Variola virus (family: Poxviridae, genus: Orthopoxvirus), was responsible for smallpox, the most lethal and devastating viral infection in history. After an intense campaign of vaccination led by the World Health Organization, smallpox was declared eradicated in 1979. With the arrest of the vaccination program, a high proportion of the world population are no longer immunised. In this context, variola virus, if used as a biological weapon, could represent a serious threat to the civilian population since no specific antiviral treatment is yet available against orthopoxvirus infections.

One line of research carried out as a collaboration between the IRBA (Institut de Recherche Biomédicale des Armées) and the “Integrated biology of persistent viruses” group at the UVHCI focuses on the structural study of essential proteins involved in poxvirus DNA synthesis. Ultimately this work will facilitate the design of new drugs targeting the DNA replication machinery, the heart of the virus, which consists of D5, a helicase-primase, and the DNA polymerase holoenzyme comprising the catalytic subunit E9, the uracil-DNA glycosylase (UNG) D4 and A20, a protein with no known catalytic activity (Figure 1). The work presented here was performed on the proteins from vaccinia virus (the model system for orthopoxviruses) which are more than 90% identical to their variola virus counterparts.

We have set up the expression of D5, D4, A20 and E9 in the insect cell-baculovirus system. After protein purification, small-angle X-ray scattering (SAXS) data collected at the ESRF yielded the envelopes of E9, of the A20-D4 heterodimer and of the E9-A20-D4 complex (Figure 1, [1]). This first structural information revealed the elongated shape of the DNA polymerase holoenzyme with a 150 Å distance between the polymerase active site of E9 and the DNA-binding site of D4. This suggests that at least 50 base-pairs of DNA would fit between the two sites [1]. Electron microscopy carried out in collaboration with the IBS EM-platform also showed the hexameric organization of the helicase-primase D5 (Figure 1). We continue to push forward to high-resolution structures of the replication complex. A first success is the crystal structure of D4 bound to the first 50 residues of A20 (A20_50) which are necessary and sufficient for its interaction with D4 (Figure 2, [2]). The structure shows that complex formation does not interfere with the UNG activity and DNA-binding property of D4 as these functions are located on different sides of the protein. Our structure solved at 1.85 Å reveals the contact surface engaged in the D4/A20 interaction in particular the important role of the A20 Trp43 involved in stacking interactions with Arg167 and Pro173 of D4. We further showed that point mutations of these residues disturb D4-A20_50 complex formation and reduce significantly its thermal stability [2].

An ongoing collaboration with X. Morelli’s group (CNRS UMR 7258, INSERM U 1068, Marseille) aims at the structure-based drug design of compounds binding at the D4/A20 interface and interfering with complex assembly.

**Scientific highlights**

**Zooming into the heart of a killer**

Variola virus (family: Poxviridae, genus: Orthopoxvirus), was responsible for smallpox, the most lethal and devastating viral infection in history. After an intense campaign of vaccination led by the World Health Organization, smallpox was declared eradicated in 1979. With the arrest of the vaccination program, a high proportion of the world population are no longer immunised. In this context, variola virus, if used as a biological weapon, could represent a serious threat to the civilian population since no specific antiviral treatment is yet available against orthopoxvirus infections.

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Probing enzymatic mechanisms through combined crystallography and bioSAXS

