructure Française de Protéomique
----	-------	---

IR	ChemBioFrance	Plateforme de découverte de molécules bioactives pour comprendre et soigner le vivant
IR	FBI	France-BioImaging
IR	FLI	France Life Imaging

France-BioImaging

A National Research Infrastructure for Biological Imaging



One portal for access

Web site: accessible via the Instruct, CNRS, ReNaFoBis & ITMO websites

<http://www.frisbi.eu>

contact@frisbi.eu

Working group and FRISBI user community

HOME

The French Infrastructure for Integrated Structural Biology (**FRISBI**) provides an infrastructure for integrative structural biology approaches, from the molecular to the cellular level, integrating multi-resolution data from X-ray crystallography, small angle X-ray scattering, NMR, Cryo-EM and functional data including development for protein expression and crystallization. **FRISBI is open to structural and molecular and cell biologists from both academia and industry from France and Europe.** A simple, transparent reviewed process will provide access based on its feasibility and resource availability. **Applications for access can be submitted at any time.** Users will be required to contribute towards the costs of access.

LATEST NEWS

Currently no news

ALL NEWS ☰

EVENTS TO COME

Currently no events



FRENCH INFRASTRUCTURE FOR INTEGRATED STRUCTURAL BIOLOGY

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HOME

The French Infrastructure for Integrated Structural Biology (**FRISBI**) provides an infrastructure for integrative structural biology approaches, from the molecular to the cellular level, integrating multi-resolution data from X-ray crystallography, small angle X-ray scattering, NMR, Cryo-EM and functional data including development for protein expression and crystallization. **FRISBI is open to structural and molecular and cell biologists from both academia and industry from France and Europe.** A simple, transparent reviewed process will provide access based on its feasibility and resource availability. **Applications for access can be submitted at any time.** Users will be required to contribute towards the costs of access.

FRISBI offers priority of access for research proposals relating to covid-19

The non-infectious character of the samples needs to be confirmed by the director of the applying institute.

For application please "**submit proposals**"

Two of the FRISBI centers are part of the european Instruct-ERIC infrastructure 

Sixth FRISBI call for proposals for Structural Biology Training Courses (to be held in 2021 in France).

LATEST NEWS

Currently no news

[ALL NEWS](#) 

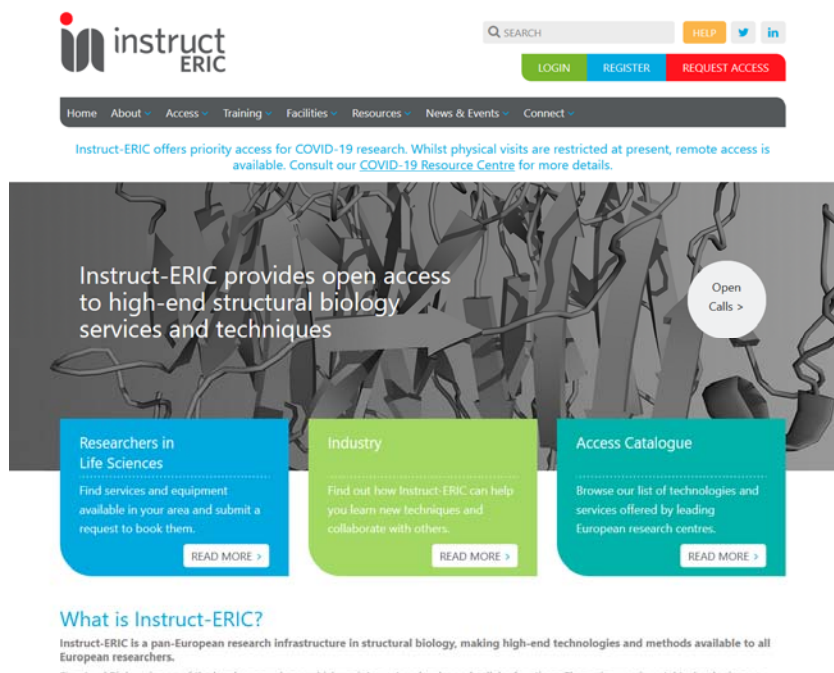
EVENTS TO COME

Currently no events

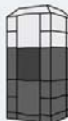
CENTERS

- **INSTRUCT CENTER - FRANCE 1 - IGBMC**
- **INSTRUCT CENTRE - FRANCE 2 - IBS - ISBG**
- **CBS**
- **AFMB**
- **South Paris**

