PSB et al.
Partnership for Structural Biology Newsletter
N° 7
July 2010

Building for the future

The success of the Institut de Biologie Structurale (IBS) has led to plans for a new initiative aimed at bringing the partnership's groups closer together and maximising their capabilities

IBS, created in 1992 by the CEA and the CNRS and subsequently joined by the University Joseph Fourier in 1999, has become a very attractive institute as exemplified by its staff that doubled over the past 18 years. Quite logically, most of the teams are now facing major space problems. In addition, being outside the EPN campus hinders an optimal integration into the PSB. It thus became obvious that the IBS had either to expand or to relocate into a larger building.

The project was officially initiated in 2006 and deposited to the CPER program (contrat de projet état-région). Its success hangs on the dynamics of the "Giant" campus project later on amplified by the "Plan campus" launched by the French government in 2008 to boost the development of 12 higher ranked universities such as Grenoble University. The plans integrating fundamental science, large scale European instruments, technology, as well as housing, restaurants and shops, within the whole "Polygone scientifique" convinced the city of Grenoble, the Région Rhône-Alpes and other local authorities (Métro, Conseil Genéral) and rapidly the new IBS building became part of these plans. The directors of the European Institutes, ESRF and ILL, with a strong support from EMBL, helped present the land request to their councils which agreed to part with sufficient land for the new IBS building. In total €23m was allocated to the IBS project (including the sale of the current building), €20m for the building itself and €3m for the ESRF/ILL site (dedicated to the construction of the science building and other smaller items).

After a few years of intense preparation, the new IBS building is now

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becoming a reality. The architect, Nickl and partners (Munich), has been selected in November 2009 among 5 preselected groups that presented their project to a jury. The project fulfils requirements for the locations of NMR and EM platforms, flexibility for laboratory spaces and even reduced energy consumption. The building will have 5 levels including the ground level. The available surface (around 8000m^2) is roughly 50% larger than the present building, allowing future expansion of our teams, installation of new coming teams or breading of spin-off companies as exemplified in the past by ProteinExpert or currently by NatXRay. The closer proximity to the PSB partners and the available space will facilitate PSB common operations such as the IBS-UVHCI joint acquisition of the latest Polara for cryo-electron tomography (the second of this type in France). Space will also be available for external users and collaborators within the frame of European projects favoured by INSTRUCT. Such users could stay several months and benefit from the unique ensemble of expertise and platforms provided by the PSB as planned in INSTRUCT Centres. The time was also appropriate for an internal reorganization of our groups, the challenge being to both favour emerging teams and create the critical mass by grouping activities that gained to be reinforced. The new scheme presented for evaluation to the AERES last February will be settled in January 2011. As highlighted by the evaluation committee, the new organisation in 15 groups is now biology-oriented rather than methodology-oriented.

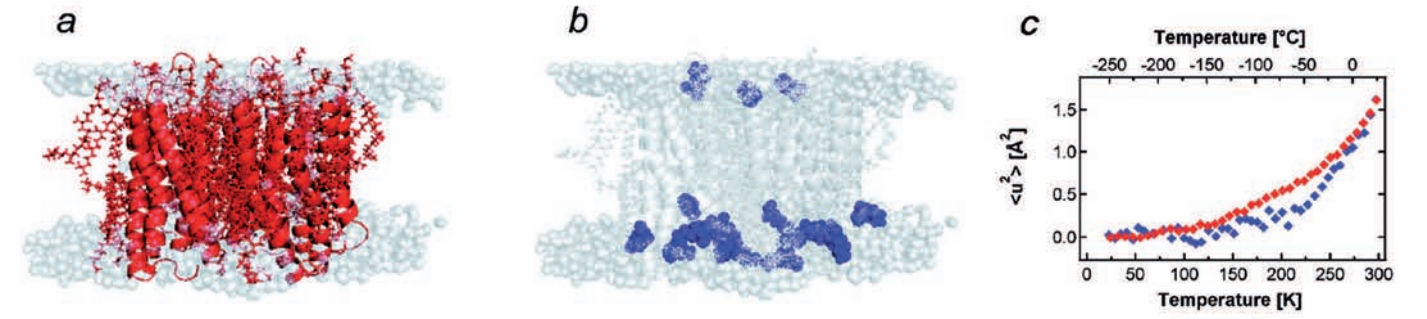
After a few years of intense preparation, the new IBS building is now becoming a reality

The building construction will be supervised by the CEA with the help of Joseph Sedita from EMBL as the project manager. The construction itself will start in spring 2011 and should be completed by the end of 2012. The IBS will continue to run under the governance of the CEA, the CNRS and the Grenoble University but this move towards a European centre is a fabulous event, quite unique for a French research unit.

