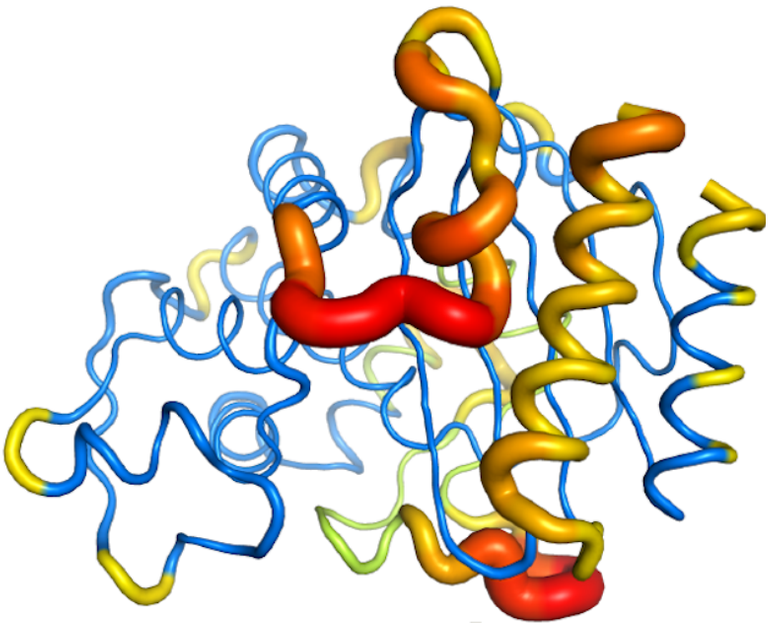
19e Symposium annuel de PROTEO

PROTEO
FONCTION | INGÉNIERIE APPLICATIONS DES PROTÉINES



19e Symposium annuel de PROTEO

Vendredi 10 mai 2019
Friday May 10th 2019

Pavillon Palasis-Prince
Théatre de la Cité Universitaire
Université Laval, Québec

PROGRAMME

Ouverture et bienvenue	
Accueil et inscription	8h00 – 8h30
Mot de bienvenue	8h30 – 8h35

Première séance : Présidente de séance Corinne Hoesli, McGill University	
Matt Shoulders, MIT, Cambridge, MA, USA *Surviving Extreme Mutation Rates to Enable Rapid Adaptation: How Viruses Solve the Protein Folding Problem*	8h35 –9h25
Michelle Arkin, UCSF, San Francisco, CA, USA *Hacking Protein-Protein Interaction Network*	9h25 – 10h15
Pause, Hall	10h15 – 10h35
Samaneh Dastpeyman, Concordia University, QC, Canada *Visualizing the Heme Loading of a Protein in Live Cells Using Green Fluorescent Protein*	10h35 – 10h55
Benjamin Martial, Université Laval, QC, Canada *Vibrational Circular Dichroism Reveals Supramolecular Chirality Inversion of α-Synclein Peptide Assemblies upon Interactions with Anionic Membranes*	10h55 – 11h15
Kevin Plaxco, UC Santa Barbara, CA, USA *Stealing Nature's Tricks to Build Better Biosensors*	11h15 – 12h05

Diner	12h05 – 13h15
Les affiches peuvent être visitées sur l'heure du diner	

Deuxième séance : Président de séance David Kwan, Concordia University	
Vicki Wysocki, Ohio State University, Colombus, OH, USA *Native MS: A Structural Biology Tool*	13h15 – 14h05
Adam Damry, Université d'Ottawa, ON, Canada *Brighter Red Fluorescent Proteins Display Reduced Structural Dynamics*	14h05 – 14h25
Marie-Laurence Lemay, Université Laval, QC, Canada *A Phage Protein Impedes Bacterial Resistance to Phage Infection*	14h25 – 14h45
Pause, Hall	14h45 – 15h10
Petra Fromme, Arizona State University, Tempe, AZ, USA *Towards Molecular Movies of Biomolecules with X-ray Free Electron Lasers*	15h10 – 16h00

Séance de présentation d'affiches	
Séance de présentation d'affiches	16h00 – 18h00
Remise des prix pour les meilleures affiches	18h00