<https://instruct-eric.eu/>



The screenshot shows the Instruct-ERIC website homepage. At the top is the Instruct-ERIC logo, a search bar, and navigation links for LOGIN, REGISTER, and REQUEST ACCESS. Below the header is a navigation menu with links to Home, About, Access, Training, Facilities, Resources, News & Events, and Connect. A banner below the menu states: "Instruct-ERIC offers priority access for COVID-19 research. Whilst physical visits are restricted at present, remote access is available. Consult our COVID-19 Resource Centre for more details." The main content area features a large image of a protein structure with the text "Instruct-ERIC provides open access to high-end structural biology services and techniques" and a button labeled "Open Calls >". Below this are three colored boxes: "Researchers in Life Sciences" (blue), "Industry" (green), and "Access Catalogue" (teal), each with a brief description and a "READ MORE >" button. At the bottom, a section titled "What is Instruct-ERIC?" explains that it is a pan-European research infrastructure in structural biology, making high-end technologies and methods available to all European researchers.



Cryo-Electron Microscopy

A sophisticated technique to obtain quantitative structural information on the atomic scale. Includes electron crystallography, single particle analysis and electron tomography.



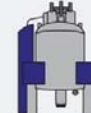
Protein Production

Includes cloning, high throughput expression and purification for the production of challenging proteins.



X-ray Techniques

Includes a variety of approaches to determine the 3D shape of biomolecules at the atomic level, including diffraction and Bio-SAXS at European synchrotrons. XChem fragment screening also available.



Magnetic Resonance (NMR)

Used to obtain three-dimensional structural and dynamic information about biomolecules in conditions as close as possible to physiological ones. Solution and solid-state NMR available.



Computational Support

A variety of computing services for bioinformatics, modelling, and image processing for electron microscopy and X-ray crystallography.



Mass Spectrometry

Used to determine protein identity, abundance, modifications (proteomics), shape and topology (ion mobility), inter-subunit connectivity, and equilibrium dynamics (native MS).



Molecular Biophysics

An extensive range of techniques to characterise the structure, function and stability of biological macromolecules, and to obtain kinetic and thermodynamic parameters.



Fragment Screening

A method of identifying small organic molecules (fragments) that bind a biological target (eg protein or nucleic acid). Used to find lead compounds as part of the drug discovery process.


15
COUNTRIES


11
CENTRES


26
FACILITIES


82
SERVICES


1259
PUBLICATIONS





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INFRASTRUCTURES DE RECHERCHE
Résonance Magnétique Nucléaire, Très Hauts Champs
FR3050 CNRS