Eva Pebay-Peyroula (IBS)

Dissecting protein dynamics - the role of methyl groups

Below: Bacterio-rhodopsin in the purple membrane (a) is animated by internal motions at temperatures as low as -100°C as shown by mean square displacements measured by neutron scattering in the temperature range from 20 to 300 K (red data points in panel c). These motions are almost absent if the hydrogenated lysine side chains (b) in an otherwise deuterated purple membrane are examined by neutron scattering (blue data points in panel c).



The dynamic nature of protein structures is essential for macromolecular function and biological activity. Like in a motor operating at full speed, a multitude of motions on various length and time scales characterize a protein at work. At physiological temperatures, protein dynamics are rich and complex. At decreasing temperatures, protein motions slow down or vanish, and like in a motor turning in slow-motion mode, the various protein motions can be dissected and studied separately. Even at temperatures as low as -70°C, proteins display complex internal motions. In particular, methyl group rotations have been suspected over the last ten years to be responsible for the low-temperature flexibility of proteins, but an experimental proof has remained elusive.

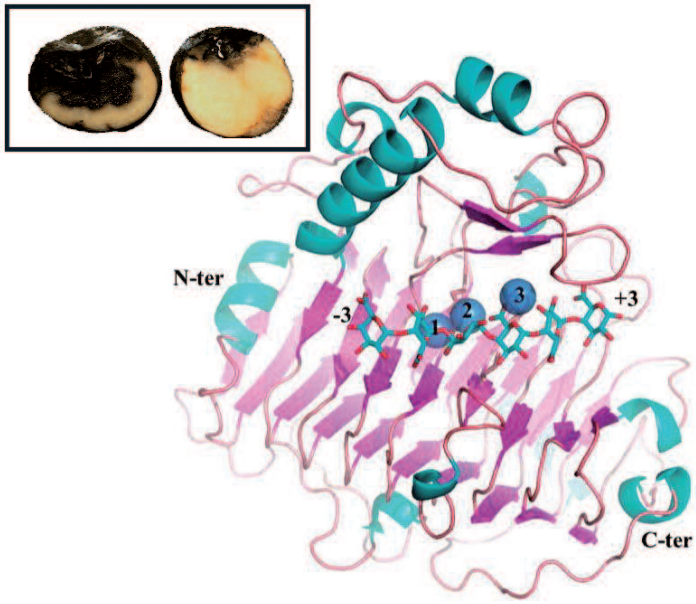
In a collaborative effort, scientists from the ILL, the IBS, the MPI in Martinsried, Germany, the University of Groningen, The Netherlands and the University of California in Irvine, USA have studied the nature of protein motions in the membrane protein bacteriorhodopsin at very low temperatures. In order to tackle the complexity of protein motions, several complementary biophysical and biochemical methodologies had to be applied, including neutron scattering, molecular dynamics simulations, NMR and specific protein deuteration.

Incoherent neutron scattering reports on motions on the nano- to picosecond time scale and is most sensitive to the contribution from hydrogen atoms. Replacing hydrogen by deuterium atoms in a particular side chain masks its dynamical contribution to the measured neutron signal. We applied the labelling strategy to the purple membrane, a membrane constituted of the protein bacteriorhodopsin and various lipid species (figure a). In order to specifically address the role of methyl dynamics we labelled a side-chain containing no methyl groups, lysine, by deuterating everything in the purple membrane but lysines (figure b). Most of the neutron signal from the specifically labelled sample is then due to lysines within their native protein environment and their dynamics is compared to an unlabelled sample where the average dynamics of the whole membrane is probed. The thermal motions (atomic mean square displacements $\langle u^2 \rangle$) as measured by neutron scattering are plotted in figure c. Lysine side chains have considerably reduced dynamics between 100 and 250 K compared to the global membrane, suggesting that methyl groups are a major source of protein flexibility in that temperature range. Molecular dynamics simulations quantitatively reproduced the neutron results and NMR data showed that it is the methyl group rotation that is observed by neutron scattering in proteins at cryo-temperatures. In the future, even more complex labelling schemes, combined with neutron scattering and complementary techniques, will provide deeper insight into the complex nature of protein dynamics. Targets of interest will not only be globular and membrane proteins, but also intrinsically disordered proteins. Eventually, uncovering a protein's dynamical personality will sharpen our understanding of its function and fundamental knowledge of protein dynamics and energetics will benefit rational drug design.

Kathleen Wood(ILL/University of California), Giuseppe Zaccai (ILL) and Martin Weik (IBS)

Wood, K. et al, 2010, J Am Chem Soc, 14, 4990-1

How to cleave one of the most stable bonds in nature



Cartoon representation of the parallel β-helix architecture of BsPel with β-strands and α-helices represented as magenta arrows and cyan helices, respectively. The cyan/red liquorice bonds represent bound hexasaccharide (pectin I). The oligosaccharide binds to the surface of the β-sheet known as PB1. The reducing end of the hexasaccharide binds toward the C-terminal end of the parallel β-helix. The three bound calcium ions are shown as blue spheres. The inset shows a photograph of an example of soft-rot disease in potatoes.