PROGRAM

Opening and Registration	
Registration	8:00 – 8:30
Welcoming Remarks	8:30 – 8:35

Plenary 1 : Chair Corinne Hoesli, McGill University	
Matt Shoulders, MIT, Cambridge, MA, USA *Surviving Extreme Mutation Rates to Enable Rapid Adaptation: How Viruses Solve the Protein Folding Problem*	8:35 –9:25
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Kevin Plaxco, UC Santa Barbara, CA, USA *Stealing Nature's Tricks to Build Better Biosensors*	11:15 – 12:05

Lunch	12:05 – 1:15
Posters can be viewed during lunch time	

Plenary 2 : Chair David Kwan, Concordia University	
Vicki Wysocki, Ohio State University, Colombus, OH, USA *Native MS: A Structural Biology Tool*	1:15 – 2:05
Adam Damry, Université d'Ottawa, ON, Canada *Brighter Red Fluorescent Proteins Display Reduced Structural Dynamics*	2:05 – 2:25
Marie-Laurence Lemay, Université Laval, QC, Canada *A Phage Protein Impedes Bacterial Resistance to Phage Infection*	2:25 – 2:45
Break, Hall	2:45 – 3:10
Petra Fromme, Arizona State University, Tempe, AZ, USA *Towards Molecular Movies of Biomolecules with X-ray Free Electron Lasers*	3:10 – 4:00

Poster Session	
Poster Session, Hall	4:00 – 6:00
Best Poster Awards Presentation	6:00

Conférencières et conférenciers invités

Keynote Speakers

Surviving Extreme Mutation Rates to Enable Rapid Adaptation: How Viruses Solve the Protein Folding Problem

Matt Shoulders

MIT, Cambridge, MA, USA

Protein homeostasis (proteostasis) networks, along with fundamental biophysics, govern protein evolution. Acquisition of adaptive amino acid mutations during evolution is often kinetically or thermodynamically destabilizing to proteins. Chaperones from the proteostasis machinery can rescue these destabilizing mutations for endogenous client proteins. Perhaps even more than native clients, rapidly evolving viral proteins also require folding assistance. The extent of viral protein's ability to tolerate mutations defines the success of their escape from antiviral drugs and immunity. We investigated viral protein mutational tolerance in different host cell proteostasis environments by pairing the high throughput deep mutational scanning method with stress-independent perturbation of the host's proteotasis components. We describe our discovery that influenza hijacks host chaperones to address folding defects of viral proteins acquired during escape from the host's innate immune system. Chaperone depletion compromises the fitness of an adaptive variant and an additional temperature increase mimicking fever condition renders the immune escape variant extremely destabilized. The positive selection pressure from the host's antiviral factor does not outweigh the magnitude of the biophysical defect, thus favoring the immune system-sensitive but biophysically more stable variant. Thus, the dependence of virus on the host's

protein folding network makes the virus highly vulnerable to immune suppression when folding assistance is limited. Therefore, host chaperones play a central role in facilitating influenza adaptation at the host–pathogen interface, a finding with potentially far-reaching implications for viral host-switching and resistance development.

Hacking Protein-Protein Interaction Networks

Michelle Arkin

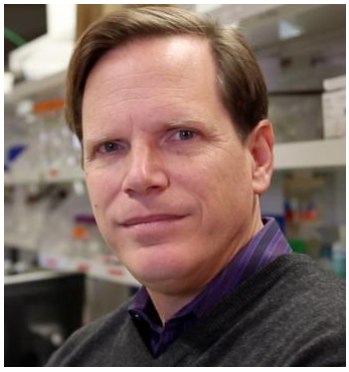
UCSF, San Francisco, CA, USA

Many potential drug targets are known to be relevant for disease, but have been ‘undruggable’ by current approaches. Our lab seeks to understand to what extent this failure has been due to the features of the biological target vs the methodologies used to discover small-molecule modulators. In particular, we have focused on protein-protein interactions and the larger networks controlled by these interactions. This seminar will describe our discoveries of first-in-class compounds with unusual mechanisms for inhibiting ‘challenging’ targets, including allosteric inhibitors of p97 and protein-protein stabilizing compounds.

Stealing Nature's Tricks to Build Better Biosensors

Kevin Plaxco

UC Santa Barbara, CA, USA



Recent years have seen the development of a broad class of optical and electrochemical sensors in which the binding of a specific molecular target is signaled via a large-scale conformational change in a protein- or nucleic-acid-based receptor. The reagentless, rapidly reversible nature of this signaling mechanism supports continuous, real-time measurement of a wide variety of analytes, and, when coupled to electrochemical read-outs, its extraordinary selectivity allows this detection to be performed in even the most complex environments, including within the living body. Like all processes reliant on single-site binding, however, these sensors still suffer from two potentially significant limitations: the useful dynamic range of single-site receptors is centered at a fixed target concentration (defined by the receptor's dissociation constant) and spans a fixed width (defined by the hyperbolic shape of the Langmuir isotherm). In this talk, I describe the various mechanisms that evolution has invented in order to circumvent these very same limitations (e.g., allostery, cooperativity), and demonstrate their value in improving the utility of a wide range of artificial biosensors.