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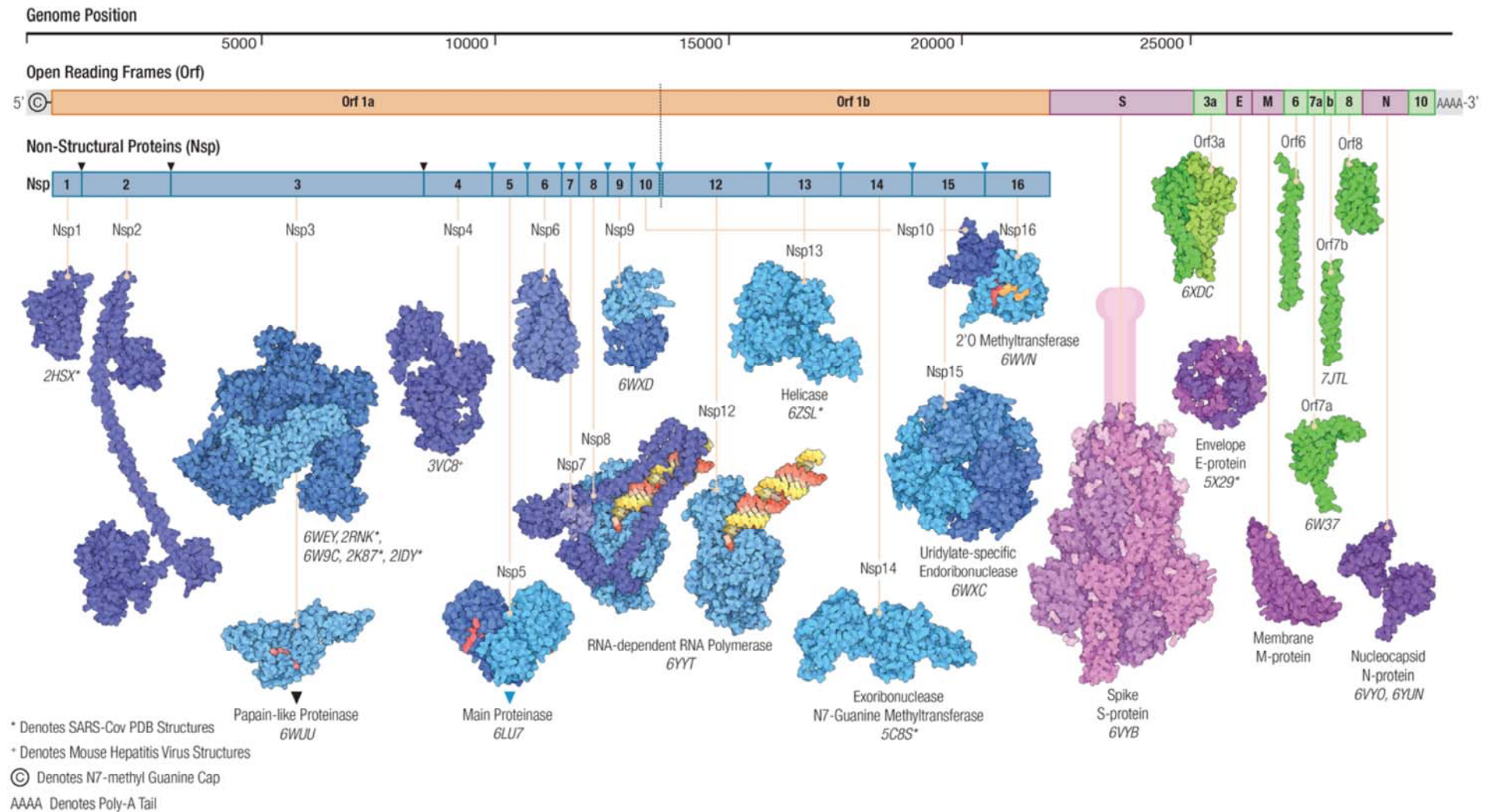
[User Dashboard](#)
[Submit Proposal](#)



Association Française de Cristallographie



Evolution of the SARS-CoV-2 proteome in three dimensions (3D) during the first six months of the COVID-19 pandemic
bioRxiv 2020.12.01.406637; doi: [10.1101/2020.12.01.406637](https://doi.org/10.1101/2020.12.01.406637)



03/03/2021

With this week's update of the PDB, over one thousand (**1018** to be exact!) SARS-CoV-2-related structures are now freely available in the PDB.

The first SARS-CoV-2 structure, a high-resolution crystal structure of the coronavirus main protease (PDB [6lu7](#)), was released early in the pandemic on February 5, 2020.