Plants use different hormones including salicylate, indole acetic acid and gibberellins to trigger diverse developmental processes, respond to external stresses and fight pathogens. Salicylic acid is a plant hormone that is critically important for defense response and often induced upon exposure to pathogenic bacteria. However, plants need to tightly control the levels of this highly active molecule. One way plants do this is to form less active amino acid conjugates of salicylate. The GH3.12 enzyme, a member of the GH3 hormone-modifying enzyme family, is able to bind salicylate, ATP and an amino acid such as glutamate or aspartate [1]. GH3.12 then performs two reactions: 1) the enzyme forms an activated acyl-adenylate intermediate via ATP hydrolysis and 2) the enzyme catalyzes the addition of an amino acid, forming a stable hormone-amino-acid conjugate. How a single enzyme is able to perform these two distinct reactions was unclear until a collaboration between researchers from the PSB partners – ESRF and EMBL Grenoble - and the University of Washington, USA was able to uncover the underlying mechanisms. Using a combination of protein crystallography and bioSAXS measurements, the different conformations of the protein were determined. High-resolution crystallography provided two "snapshots" of the protein in two distinct conformations due to a rotation of the C-terminal domain [2]. This rotation was postulated to change the topology of the active site, allowing for the different reactions to occur. BioSAXS experiments were performed to monitor the conformation of the protein in solution in the presence of the different substrates and products. By combining these two different types of data, high-resolution static snapshots from protein crystallography and low-resolution solution state data from bioSAXS, a detailed enzymatic mechanism was determined [3]. Based on the combined data, the GH3 enzymes are able to bind hormones and ATP in an open conformation and subsequently adopt a closed conformation that allows the hormone amino acid product. These studies provide the mechanism of the highly reactive acyl-adenylate intermediate. This conformation likely protects the intermediate from catalytically non-productive hydrolysis and favors the second reaction - the formation of the hormone amino acid product. These studies provide the mechanism of the entire GH3 family enzymes to perform hormone modification via amino acid conjugates. These reactions can now be manipulated and tuned in plants to favor different hormone modifications to increase pathogen resistance or alter fruit ripening, for example.

The diverse structural and biochemical techniques available through the PSB provide critical tools to explore many aspects of enzymatic catalysis at different resolutions and in crystalline and solution states. As demonstrated by the study of the GH3 enzymes, the combination of protein crystallography and bioSAXS is a powerful method to investigate conformational changes under different biologically relevant conditions.

A. Chloé Zubieta1,2, Adam Round1 (ESRF, Laboratoire de Physique Cellulaire et Végétale, CNRS - IRTSV/CEA - UJF - INRA, EMLBL)


Small RNA amplification for germline genome defense

Transposons or "jumping genes" constitute a large part of eukaryotic genomes and play an important role in development and genome evolution. However, due to their potential for genome destruction they must be tightly controlled. This regulation is normally achieved by maintaining such elements in a reversibly inactive state through the chemical modification of histones and DNA, termed "epigenetic silencing." Germlines are entrusted with the task of transmitting genetic information from one generation to the next and formation of germ cells (egg or sperm) usually involves a complete rewiring of these epigenetic markers, generally leading to a significant increase in transposon activity. To protect their genomes, animal germ cells have evolved dedicated genome defenders in the form of Pti proteins and a set of small, 24-30 nucleotides, RNA Pti-interacting RNAs (pRNA). In all animals studied so far, pRNA are perfectly complementary to endogenous transposon elements in the germ line. Since some of the Pti proteins are small RNA-guided endonucleases, target recognition by pRNA results in their cleavage by Pti, contributing to transposon silencing. This results in a significant increase in transposon activity. To protect their genomes, animal germ cells have evolved dedicated genome defenders in the form of Pti proteins and a set of small, 24-30 nucleotides, RNA Pti-interacting RNAs (pRNA). In all animals studied so far, pRNA are perfectly complementary to endogenous transposon elements in the germ line. Since some of the Pti proteins are small RNA-guided endonucleases, target recognition by pRNA results in their cleavage by Pti, contributing to transposon silencing. This results in a significant increase in transposon activity. To protect their genomes, animal germ cells have evolved dedicated genome defenders in the form of Pti proteins and a set of small, 24-30 nucleotides, RNA Pti-interacting RNAs (pRNA). In all animals studied so far, pRNA are perfectly complementary to endogenous transposon elements in the germ line. Since some of the Pti proteins are small RNA-guided endonucleases, target recognition by pRNA results in their cleavage by Pti, contributing to transposon silencing. This results in a significant increase in transposon activity. To protect their genomes, animal germ cells have evolved dedicated genome defenders in the form of Pti proteins and a set of small, 24-30 nucleotides, RNA Pti-interacting RNAs (pRNA). In all animals studied so far, pRNA are perfectly complementary to endogenous transposon elements in the germ line. Since some of the Pti proteins are small RNA-guided endonucleases, target recognition by pRNA results in their cleavage by Pti, contributing to transposon silencing. This results in a significant increase in transposon activity.