Native MS: A Structural Biology Tool

Vicki Wysocki

The Ohio State University, Columbus, OH, USA

Characterization of the overall topology and inter-subunit contacts of protein complexes, and their assembly/disassembly and unfolding pathways, is critical because protein complexes regulate key biological processes, including processes important in understanding and controlling disease. Tools to address structural biology problems continue to improve. Native mass spectrometry and associated technologies are becoming an increasingly important component of the structural biology toolbox. When the mass spectrometry approach is used early or mid-course in a structural characterization project, it can provide answers quickly using small sample amounts and samples that are not fully purified. Integration of sample preparation/purification with effective dissociation methods, ion mobility, and computational approaches provide a MS workflow that can be enabling in biochemical, synthetic biology, and systems biology approaches. Beyond what MS can provide as a stand-alone tool, MS can also guide and/or be integrated with other structural biology approaches such as NMR, X-ray crystallography, and cryoEM. MS can determine whether the complex of interest exists in a single or in multiple oligomeric states and can provide characterization of topology/intersubunit connectivity, and other structural features. Examples will be presented to illustrate the role MS and surface-induced dissociation can play in guiding a structural biology workflow and will include designed protein complexes and isolated or recombinant protein and nucleoprotein complexes.

Towards Molecular Movies of Biomolecules with X-ray Free Electron Lasers

Petra Fromme **(see references for co-authors)**

Arizona State University, Tempe, AZ, USA

Serial Femtosecond Crystallography (SFX) provides a novel concept for structure determination, where X-ray diffraction “snapshots” are collected from a fully hydrated stream of nanocrystals, using femtosecond pulses from high energy X-ray free-electron lasers (XFELs) [1-4]. The XFEL pulses are so strong that they destroy any solid material, but a femtosecond is so short (1 fs =10^{-15} s) that X-ray damage is diminished and diffraction from the crystals is observed before destruction takes effect [3]. Study of the dynamics biomolecules is one of the grand challenges of Structural Biology as most structures determined so far only provide a static picture of the molecule. Time-resolved femtosecond crystallography opens new avenues to determine molecular movies of molecules “in action” [6-10]. In this talk we will present results from recent experiments to study the dynamic processes in Biology. The talk will close with a progress report on the development of compact femto and attosecond X-ray Sources at Arizona State University (CXLS and CXFEL) and DESY (AXSIS) [11], which will provide unique new opportunities to study the ultrafast dynamics of reactions with a combination of X-ray diffraction, X-ray spectroscopy and ultrafast optical spectroscopy.

References:
[1] Chapman,HN et al 2011, Nature, 470, 73-77 ;
[2] Fromme P and Spence JC 2011 Curr Opin Struct Biol 2011, 21: 509-516;

[3] Barty,A et al. 2012 Nature Photonics 6, 35–40;
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[5] Liu W et al 2013, Science 342: 1521-1524;
[6] Aquila,A et al 2012, Optics Express, 20 (3), 2706-16;
[7] Kupitz C et al 2014, Nature 513, 261-5;
[8] Young ID et al. 2016, Nature 543, 131-135 ;
[9], Suga M et al.2017, Nature 543, 131-135 ;
[10] Ayyer, K. et al. Nature 2016, 530, 202-206
[11] Kartner, F.X. et al. 2016, Nuclear Instruments & Methods in Physics Research Section A -Accelerators Spectrometers Detectors and Associated Equipment, 829, 24-29.