Since then, structural biologists have determined the structures of most of the proteins in the SARS-CoV-2 proteome, including the spike protein binding to its ACE2 receptor and neutralizing antibodies, and the main protease, the papain-like proteinase, and other promising drug discovery targets.

Rapid public release of SARS-CoV-2 structures has greatly increased our understanding of Covid-19, allowed direct visualization of emerging variants of the virus, and facilitated structure-guided drug discovery and reuse to combat infection. Open access to PDB structures has already enabled design of effective vaccines against SARS-CoV-2.

John Berrisford
PDBe, European Bioinformatics Institute (EMBL-EBI)
Wellcome Trust Genome Campus, Hinxton, Cambridge



One year since first genomes of SARS-CoV-2 to the world 10 January 2020 00:00

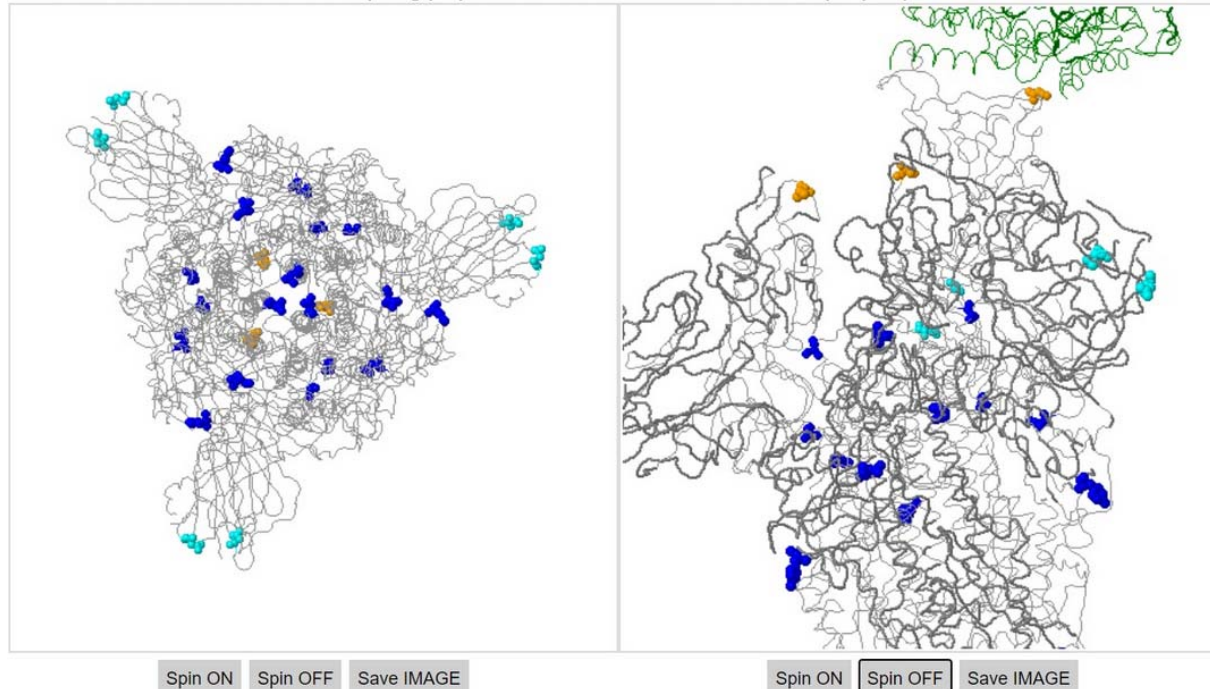
One year ago, critical public health responses kicked off, when China CDC shared via GISAID whole-genomes and associated data.

This curated, high-quality data made available the initiation of the development of the first and other responses at unprecedented speed to be approved and made available (Polack and development of the first NAAT and RT-detect the pandemic coronavirus (Bohn et al. 2020)).