Pectate lyases such as *Bacillus subtilis* pectate lyase (BsPel), are secreted microbial enzymes that play a pivotal role in plant pathogenesis. They are potent virulence factors of plant pathogenic bacteria which break down the stable pectin network loosening the adhesion between cell walls. This allows bacteria to invade and cause disease – so-called soft rot disease, one of the most serious worldwide diseases of harvested potatoes – and crop spoilage. Amazingly pectate lyases accelerate rates of reaction by factors exceeding 10^{17}-fold, cleaving very stable bonds in nature that would otherwise last 10 million years!

Through a combination of crystallographic studies using mutant enzymes (where data was collected using the ESRF and ISIS facilities), along with isothermal titration calorimetry experiments we reveal the importance of entropy in binding and gain insight into the calcium binding characteristics of BsPel in both protein/substrate complex and in the free-form. BsPel comprises a β-helix domain that binds a single calcium ion in the free-form, (which is enthalpically driven and plays a role in substrate binding) in addition to two catalytic calcium ions in complex with substrate that play a role in stabilizing the intermediate (see picture). This process of binding catalytic metal ions is reminiscent of substrate-assisted catalysis, as described in a paper published earlier this year (see reference).

To further probe into the catalytic mechanism and substrate specificity of BsPel, high-resolution neutron crystallographic studies on perdeuterated BsPel using the LADI-III quasi-Laue instrument are well under way at the ILL. Fully deuterated crystals of the protein have been produced and tested at the instrument and a joint structure refinement with neutron and X-ray diffraction data will be carried out. The outcome of these results will confirm the role of the catalytic arginine as a base which has been under investigation for many years. This is fascinating as arginine is fully protonated at physiological pH and so for it to abstract a proton (initiating the reaction) there must be a favorable change in the local pH environment facilitating the abstraction of the proton from substrate. Ultimately the direct experimental determination of the protonation state of the catalytic arginine, along with water molecule orientations, will prove the mechanism by which BsPel cleaves one of the most stable bonds in nature.

Salyha Ali (Queen Mary University of London/ILL)

Seyedarabi, A., To, T.-T., Ali, S., Hussain, S., Fries, M., Madsen, R., Clausen, M., Teixeira, S., Brocklehurst, K. & Pickersgill, R. (2010). Biochemistry 49, 539–546

Training at the PSB

The PSB Students Day 2010

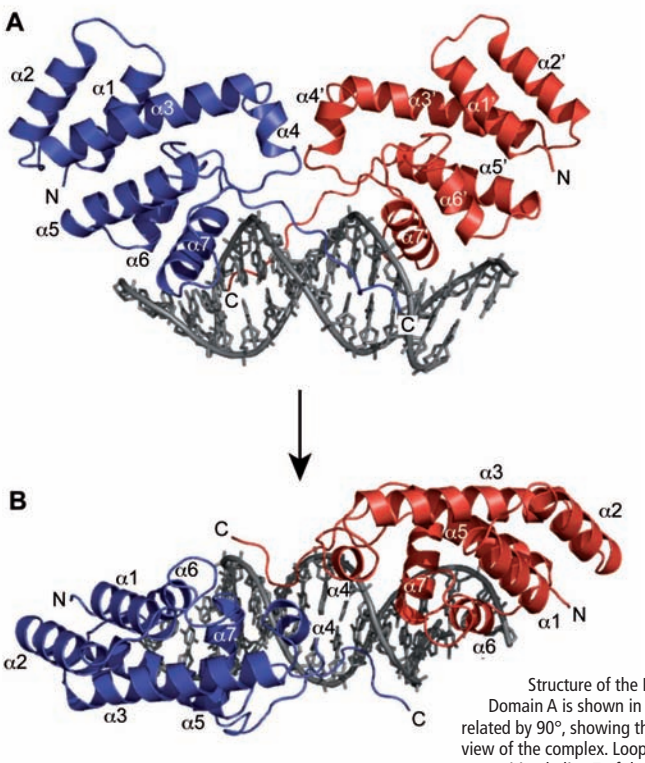
Our second PSB Students Day was held on 26 January and it was again a huge success. First, second and third year PSB PhD students came to present and discuss their work in a semi-professional environment. Throughout the day, there was a stimulating and international atmosphere – this is to be expected at PSB events as the diverse expertise, nationalities and inter-disciplinary research that is available here is extremely unique and allows us to meet and discuss with other students and scientist with similar interests.

Prizes were awarded to the best poster (second year PhD students) and best short clip presentations (first year PhD students); Celeste Sele (UVHCI) and Romain Talon (IBS) shared the prize for best poster and that for the best clip was shared by Charlotte Sueur (UVHCI) and Aili Sarre (ESRF). Well done, everyone!

On behalf of the PSB students Committee, I would like to sincerely thank Laurence Serre, without whom none of the PSB events would have been possible. We are looking forward to seeing many more group leaders and staff scientists at our next PSB Student's Day in 2011 – come and join the melting pot!