Production and Analysis of Perdeuterated Lipids from P. pastoris Cells

A collaborative effort involving the ILL, the Free University of Brussels, the CNRS Molecular Biology Institute (Strasbourg), the Laboratory for Cellular and Vegetable Physiology (CNRS/CEA/Univ. Grenoble Alpes/INRA), as well as the European Spallation Source (Lund) has been put together to optimize ways for producing biologically relevant models of cell membranes. Collecting experimental data using the same lipids found in vivo is not always possible since isotopically-labeled lipids are needed for a range of biophysical techniques (in neutron scattering or NMR studies, for example), given that these can be very difficult to prepare via synthetic routes and are not commercially available. The ability of the yeast species Pichia pastoris to grow in fully deuterated media, widely exploited in expression systems for producing detergent-labile proteins, has now been used to produce fully deuterated unsaturated glycerolipids. Perdeuterated phospholipids and sterols grown in deuterated media were extracted and analysed. It was found that when yeast cells are grown in a deuterated environment, the phospholipid headgroup is maintained - but the fatty acid composition and unsaturation level is modified. The ergosterol synthesis is not affected by the deuterated culture medium. However, remarkably, an accumulation of C18:1 fatty acid is strikingly triggered in perdeuterated lipids from this micro-organism. Lowering the growth temperature of Pichia in deuterated medium reduces this effect, but the level of unsaturated fatty acids obtained in undeuterated medium is still higher. The results confirm that the production of well-defined natural unsaturated perdeuterated lipids is possible and give new insights into the production of deuterated enzymes.

V. Laux and M. Haertlein (ILL Life Sciences Group)


Scientific highlights

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Transposons or “jumping genes” constitute a large part of eukaryotic genomes and play an important role in development and genome evolution. However, due to their potential for genome destruction they must be tightly controlled. This regulation is normally achieved by maintaining such elements in a reversibly inactive state through the chemical modification of histones and DNA, termed “epigenetic silencing.” Germlines are entrusted with the task of transmitting genetic information from one generation to the next and formation of germ cells (egg or sperm) usually involves a complete rewiring of these epigenetic markers, generally leading to a significant increase in transposon activity. To protect their genomes, animal germ cells have evolved dedicated genome defenders in the form of Pti proteins and a set of small, 24-30 nucleotides, RNA Pti-interacting RNAs (pRNA). In all animals studied so far, pRNA are perfectly complementary to endogenous transposon elements in the germ line. Since some of the Pti proteins are small RNA-guided endonucleases, target recognition by pRNA results in their cleavage by Pti, contributing to transposon silencing. This results in a significant increase in transposon activity.

The three-dimensional structure of a protein spontaneously adopts in its environment is dictated by a subtle balance of numerous interactions, which are all individually weak. At physiologically relevant temperatures, these interactions are cent mola ry rearranged, such that proteins visit a range of different conformations. The function of proteins is inherently crucial on motions on conformational states that are transient and low-populated, in exchange with a major conformer. Such transient states with life times often in the range of only a few milliseconds to a millisecond or more, correspond to binding competent conformers in allosteric proteins [1] or to the actual functional states in enzymes [2]. Due to their transient nature, detecting and characterizing these alternative structures is a difficult task, and even determine structural models of these “excited” states [3]. Solution-state NMR, however, is faced with an inherent technical limitation: it is restricted to proteins that generally only deal with proteins of rather small size. Many interesting systems in biology, such as membrane proteins embedded in liposomes, viral capsids, secretion systems, amyloid and many other supramolecular ensembles are generally out of reach for solution-state NMR.

A recently emerging variant of NMR spectroscopy, solid-state NMR, or SSNMR, is not bound to these limitations, and is rapidly emerging for atomic-resolution studies of biological objects that are inaccessible to X-ray crystallography and solution-state NMR. For technical reasons it is so far been difficult to detect conformational dynamics, such as the above-mentioned rare excursions to low populated states, by SSNMR. Researchers in the NMR group at IBS have established a novel method that provides insight into short-lived conformational states. The technique can provide information about the life times and population of these conformers, and importantly, it can also provide atomic-resolution insight into structural properties of these states, such as the difference in bond orientation between the readily visible “ground” state and the excited state. In a first application, the method has been applied to the crystalline protein ubiquitin, for which conformational dynamics can also be seen in solution-state, thus allowing to benchmark this method. A minor conformational state, populated to about 9% could be revealed, in which a peptide plane is flipped, resulting in hydrogen bond and side chain rearrangements. Interestingly, the study revealed that the dynamic process in the microcrystals – which is also present in the protein in solution – is significantly impacted by the crystalline environment (Figure A).