UK reports new variant, termed VUI 202012/01

The United Kingdom reported a new variant, termed VUI 202012/01 (Variant Under Investigation, year 2020, month 12, variant 01). It was defined by multiple spike protein changes (deletion 69-70, deletion 145, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H). An increasing fraction in Southern England (all from clade GR) share several of these changes and a handful have been seen through imports in other countries. Based on evaluation of effect on virus structure and function, the most relevant might be N501Y (orange in Figure; host receptor and antibody binding, also reported at gisaid.org/spike) and the deletions (cyan in Figure) in positions contributing to potential spike surface variation (Y145del is where some antibodies like neutralizing 4A8 bind).

3D structural visualization of the spike glycoprotein with mutations identified in the query sequences shown as colored balls



Spike glycoprotein (PDB: 6acc, EM 3.6 Angstrom) with RBD in down conformation.

Spike glycoprotein (PDB: 6acj, EM 4.2 Angstrom) in complex with host cell receptor ACE2 (green ribbon).

List of variations displayed in structure (nearest residue if in loop/termini region)
H69del V70del(69) Y145del(143) N501Y A570D D614G P681H(674) T716I S982A D1118H

At the end of
the day,
biology is just
chemistry

French Infrastructure for Integrated Structural Biology

Education and Training

Workshops/Symposia

PhD



Master

Developments of Methods
and Techniques
to shape and build the
future of Integrate
Structural Biology

helping “people” to
understand the core
principles of Integrated
Structural Biology

Exp
Researcher

FRISBI platforms

Provide access to cutting-edge
instruments and expertise in structural
biology





2013

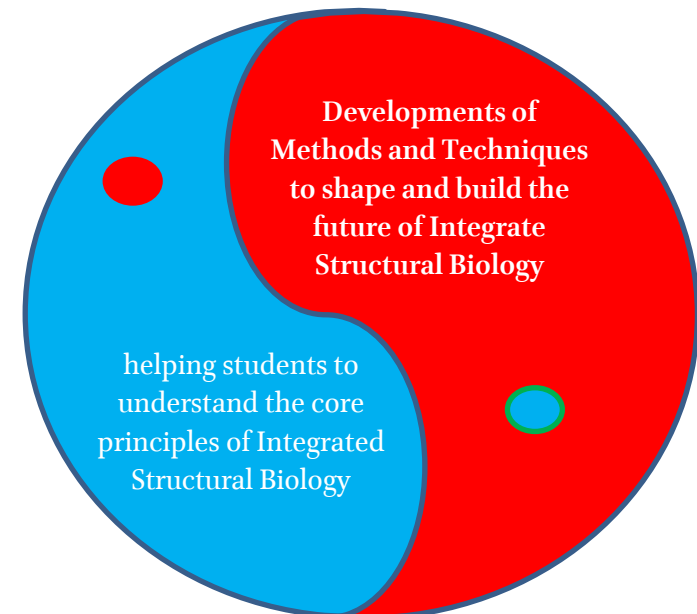
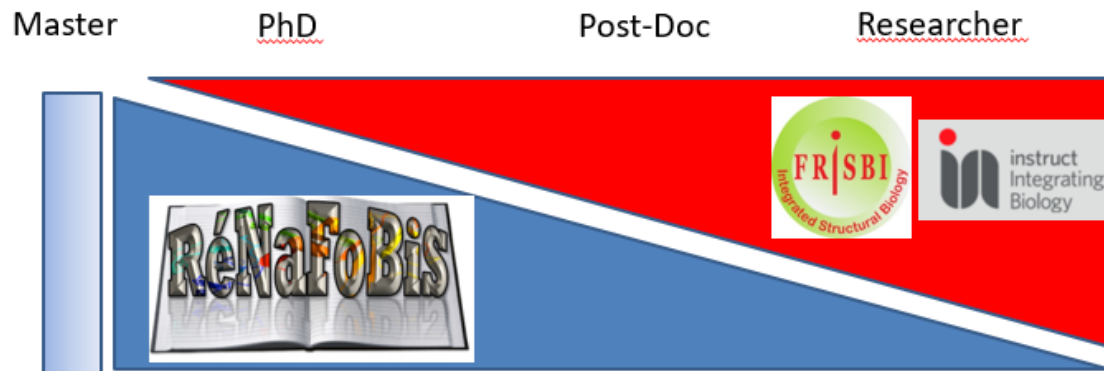