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Conférencières et conférenciers étudiants et stagiaires postdoctoraux

Students and Postdocs Lectures

Visualizing the heme loading of a protein in live cells using green fluorescent protein

Samaneh Dastpeyman[1], Gonzalo Cosa[2], Ann English[1]

[1]Concordia University, [2]McGill University

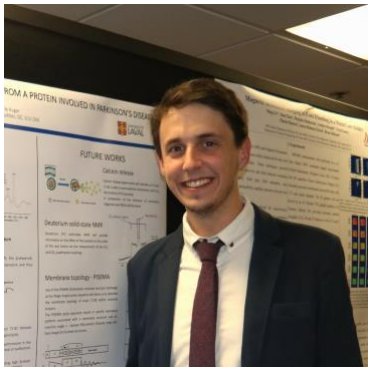
Heme proteins are involved in numerous biological processes, including aerobic respiration, cell signaling, antioxidant stress and xenobiotic metabolism. Despite its role as an essential prosthetic group, we do not known how heme is distributed from the mitochondrial matrix, where it is synthesized, to the proteins that need it. We do know, however, that apocatalase A (Cta1) maturation involves recruitment of heme from cytochrome c peroxidase (Ccp1) in yeast mitochondria. Thus, tracking Ccp1's heme loading in live cells is of interest but this has not been achieved for a heme protein to date. Heme is a highly efficient quencher of green fluorescent protein (GFP) so we chose to use yeast chromosomally expressing the Ccp1-GFP fusion under the native Ccp1 promotor to monitor the heme status of Ccp1 in live cells. We first characterized the time-resolved fluorescence of recombinant apo- and holoCcp1-GFP in vitro. ApoCcp1-GFP exhibits a fluorescence lifetime of 2.86 ns whereas holoCcp1-GFP decays with two lifetimes, 0.96 ns and 2.45 ns. The fractional amplitude of the 0.96-ns lifetime increases linearly with heme loading of apoCcp1-GFP. With this knowledge, we followed by fluorescence lifetime imaging microscopy (FLIM) the heme loading of Ccp1 in the live yeast cells expressing Ccp1-GFP. From the lifetime amplitudes of GFP fluorescence, we find that Ccp1-GFP is ~ 90% heme loaded and resides in the mitochondria of 2-day cells. In contrast, in 7-day cells, half of Ccp1-GFP is extra-

mitochondrial and 100% heme-free. Overall, our unprecedented study reveals the power of FLIM in monitoring both the heme loading and location of a GFP-fusion protein in live cells. We also have enlarged the toolkit for monitoring intracellular heme trafficking as well as expanding the functional repertoire of genetically encoded fluorescent probes.

Vibrational Circular Dichroism Reveals Supramolecular Chirality Inversion of α-Synuclein Peptide Assemblies upon Interactions with Anionic Membranes

Benjamin Martial[1], Thierry Lefèvre[1], Thierry Buffeteau[2], Michèle Auger[1]

[1]Université Laval, [2]Université Bordeaux 1



Parkinson's disease is an incurable neurodegenerative disorder caused by the aggregation of α-synuclein (AS). This amyloid protein contains a 12-residue-long segment, AS_{71-82}, that triggers AS pathological aggregation [1]. This peptide is then essential to better understand the polymorphism and the dynamics of formation of AS fibrillar structures. In this work, vibrational circular dichroism showed that AS_{71-82} is random coil in solution and forms parallel β-sheet fibrillar aggregates in the presence of anionic vesicles. Vibrational circular dichroism, with transmission electronic microscopy, revealed that the fibrillar structures exhibit a nanoscale tape-like morphology with a preferential supramolecular helicity. Whereas the structure handedness of some other amyloid peptides has been shown to be driven by pH, that of AS_{71-82} is controlled by peptide concentration and peptide-to-lipid (P:L) molar ratio. At low concentrations and low P:L molar ratios, AS_{71-82} assemblies have a left-twisted handedness, while at high concentrations and high P:L ratios, a right-twisted handedness is adopted. Left-twisted assemblies interconvert into right-twisted ones with time, suggesting a maturation of the amyloid structures [2]. Since fibril species with two chiralities have also been reported previously in Parkinson's disease Lewy bodies and fibrils, the present results seem relevant to better understand AS amyloid assembly and fibrillization in vivo. From a diagnosis or

therapeutic point of view, it becomes essential that future fibril probes, inhibitors or breakers target pathological assemblies with specific chirality and morphology, in particular because they may change with the stage of the disease.