The thermodynamic, kinetic and structural insight into a transient conformational state in the microcrystalline protein ubiquitin (A model of the exchange process, in which the ground state – readily observed by X-ray diffraction – is in exchange with a minor state, populated to 9%). The flipped peptide plane is highlighted in yellow. (B) Structural information of the “excited” state obtained from this technique is used to extract as differences between the observable major state and the transient excited state. Left: chemical shift differences, which are sensitive to the local environment around each nitrogen atom (spin). Right: difference of the orientation of the H-N bond between major state and excited state. In the excited state, on average, the orientation of the peptide plane changes around the peptide plane which flips by ~180°. These data allow testing structural hypotheses of the excited state.

The methodology, tested on a well-characterized system in a first step, paves the way to studying challenging biomolecules that inherently rely on motion for their function: for example, it may provide important clues about the function and conformational dynamics of membrane proteins in native-like lipid environments, or megadalton large enzymatic assemblies.

The figure shows typical cells a few seconds after the bleaching event. The plot (B) clearly shows the FRET signal correlation with the photobleaching of the acceptor in the nucleus of the positive cell. In parallel, the cells can be analyzed using the multichannel flow cytometer of the cell-imaging platform (C). The dot-plots presented illustrate the high yield FRET obtained in positive cells (right) but not in control population (left). Unlike imaging that can only illustrate a few cells, and may need to continue for six months, to evaluate user demand and advance the level of reliability of automated diffraction data analysis and collection pipelines. During this phase, scientists from ESRF HAGs, including members of the PSB are strongly encouraged to send their samples to MASSIF-1 to have them automatically evaluated. Feedback on the experiments performed and results will be returned to users via ISPyB. More information on these processes can be found here: www.esrf.eu/MXPressE

The first of the three MASSIF (Massively Automated Sample evaluation and Screening Integrated Facility) beam lines, MASSIF-1 will be available for ESRF users from July 2014. This unique and highly automated end station is designed to perform sample evaluation i.e. sample screening and diffraction data collection using automatic pipelines based on users’ demands. The beam line is equipped with BobDiff, a robot acting both as a sample changer and goniometer in tandem with a high-capacity dewar (240 current SPINE standard vials) and a Pilatus 3M detector. A pilot study for MASSIF-1 will be launched in September, and to continue for six months, to evaluate user demand and advance the level of reliability of automated diffraction data analysis and collection pipelines. During this phase, scientists from ESRF HAGs, including members of the PSB are strongly encouraged to send their samples to MASSIF-1 to have them automatically evaluated. Feedback on the experiments performed and results will be returned to users via ISPyB. More information on these processes can be found here: www.esrf.eu/MXPressE

MASSIF-3, which will become operational from December 2014, will provide a highly intense beam of about 10μm in diameter in size at the sample position and will be equipped with an EIGER detector capable of recording images at a frame rate of 750 Hz. This setup not only allows diffraction experiments from very small samples, but also opens perspectives to perform time-resolved experiments at both cryogenic and room temperatures.

C. Mueller-Dieckmann (ESRF)

Events

GRAL-48H

Within the framework of the Labex GRAL (Grenoble Alliance for Integrated Structural Cell Biology), the first GRAL-48H Workshop took place in Autrans on April 7th and 8th 2014. This meeting gathering 100 participants from the GRAL community (RTSv, IBS, VHCRI and their PSB partners), was a great opportunity to get a global overview of the multidisciplinary research performed in the GRAL partner institutes. The workshop consisted of four oral sessions including key lectures by three outstanding international speakers, Prof. Paul Jarvis (Oxford University, UK), Prof. Guy Cornélis (Namur University, Belgium) and Prof. Dento Hansuy (Sanford-Burnham Medical Research Institute, USA), as well as a poster session. Three of the oral sessions were dedicated to the presentation of the Labex's pilot projects on Host-Pathogen Interactions, the Compartments of the Choleplast and its Substructures, and Methodological Developments. The fourth session was dedicated to other ongoing projects developed within the GRAL community.

A strong emphasis was dedicated to young researchers that were able to present their work through the poster session and a 2-minutes “flash presentation”. The participants were very pleased with the content, the location and the organization of these two days and wished for the meeting to take place again every 18-24 months. The organizers would like to thank all participants and confirm that this will be done!