initially driven by the FRISBI centers



A “national” high-level training program in integrated structural biology

A dream of a national graduate School in Structural biology



ReNaFoBiS is an open initiative, Open Network

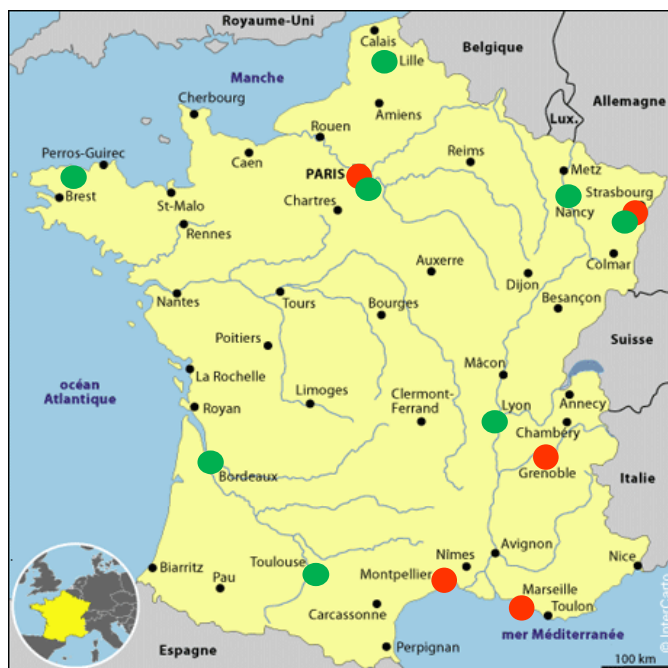


" National Training Network in Integrated Structural Biology "

« Réseau National de Formation en Biologie Structurale Intégrative »

A dream of a national graduate School in Structural biology

Structural biology Institutes in 12 cities



<https://www.renafobis.fr/>

RéNaFoBiS
Fédérer et proposer des formations en Biologie Structurale Intégrative en France.

Oléron 2021 : 18-25 juin 2021. Inscriptions à partir de Janvier 2021.

Vous préparez un doctorat ? Vous êtes postdoctorant ou chercheur ?

RéNaFoBiS est une structure nationale qui vous propose des formations aux différentes facettes de la Biologie Structurale Intégrative, au niveau doctoral (post-master), en lien avec de nombreuses universités françaises et les instituts de recherche.

Objectifs:

- Proposer des enseignements labellisés, reconnus par les Ecoles Doctorales de chaque Université, gage de formation de haut niveau.
- Intégrer les aspects connaissances fondamentales et développements pratiques actuels et futurs.
- Intégrer, coordonner et mutualiser les formations offertes en Biologie Structurale Intégrative à l'échelle nationale.
- Proposer/développer/encourager les collaborations nationales et internationales, tout en gardant la spécificité de chaque site partenaire.
- Offrir une visibilité et une unité à la communauté nationale.

Actions:

- RéNaFoBiS propose chaque année à quelques étudiants des écoles thématiques en biologie structurale intégrative, axées sur les aspects applicatifs, animées par les plus grands spécialistes, et visant à donner les compétences les plus en pointe.
- Une aide financière est proposée par Aviesan, aux étudiants sélectionnés.
- Une Ecole tutorale RéNaFoBiS permet chaque année à l'ensemble des partenaires du réseau (intervenants et participants) de faire le point sur l'ensemble des derniers développements en Biologie Structurale Intégrative.