Bridget Connell (IBS)

Get into the groove



Structure of the MogR-DNA complex. MogR bind DNA as a dimer. Domain A is shown in red and domain B in blue. Two views of the complex, related by 90°, showing the overlapping DNA contacts of both domains. (A) Side view of the complex. Loop L3 of domain A inserts into the minor groove opposite recognition helix a7 of domain B and vice versa. (B) Top view of the complex.

Work from Daniel Panne at EMBL Grenoble has pointed to a new possibility for DNA sequence recognition by transcription factors. In a Structure paper in May last year, he and his group presented the structure of a transcriptional repressor, MogR, bound to DNA – and found that, unlike most transcription factors we know, its binding specificity seems to rely on the shape of DNA rather than its sequence. The conventional view is that transcription factors literally read out the four-letter code by binding to bases directly. The arrangement of atoms in a DNA molecule creates two grooves – major and minor – that wind along its length, carving out the double helix shape. Many transcription factors bind in the larger major groove as it gives better access to the bases to read their sequence.

"What's special about MogR is that it binds to a DNA sequence composed exclusively of 'A's and 'T's," explains Daniel. "These 'Atracts' cause the DNA to bend, narrowing the minor groove and concentrating its negative charge." In other words, MogR recognizes its target not so much by the literal sequence of bases, but by the shape and electrostatic pull of the minor groove that this sequence creates. Since Daniel's discovery, another group at the Howard Hughes Medical Institute at Columbia University trawled the protein structure databases using MogR as a prime example. Their findings suggest that shape dependent readout could actually be a universal method of sequence recognition. "It seems that a whole number of structures exhibit this feature and that this is a general phenomenon in protein-DNA recognition," Daniel says. "MogR illustrates these principles beautifully."

Lucy Patterson (EMBL)

Shen, A., Higgins, D.E. & Panne, D. (2009). Structure 17, 769-77

Events

MaM2010: Membranes and Molecules Symposium

A symposium took place earlier this year to honour Peter Timmins and Roland May, both recently retired from the ILL. Invited scientists presented past, present and future developments made possible thanks to Peter and Roland's important contributions towards the use of neutron scattering in challenging structural biology studies, such as the determination of membrane protein structures and their interactions with lipids, nucleic acid-protein complex structures and many other studies of macromolecular assemblies. We will all remember an inspirational speech from Roland when he reminded us of the importance of pursuing new ideas with enthusiasm, even when they are first received with the well known scientific skepticism. Peter and Roland definitely made things happen with their original approaches to scientific challenges and left very big shoes to fill!

Susana Teixeira (Keele Uni./ILL)

PSB Science Day: dynamics in biology

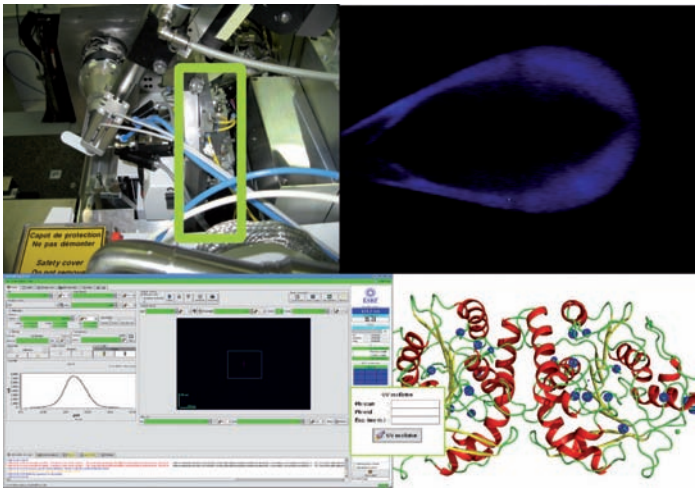
On June 28, the PSB organised a Science Day on Dynamics in Biology at the IBS. The PSB competences in this field were particularly well represented by all the partners. Martin Field (IBS), creator of DYNAMO, opened the session by giving a very didactic overview of molecular simulations applied to enzyme catalysis. Michael Wulff (ESRF) described his activity on the ID09 beamline and some exciting perspectives for the study of proteins. The first session, chaired by Christian Schaffitzel (EMBL), ended by the presentations of two young PSB scientists: Colin Jackson, a post-doc working with Martin Weik (IBS), gave an interesting talk relating protein evolution and dynamics, while Cedric Leyrat PhD student under Marc Jamin (UVHCI) presented data obtained by NMR and molecular dynamics simulations on Rhabdoviridae replication complex. The second session was chaired by Dominique Housset (IBS). Jo Zaccai (ILL) highlighted the contribution of neutron scattering to the understanding of protein dynamics and Martin Blackledge (IBS) presented various NMR approaches to tackle the role of molecular flexibility in protein function. The PSB would like to thank all speakers for their participation.