References

[1] B. Giasson et al., J. Biol. Chem. 276, 2380-2386 (2001)
[2] B. Martial et al., ACS Nano, 13, 3232-3242 (2019)

Brighter red fluorescent proteins display reduced structural dynamics

Adam M. Damry, Serena E. Hunt, Natalie K. Goto, Roberto A. Chica

Université d'Ottawa

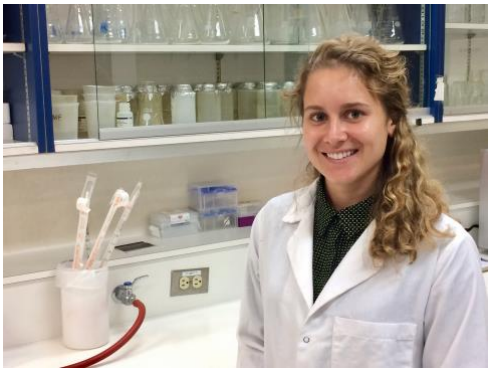
Red fluorescent proteins (RFPs) are genetically-encoded fluorophores that are extensively used in biological research. For all imaging applications, brighter variants are desired. Brightness is directly proportional to quantum yield (QY), and QY improvements can theoretically be achieved by decreasing dynamics of the chromophore responsible for fluorescence by optimizing packing interactions. Although it has been demonstrated that optimization of local packing interactions around the chromophore can provide brighter FPs, mutations proximal to the chromophore often cause unwanted hypsochromic shifts in emission wavelength. Distal sites provide the possibility of rigidifying the chromophore through trickle-down dynamics without directly affecting its electrostatic environment, but the magnitude and extent of their contributions to dynamics has never been systematically evaluated. Here, we study this relationship using nuclear magnetic resonance (NMR) spectroscopy of a family of related monomeric RFPs with a range of QY between 0.02 and 0.70. A residue-by-residue comparison using $^{1}H–^{15}N$ HSQC spectra showed line-width broadening correlating with QY in roughly 12% of backbone amide peaks. As peak line-widths are influenced by microsecond–second timescale motions, T1 and T2 relaxation measurements were performed to probe picosecond–nanosecond timescale dynamics. These measurements showed that apparent correlation time increases with QY in roughly 6% of backbone

amide peaks. While many positions selected by these experiments are dispersed throughout the RFP scaffold, the β strand 7-–10 region shows a cluster of residues whose dynamics correlate with QY. This indicates a potential link between dynamics in this region and chromophore flexibility and brightness. To further probe this relationship, we saturated six sites along this face in mPlum-E16P (QY = 0.14), resulting in the production of mutants displaying QY enhanced by up to 35% without significant alteration of their emission wavelength. Our results show that RFP QY can be increased through mutagenesis of sites distal to the chromophore identified by NMR, opening the door to the rational design of more rigid, brighter RFPs.

A Phage Protein Impedes Bacterial Resistance to Phage Infection

Marie-Laurence Lemay[1], Sandra Maaß[2], Andreas Otto[2], Jérémie Hamel[1], Geneviève M. Rousseau[1], Denise M. Tremblay[1], Rong Shi[1], Stéphane M. Gagné[1], Dörte Becher[2], Sylvain Moineau[1]

[1]Université Laval, [2]University of Greifswald



The unequalled abundance and diversity of bacterial viruses (phages) partly explain why so many of the deduced proteins encoded by phage genomes have no known function and no homologue in public databases. While structural proteins are found in the virion particles, non-structural phage proteins are produced inside the bacterial host where it is presumed that they play a role in hijacking the cellular machinery for viral production. Virulent lactococcal phages belonging to the Skunavirus genus (Siphoviridae family) are by far the most endemic and problematic in the dairy industry worldwide. Phage p2 is a model for this viral genus and it infects Lactococcus lactis MG1363, the international reference strain for lactococcal research. Phage p2 structural proteins have been analyzed in great details, but most of its non-structural proteins are still uncharacterized. To study these proteins, a multidisciplinary approach is required.

Here, we made use of structural biology, genomics, physiology, and proteomics to provide insights into the function of phage p2 protein ORF47, the most conserved non-structural protein of unknown function among members of the Skunavirus genus. We solved the protein structure through circular dichroism and nuclear magnetic resonance. Using CRISPR-Cas9, we knocked out orf47 from phage p2

genome and confirmed gene disruption in a recombinant phage (p2Δ47) by whole genome sequencing. The lack of ORF47 did not affect the duration of the phage lytic cycle, but the number of infective particles released per infected bacterium was significantly lower with p2Δ47 yielding a burst size of 80 ± 7 in comparison to 129 ± 17 for p2. Moreover, we made use of label-free quantitative proteomics to compare the proteotypes of L. lactis MG1363 infected by phage p2Δ47 or phage p2. Infection by p2 resulted in an increase of most metabolic pathways while a global decrease was observed during the infection by p2Δ47. Our data showed that ORF47 is inducing the expression of many genes that are not functionally related and that without this protein, the phage induces a dormancy-like state in the bacterial host. Most interestingly, we found that ORF47 hinders L. lactis MG1363 resistance to phage infection.