C. Guillouret (GRAL Executive Manager)
FOCUS MEETING ON LIGAND SCREENING

The PSB “FOCUS MEETING ON LIGAND SCREENING” took place on the EPN campus on the morning of the 25th of April 2014 and gathered red more than 50 participants in the PSB seminar room. The purpose of this meeting was to help identify unique opportunities to establish pipelines for efficient ligand screening within the Grenoble area. The meeting opened with a lecture by Marc O’Reilly (Astex Pharmaceuticals, U.K) on the challenges of fragment based drug discovery, followed by the presentations of several technical platforms located at the PSB and iRTSV (CEA Grenoble), on their latest developments and potential applications in ligand screening. After coffee, the meeting continued with 5-minutes clips from PSB and iRTSV groups on potential high-value targets that could be studied in pilot projects for the development of new ligand-screening pipelines. A closing lecture by Teresa Carlsgaard (EMBL, Heidelberg) informed the audience on the structural mechanisms of drugs studied by NMR.

In the afternoon, an open round table was organized with the internal speakers, group leaders and platform managers (approximately 20 participants). The external speakers contributed greatly to the discussion which proved to be very lively and fruitful, leading to potential future new collaborations and interactions.

F. Bernardat (PSB Coordinator)

Neutrons in Biology and Biotechnology 2014 meeting

The Neutrons in Biology and Biotechnology (NIBB) meeting took place at the IBS (19th-21st April 2014) and gathered more than 20 participants. The purpose of the meeting was to highlight the amazing structural discoveries it contributed to, including X-rays, NMR, EM, ... This is very well illustrated within the PSB.

The talks ranged from molecular details on the fundamental biology of photosynthesis (J. Anderson and N. Nelson) and protein synthesis (Nobel-laureate Prof. Venki Ramakrishnan) to the intricacies of how the innate immune complement system works. The success of the symposium is probably best summarized by Prof. Peter Gough, who remarked that “ID14 probably made my scientific career in the complement field”.

A. McCarthy (EMBL) - on behalf of the organising committee

ESRF Um2014 and fond farewell to ID14

A special symposium on the 3rd of February 2014 to commemorate the closure of the ID14 complex was organized in conjunction with this year's ESRF users' meeting. Over 100 people attended the “Celebrating 15 years of scientific achievement on ID14” symposium at the BSS and heard how the vision of ID14 was realized (K. Wakabayashi) and some of the amazing structural discoveries it contributed to.

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Training the next generation of structural biologists

The month of June saw twenty young scientists from seventeen different countries spend a week at the PSB learning how to solve challenging problems in structural biology. The group was attending the EMBO Practical Course on the Structural Characterization of Macromolecular Complexes, an event organized biennially on the EPN campus since 2002.

Hailing from laboratories from across Europe, the US and Mexico, the twelve PhD students and eight postdoctoral fellows all shared a keen interest in the 3D architecture of macromolecular complexes. During their stay, course participants learned how to identify, produce and purify complexes, analyze macromolecular interactions through biochemical and biophysical techniques, and structurally characterise...
Native mass spectrometry

Native mass spectrometry (MS) represents a powerful tool to study the architecture of protein complexes when high-resolution structural data are not available. On January 23rd 2014, the IBS hosted the first symposium “Native MS and its Applications in Structural Biology”, organized by the MS team of the IBS and sponsored by the company MS Vision. The 60 participants listened to the presentations given by three international speakers and five local ones. In the first session, Dr. Baran (Manchester University) illustrated the use of MS to characterise biosimilars, Dr. Snijder (Utrecht University) described his work, probing the limits of MS to analyse mega-dalton assemblies (molecular viruses), Dr. Uetrecht (European XFEL, Hamburg) discussed the combination of native MS with X-ray free-electron lasers to resolve the structure and dynamics of biomolecules. Then, Dr. Masselon and Hentz (both at CEA, Grenoble) illustrated their efforts to develop the next generation of instruments whose sensitivity will be boosted by nano-electromechanical detection. Dr. Signor and Dr. Forest (both from the IBS) provided an overview of the IBS MS facility activity and hydrogents/deuterium exchange MS, respectively. Finally, Dr. Boeri Erba discussed her research activity at the IBS using native MS and gave also a practical demonstration of the IBS MS spectrometer specially modified to analyse intact protein complexes (see photo). Encouraged by the excellent feedback from attendees, the IBS MS team will continue to communicate the latest developments in the field of native MS and to promote its use within the structural biology community.