Laurence Serre (ESRF) and Dominique Housset (IBS)

Routine use of UVRIP as phasing technique on ID23EH1

Radiation damage is a side effect of protein crystallography because of which the diffraction limit of the crystal exposed to x-ray is dramatically decreased and structural changes occurs in the structure, in some cases affecting isomorphism inside the same crystal. However it has been shown how these structural changes can be used, in favourable cases, as derivative sites if two different data sets are collected, a low dose exposed data set (or before) and a high dose exposed data set (or after). More recently the use of UV as source to induce specific damage in a protein crystal has been proved successful. The difference between a 'before' and an "after" UV exposure data sets are in some cases enough to obtain experimental phases.

The possibility to perform such an experiment on routine base is given on ID23EH1, where a 266 nm UV source is installed. UV radiation is coming through the on-axis-viewer, coaxial with x-ray radiation. UV exposure is completely user accessible, and is entirely controlled by mxCuBE, as version installed on ID23EH1. Users need to provide as input information the oscillation range, over which the crystal will be exposed and time of the exposure. The software macro will take care of irradiating the crystal on two sides, over the oscillation sweep defined, to maximize the damaged volume of the crystal.

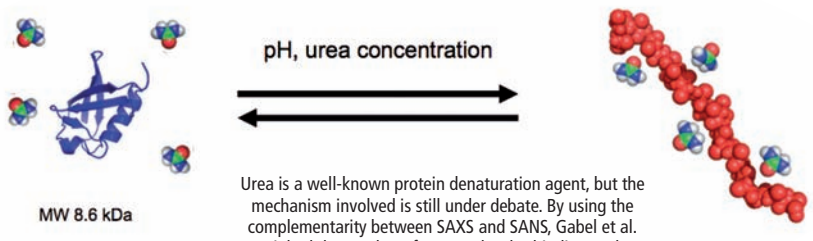


UV radiation has been proved effective in disulphide bridges containing protein, but not only. Recent results showed that information contained in UV damaged structure can be combined with Selenium Methionine labelled protein, enhancing substructure determination and quality of the first experimental map. Currently we are investigating the combined use of UV damage with other anomalous scattering phasing experiment. As the technique is very new and its application has been very limited, it is expected that there is still room for improvement, and to use it in new phasing experimental approaches, thus it is not possible to foresee the limit of applicability.

Daniele de Sanctis (ESRF)

Combined applications of SANS and SAXS

Happily, the days are gone when champions of SANS and SAXS would stand up at conferences and have it out on the respective merits of each technique. The debate was not entirely scientific, but also included the political confrontation between a laboratory-based method and one that required access to a large facility, with the inherent competition for funding in an atmosphere of shrinking budgets for fundamental research. Neutron beam allocation committees were given strict instructions not to accept proposals that 'could be done by X-rays', leaving it up to the appreciation of the referees as to how to interpret this. It did not help matters that there were very few places that had laboratory SAXS instrumentation, and that it was not accessible widely to the community. The situation changed with the advent of synchrotron radiation sources, and SAXS joined SANS as a predominantly large facility technique. Both techniques now have similar access rules. Dedicated scientists are developing and building state of the art instrumentation and data analysis procedures that are openly made available to structural biology (SB). A block allocation group system was introduced into SANS at ILL to facilitate SB access, and a new beam line dedicated to SB SAXS is now available at ESRF. The SB community has not been slow in responding, and in making use of the strong scientific complementarity between these methods. Recent publications of members of the PSB in international collaborations, based on combined SANS/SAXS experiments often with other techniques, include studies of interactions between membrane proteins involved in bacterial division, interactions of the alpha-crystallin protein in the eye lens and interactions with urea in the unfolding of ubiquitin . The essential complementarity of SAXS and SANS is beautifully illustrated in a paper by Gabel et al. (see reference). In what could be described as a radiation-dependent contrast variation approach, these authors describe how they measured the different interacting partners in the system, urea, protein and water, by weighing their respectively different contributions to the X-ray and neutron scattering (see figure). Now, the PSB SAS platform (previously called the SANS/SAXS platform) has participated in the putting into place by ILL and ESRF of a system for joint SANS/SAXS proposals. Successful applicants will have their beam allocations scheduled most conveniently, on the two instruments, to facilitate the best possible experimental conditions for their samples. First official users using both facilities in a single visit to the Grenoble site are expected this summer. Further details and information for the PSB SAS platform is available on the official web page (www.ill.eu/fileadmin/users_files/Other_Sites/saxs-sans/Front_Page.htm).