Téléchargez la plaquette au format pdf: [plaquette 2020](#)

<https://listes.services.cnrs.fr/www/info/renafobis.bb>



Ecole RéNaFoBiS Oléron Juin 2014

Programme et supports de cours



Ecole RéNaFoBiS Oléron 2015

Bienvenue sur la section de l'école RéNaFoBiS 2015 à Oléron!



Oléron 2016: Troisième Ecole Nationale RéNaFoBiS



Oléron 2017: Quatrième Ecole Nationale RéNaFoBiS



5^e École de Biologie Structurale Intégrative



6^{ème} Ecole RéNaFoBiS - Oléron 2019



7^{ème} Ecole RéNaFoBiS - Oléron 2020



Accueil

8^e École de Biologie Structurale Intégrative Oléron - du 18 au 25 Juin 2021

Cette **école** propose une formation théorique et appliquée aux différentes approches utilisées en biologie structurale (diffraction et diffusion des rayons X, RMN, cryo-microscopie, préparations des échantillons en vue des études structurales, interactions macromoléculaires). Elle mettra l'accent sur l'intégration de plusieurs de ces méthodes pour répondre aux grandes questions de la biologie fonctionnelle à l'échelle atomique.

Ciblée pour un public de **doctorants** ou de **jeunes chercheurs**, cette formation montrera les apports et les limites de chaque méthode et leur complémentarité. Elle inclura des sessions théoriques le matin et des travaux pratiques en groupes l'après-midi. Cette école est ouverte aux techniciens et ingénieurs (domaine académique et industriel) dans la cadre de la **formation continue**.

Les conférences seront données principalement en Français. Les supports des présentations seront en **Anglais**, afin de permettre aux participants non-francophones de suivre plus facilement. Lors des sessions pratiques (TP), des groupes anglophones pourront être proposés si besoin.

Le nombre de places étant limité (28), les participants seront sélectionnés sur la base d'une lettre de motivation. Les dossiers seront examinés et validés au fur et à mesure de leur arrivée. **Les inscriptions seront closes lorsque le nombre de candidatures acceptées atteindra le nombre de places possibles.**

En préparation et en complément de l'école, le MOOC "Voyage au coeur du Vivant avec les rayons X", accessible sur [FUN-MOOC](#) sera ouvert en SPOC aux étudiants retenus.

Ce SPOC, adapté spécifiquement pour les participants à Oléron2021, comportera des compléments nécessaires à l'école (initiation à LINUX, utilisation de programmes de construction/visualisation 3D, vision unifiée de la diffraction/diffusion des rayonnements). Les informations détaillées seront communiquées aux étudiants sélectionnés.

Formateurs et conférenciers

Guillaume Bouvignies (ENS, Paris), Jean Cavarelli (IGBMC, Strasbourg-Illkirch), Marc-André Delsuc (IGBMC, Strasbourg-Illkirch), Samuel Holweg (IGBMC, Strasbourg), Bruno Klaholz (IGBMC, Strasbourg-Illkirch), Olivier Lambert (CBMN, Bordeaux), Marie-Helene Le Du (CEA Saclay), Amélie Leforestier (LPS, Orsay), Gordon Leonard (ESRF, Grenoble), Arnaud Poterszman (IGBMC, Strasbourg-Illkirch), Alain Roussel (AFMB, Marseille), Robert Schneider (Biologie Structurale Intégrative, Lille), William Shepard (SOLEIL, Gif/Yvette), Christina Sizun (ICSN, Gif/Yvette), Jean-Christophe Taveau (CBMN, Bordeaux).