E. Boeri Erba (IBS)

IYCr 2014 International Year of Crystallography

Crystallography encompasses a range of areas and techniques where developments are often symptomatic of general biological and conceptual trends. The IYCr sets the scenario for timely discussions on the role of Science in society. Crystallography has a pivotal role within Structural Biology and has become an integral part of the high-throughput screening and target validation tools, where the native beauty of crystals is an undeniable asset.

Early this year an official inauguration ceremony (where the PSB partners were present) took place in Paris to set the pace for a busy year. Worldwide events and crystallographic tools are listed on the IYCr1 and other websites, such as “100 ans de Cristallographie”2, delivering solutions structural data are not available. On January 23rd 2014, the PSB community is here called to contribute! Send us images of unique crystals for consideration either to ESRF or to ILL or to IBS, and introduce at the inaugural ceremony of the IYCr. A test version will soon be released, where a collection of photos of biological crystals will provide examples of research samples.

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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.

PROFILE: Monserrat Soler-López

I received my PhD from the Universitat Politècnica de Catalunya in 2000, based on the structural biology of DNA and DNA-drug complexes. I gained further experience in nucleic acid crystallography at the Hauptman-Woodward Medical Research Institute in Buffalo and at Northwestern University Medical School in Chicago. I was a postdoctoral fellow from 2000 to 2005 at the EMBL, where I worked on the structure determination of proteins involved in transcriptional regulation and nuclear transport. I was subsequently involved in the set up of a semi-automated cloning and protein expression pipeline for structural studies on the bromodomain protein family. In March 2005, I joined a structure-based drug discovery biotechnology company, Crystax Pharmaceuticals, and was appointed Unit Head to manage and expedite the structural analysis of diverse pharmaceutical targets. In January 2008, I joined the Experimental Bioinformatics Lab (EBL) at the Institute of Research in Biomedicine (IRB Barcelona) as a Lab Director, where we evaluated the structural organization of chromatin at the molecular and genome-wide levels. Furthermore, we implemented diverse large-scale methods and ‘omic’ technologies to identify and characterize protein interaction networks associated with complex diseases, in particular Alzheimer’s disease. Since April 2014, I am the Manager of the Molecular Biology Laboratory within the Structural Biology Group at the ESRF. In parallel to the support of in-house research, my aim is to combine large-scale biology approaches with more focused structural biology efforts in order to achieve a detailed, mechanistic understanding of neurodegenerative pathologies.

Newcomers

Florine Dupeux joined Valentin Gordeliy’s team at the IBS in December 2013 as a CNRS research engineer to further develop the membrane protein crystallisation facility. (see “News from the Platforms” on page 5).

For more information you can contact Florine at: florine.dupeux@ibs.fr

Previously at EMBL, Philippe Mas has joined the CNRS-ISBG to run ESPRIT and the Thermal Shift Assay platform at the PSB. For more information about platform applications you can contact him at: mas@embl.fr

Following the closure last year of the French Armed Biomedical Research Institute (IRBA) site in La Tronche, several scientists arrived on the EPN science campus as visitors. Dr Florian Nachon, Dr Marie Trovaslet and Dr Xavier Brazzolotto joined the DYNAMOP group and Dr Anne-Laure Favier the IRPAS group at the IBS.

Dr Céline Contexto-Richefeu, Dr Frédéric Iseini and Corinne Ducournau joined the UVHCI.

ANNOUNCEMENTS

GTBio2014 Conference

The GTBio2014, the meeting of the Biology thematic group of the French Crystallographic Association (AFC) will be held in Grenoble on the EPN Campus (IBS and ESRF auditoriums), from Tuesday October 7th until Friday October 10th, 2014. Registrations are open and abstracts for either oral or poster presentations can be submitted. Languages of the meeting will be both French and English.

Important dates to remember:
June 30th, 2014: deadline for submitting an abstract for a talk
June 30th, 2014: deadline for requesting student fellowships (see web site).
September 7th, 2014: deadline for registration and for submitting an abstract for a poster.

For more information please visit the website: http://gtbio2014.ibs.fr

Contact: gtbio2014@ibs.fr

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