Urea is a well-known protein denaturation agent, but the mechanism involved is still under debate. By using the complementarity between SAXS and SANS, Gabel et al. weighed the number of urea molecules binding to the unfolded chain of ubiquitin

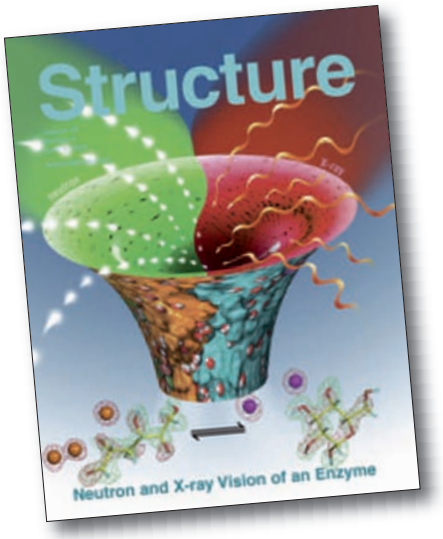
Joe Zaccai (ILL)

Gabel, F., Jensen, M. R., Zaccai, G. & Blackledge, M. (2009). J. Am. Chem. Soc. 131, 8769-71.

Hydrogen transfer during the reaction catalysed by d-xylose isomerase

A monochromatic neutron crystallographic study using ILL's D19 diffractometer

D-xylose isomerase (XI) catalyses the conversion of aldo to keto sugars. This occurs through a multi-step reaction involving the transfer of hydrogen. Structural information derived from X-ray crystallography has resulted in the proposal of several models for the reaction. These models differ in the way hydrogen is located and transferred.



As part of a collaboration between ILL, Los Alamos National Laboratory (New Mexico), Fox Chase Cancer Centre (Philadelphia), and ISIS at Rutherford-Appleton Laboratory, the D19 monochromatic diffractometer at the ILL has been used to carry out a neutron crystallographic study of XI to a resolution of 1.4Å. This study provides direct information on the side-chain and ligand ionization states, and on the coordination of metal ions in complexes of XI that are important for the reaction mechanism. During ring opening, hydrogen is moved from O1 and to Lys289. During subsequent isomerization hydrogen is moved from the catalytic water, C2, and O2, and to O1 and C1, as a metal ion moves towards the aldehyde terminus of the linear sugar to bind to O1 and O2. These results have led to new suggestions as to how changes might take place over the course of the reaction.

This work is the first study of its type at the D19 diffractometer, and illustrates the scientific scope available when detailed information on hydrogen atoms and hydration is available in structural studies. D19 is one of ILL's diffraction group instruments, and was recently refurbished with major funding from the UK Engineering and Physical Sciences Research Council (EPSRC) to Durham, Keele and Bath Universities, producing a signal gain factor of approximately 25. The new instrument has opened up new areas for crystallography and partially ordered systems for chemistry, soft matter, and the biosciences. D19 (www.ill.eu/d19) is strongly complementary to the LADI-III neutron Laue diffractometer which since being commissioned in 2007 has delivered striking results for a large number of protein systems, and to D16, which now includes a low resolution (long wavelength) biological crystallography mode of operation. As in this study of XI, these instruments yield information of key importance to biological structure/function – information that is not accessible to X-ray methods alone.

Trevor Forsyth (ILL/Keele University)

Kovalevsky, A., Hanson, L., Fisher, Z.,, Mustyakimov, M., Mason, S., Forsyth, T., Blakeley, M., Keen, D., Wagner, T., Carrell, H., Katz, A., Glusker, J., Langan, P. (2010). Structure 18, 688-699

Training at the PSB

Shaping a new generation of structural biologists

In June the PSB welcomed twenty-six young scientists from 13 countries to spend a week learning how to tackle challenging problems in structural biology. The group was attending the fifth biennial EMBO Practical Course on the Structural Characterization of Macromolecular Complexes, a course organized and run by members of the IBS, EMBL, UVHCI, ESRF and ILL – a truly PSB-wide initiative.

The 17 predoctoral students and 9 postdocs came primarily from laboratories in Europe, but also from Israel, India, and Australia. With backgrounds primarily in crystallography, electron microscopy, and NMR, they all shared a keen interest in the 3D architecture of macromolecular complexes. During their stay, the students learned about the different strategies and techniques required to produce, purify and characterise multi-protein and protein-nucleic acid complexes. They also learned about P-CUBE – the new EU initiative that allows researchers access to protein production and characterization platforms – which co-sponsored the course.

Teaching the course were twenty-four highly motivated speakers from across Europe and the US, including several P-CUBE partners and local scientists. They lectured on topics that ranged from basic laboratory protocols to the description of complex macromolecular assemblies. Some focused on practical matters – how to express recombinant protein in mammalian cells or to determine binding constants by isothermal calorimetry – while others outlined an entire discipline, for example small-angle scattering, nuclear magnetic resonance or electron microscopy. Still others presented case studies, outlining the chronology of events and strategy used to crack a tough structure.

The talks were complemented by practical sessions run by local tutors, allowing students to gain hands-on experience with techniques and instruments presented during the lectures. Among other things, students prepared sample grids for electron microscopy, carried out measurements by CD spectroscopy and multi-angle laser light scattering, and optimized protein buffer conditions in a thermofluor stability assay, often using their own samples.