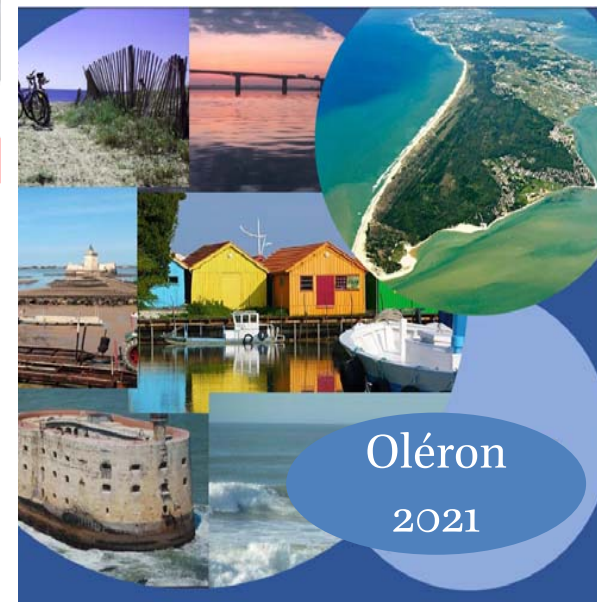
Contacts administratifs

Marie-Christine Poterszman: pmarie@igbmc.fr

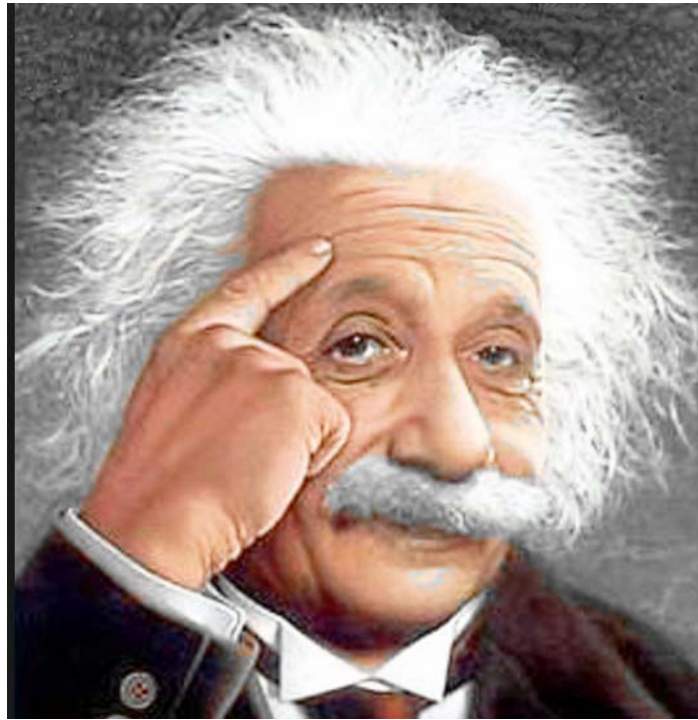
Informations

Inscriptions

Effectif Complet pour 2021



Oléron
2021



What we hope to do in *ReNaFoBiS/Oleron* is to give you a feel for the fundamental ideas that come into play in a variety of structural biology approaches and applications, and to do so with enough detail to allow you to go off and invent new approaches of your own.

We look forward to seeing your contributions to Structural biology !



*Modify without permission from Jacobsen 2020
"X-ray microscopy"*



Aimeur



Ammar Khodja



Ayala



Bretagne



Cargemel



Claire

Cirio

Charles



Coudray

Léna



Degaugue

Augustin



Donker

Helena

Sana-Zineb

Liza

Isabel

Damien



Gauffre



Gervason



Hepp



Kra



Lahfa

Pierre

SYLVAIN

Benjamin

Kalouna

Mounia



Lo Bello



Lopez-Lozano



Lublin



Mochetti



Paris

Lea

Nina

Victoria

Eva

Théo



Parpinel



Rollet



Royet



Ruedas



Schmitt



Seif El Dahan

Aline

Kévin

Adrien

Rémi

Alain

Murielle



Sobron

Lua



Vuillemot

Rémi



Welker

Lisa



Zachayus

Amélie



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Christina Sizun (ICSN, Gif/Yvette)



Jean-Christophe Taveau (CBMN, Bordeaux)



Aurélien Thureau (SOLEIL, Gif/Yvette)