"The course was very inspiring and motivating," said one student. "It opened up many opportunities for collaboration and discussion and helped me make many contacts that will be useful in the future." Another said, "I especially liked the informal atmosphere, the ability of participants and tutors to interact and the structure of the course, which allowed extensive time for networking alongside the lectures and practicals."

Carlo Petosa (IBS), Elspeth Gordon (ESRF), Darren Hart, Mary Jane Villot (EMBL), Guy Schoehn, Winfried Weissenhorn (UVHCI)

Profile

Serge Pérez

Director of research, ESRF

Interview by Dominique Housset (IBS) and José A. Márquez (EMBL)

Serge Pérez took up the position of director of research at the ESRF in June 2009, replacing Sine Larsen. He was previously director of the Centre de Recherches sur les Macromolécules Végétales in Grenoble, and prior to that, director at the Centre de Recherches Agro-Alimentaires.

After one year in your new position, you've had the opportunity of seeing the PSB both from the outside and from the inside. What is your view of the PSB?

The PSB has fostered an atmosphere of collaboration and cooperation in bringing cutting-edge technologies to bear on the most challenging research problems in biology. This approach is a model for the international scientific community.

In your opinion, what will be the next challenges the now mature PSB will need to undertake?

Maintain the quality and the access to the technological platforms and make sure that staffing continuity is committed. The PSB is in a strong position to explore synergies with other major facilities across Europe and to work with these facilities to take the leadership in developing a coherent front for the benefit of the structural biology user community. Whereas its scientific case is very strong, the PSB may be handicapped by the fact that it is not a legal entity. The question remains to see how the PSB can overcome this administrative handicap and be recognized as a whole on the national and international level by the funding agencies.

What should the PSB develop in priority in the coming years?

New PSB platforms could be developed for example in the field of low resolution crystallography (combining low resolution X-ray and neutron crystallography with electron microscopy) and biophysical characterization. For the time being the computational biology is not covered within the PSB, in the sense of offering access to the tools and computational resources.

How would the upgrade of the ESRF impact the PSB and vice versa?

The part of the ESRF upgrade which deals with "Macromolecular Crystallography" is a most ambitious project that sets the pace towards a very high through put analysis of protein crystals. Such an unprecedented endeavor will initiate new initiative towards opening the doors to integrated facility on going from protein in solution to X-ray data measurement and analysis. Some of these developments will be performed in close collaboration with partners within the PSB. The concomitant developments in automation and data management that will be developed within the upgrade are likely to benefit to other aspects of structural biology.

And how would all this benefit the European life science research community?

The PSB is now poised to be a leader in Europe of international efforts to coordinate and synergize activities across institutions and disciplines. The PSB is already a recognized site within the landscape of the structural biology in Europe. With the increasing importance of the "System Biology" it is important not only to maintain the quality of the several technological platforms within the PSB, but also to participate in the integration of the results obtained at the structural level in broader questions related to fundamental questions in life sciences as well as to issues pertinent to health and sustainability.

IBS will be moving on the EPN site campus in 2013. What will be the major consequences of this move for ESRF and the PSB?

This is considered as a positive development that will further enhance communication and collaboration of research groups and lead to a better integration of the technology platforms that are unique in the Grenoble environment. This resulting spatial proximity of the structural biologists will enhance the density of collaborations and facilitate the formal and informal exchanges among the scientists. These informal exchanges are very often keys towards innovation and creativity. Beside, the international visibility of the site, in all aspects of structural biology will be enhanced.

You also hold the position of director of the PhD programme in Chemistry and Life Sciences at the University Joseph Fourier in Grenoble. Are the PSB and the Doctoral school taking full advantage of each other?

Actually, I resigned from the position, and I'm acting as a deputy of the new director, with the role of liaising the Doctoral School with the International Large Scale Facilities located on the European Photon and Neutron Scientific Campus. The Doctoral School has been rated very high by the recent evaluation conducted by the Agence d'Evaluation de la Recherche et de l'Enseignement Supérieur. It provides a large spectrum of educational modules which can be followed by all the doctoral students present on the site. It is also a forum for promoting the research conducted in the PSB laboratories at the European level. Special training sessions can be organized as the one which has been co-organized by some of the members of the PSB dealing with the theoretical and practical aspects of "Structural Glycoscience".

Newcomers

Robert Cubitt is now the new group leader of the Large Scale Structures (LSS) group at the ILL, where he will be leading a team carrying out structural studies on a scale of one to hundreds of nanometers. These require neutron beamlines for small-angle scattering, reflectometry, diffraction from single crystals or one or two-dimensionally ordered materials.

Previously Robert was an instrument scientist at D17, the first ILL dedicated reflectometer. He has worked at the ILL for 15 years where his research interests focused mainly in studying the flux lattice in superconductors, the casimir force and the development of neutron optics.

Cécile Morlot as joined the IBS in January as a CNRS Chargée de recherche in the team of T. Vernet.

Maxime Terrier has joined the IBS as a CEA Engineer in the FIP beamline team.

Spotlight

MASSIF and the ESRF upgrade

The upgrade programme beam line UPBL10, combined with ID23 and ID29, will ensure that the ESRF provides the synchrotron radiation facilities required by Structural Biologists for the next 10 to 15 years. UPBL10 will provide an upgraded suite of beam lines regenerating ID14 A&B (in operation since 1997) on ID30. MASSIF (ID30A) will consist of three end-stations and will provide a state-of-the-art facility for high throughput sample evaluation, ranking and data collection. Two stations will provide an X-ray beam 100 µm in diameter at the sample position. The third station will be a micro beam facility producing a beam 15 µm in diameter.

As identifying the "best" crystal is only the beginning of a successful MX experiment, UPBL10 will also provide a tunable end-station (ID30B), from an independent canted undulator source. This resource will be optimised for the requirements of the crystals identified as being suitable for full data collection by MASSIF. Exploiting the potential of a high β-section source, the end-station will have a flexible beam size (ranging from 20 x 20 µm² to 200 x 200 µm²) with an X-ray collimation system able to further tailor the size and shape of the X-ray beam to that of the sample.

The bending magnet beam line BM29 will become a facility fully dedicated to Protein Solution Scattering and will replace the current ID14-3 end-station. A highly intense and tunable beam will enable sample volumes to become smaller and changes in experimental environment easier to achieve. As the equipment of the experimental station has only recently been installed and commissioned on ID14-3 it will be placed directly on BM29. A reasonably rapid transition from ID14-3 to BM29 is thus anticipated. Table 1 gives a comparative overview of the existing ID14 and the new ID30/BM29 beam lines and Figure 1 shows a top-view perspective of the floor plan of BM29 and ID30A with ID29, together with the CRG BM30A (FIP), these beam lines form the future "Structural Biology" village.

Christoph Müller-Dieckmann (ESRF)

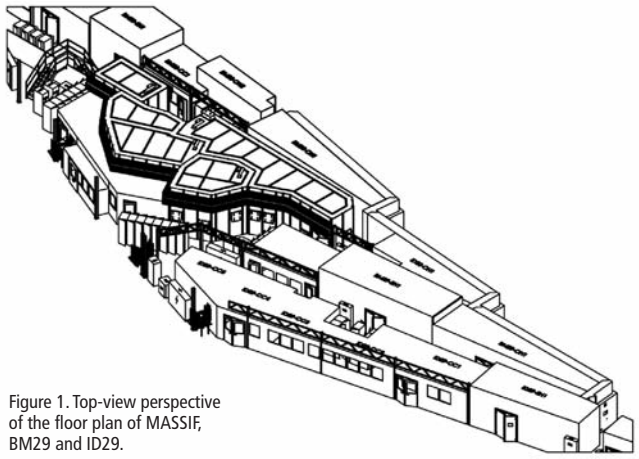


Figure 1. Top-view perspective of the floor plan of MASSIF, BM29 and ID29.

		Now				Upgrade	
Beam line	Energy	Beam size	Flux	Beam line	Energy	Beam size	Flux
14-1	13.3	200	10^{11}	30-1	12.8	100	$> 10^{12}$
14-2	13.3	200	10^{11}	30-2/3	12.8	100/10	$> 10^{12}$
14-3	13.3	700	3×10^{11}	BM29		700	$> 5 \times 10^{11}$
14-4	10-18	150		30B	6-20	20-200	5×10^{12}
29	6-18	40		29	5-20	5-30	
23-1	6-20	30		23-1	6-20	10-150	
23-2	14.2	7		23-2	14.2	1 or 7	

Announcements

Eva Pebay-Peyroula, head of the IBS, has been appointed in May president of the Agence Nationale de la Recherche (ANR) by Valérie Pécresse, the french minister of research. She is taking over from Jacques Stern, who chaired this major research funding agency since its creation in 2005.

The first User Meeting of the EC-funded Protein Production Platform (P-CUBE) project will take place on 9 September 2010 in Grenoble. The meeting will be open to all former users of the P-CUBE platforms as well as to all prospective users from EU Member and/or Associated States. Prior to the meeting, a one-day workshop on 'Advanced Protein Expression and Crystallization Methods' will be held on 8 September and will focus on the newest developments in MultiBac, ESPRIT and HT crystallization technologies.

The Partnership for Structural Biology (PSB) is a collaboration between a number of prestigious European and French scientific laboratories in Grenoble which has received support from the EU FP6 programme. The PSB is unique in combining world leading user facilities for synchrotron X-ray and neutron scattering with NMR, electron microscopy, molecular biology and high throughput techniques on a single site together with strong projects in a broad range of structural biology, notably host-pathogen interactions.

Contacts

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