Présentations d’affiches

Poster presentations

1 - Des peptoïdes perméants comme transporteurs de molécules imperméables à travers la membrane cellulaire

Andréanne Laniel[1], Claire McCartney[2], Étienne Marouseau[1], Christine Lavoie[1], Éric Marsault[1]

[1]Université de Sherbrooke, [2]Université Bishop's

2 - 15N-Heteronuclear Single Quantum Coherence (HSQC) titration of Galectin 7: comparison between two ligands

Carolina Perusquía Hernández[1], Myriam Létourneau[1], David Bernard[1], Nicolas Doucet[1,2]

[1]INRS - University of Quebec, [2]PROTEO

3 - Peptide assemblies as self-adjuvanted platform for nanovaccine design

Ximena Zottig[1,2], Al Halifa Soultan[1,2], Mélanie Côté-Cyr[1,2], Margaryta Babych[1,2], Laurie Gauthier[1,2], Jessica Dion[1,2], Denis Archambault[1], Steve Bourgault[1,2]

[1]Université du Québec à Montréal, [2]PROTEO

4 - A Controlled Method to Immobilize Antibodies for the Surface Modification of Vascular Stent

Omar S. Bashth[1], Mohamed A. Elkhodiry[1], Gaétan Laroche[2], Corinne A. Hoesli[1]
[1]1. Department of Chemical Engineering, McGill University, Montréal, Québec, Canada., [2]2. Centre de Recherche du CHU de Québec, Département de Génie des Mines, des Matériaux et de la Métallurgie, Université Laval, QC

5 - Analyse des interactions médiées par les domaines SRC homology 3 (SH3) de SLA1 en les substituant par CRISPR-Cas9

Émilie Bourgault[1,2], Ugo Dionne[2,3,4], Alexandre Dubé[1,2,5], Philippe Despré[1,2], Nicolas Bisson[2,3,4,6], Christian Landry[1,2,5]

[1]Département de Biochimie, Microbiologie et Bio-Informatique, Université Laval, Québec, QC, Canada., [2]PROTEO-regroupement québécois de recherche sur la fonction, l'ingénierie et les applications des protéines., [3]Centre de recherche du Centre Hospitalier Universitaire (CHU) de Québec-Université Laval, Québec, QC, Canada., [4]Centre de recherche sur le cancer de l'Université Laval, Québec, QC, Canada., [5]Département de Biologie, Université Laval, Québec, QC, Canada., [6]Département de biologie moléculaire, de biochimie médicale et pathologie, Université Laval, Québec, Canada.

6 - Analysis of the Impact of Conformational Entropy on the Accuracy of the Molecular Docking Software FlexAID in Binding Mode Prediction

Louis-Philippe Morency[1,2], Rafael Najmanovich[1,2]

[1]Université de Montréal, [2]PROTÉO

7 - Brighter Red Fluorescent Proteins through Improved Chromophore Packing

Sandrine Legault[1], Matthew G. Eason[1], Erin Nguyen[1], Roberto A. Chica[1]

[1]University of Ottawa, Department of Chemistry and Biomolecular Sciences

8 - Caractérisation de la liaison membranaire de l'arrestine

Marc-Antoine Millette[1,2,3], Sergey Vishnivetskiy[4], Vsevolod V. Gurevich[4], Christian Salesse[1,2,3]

[1]Département d'ophtalmologie et d'ORL-CCF, Faculté de médecine, Université Laval, [2]CUO–Recherche, Centre de recherche du CHU de Québec, Hôpital du Saint-Sacrement, CHU de Québec-Université Laval, [3]Regroupement stratégique PROTEO, Université Laval, [4]Department of Pharmacology, Vanderbilt University, Etats-Unis

9 - Caractérisation des mécanismes moléculaires de la liaison des doigts de zinc 10 à 12 de Miz-1 à l'ADN par RMN en solution

Olivier Boisvert[1], Jean-Michel Moreau[1], Patrick Delattre[1], Danny Letourneau[1], Martin Montagne[1], Pierre Lavigne[1]

[1]Université de Sherbrooke

10 - Cell-based fluorescent assay for screening ligand-gated ion channel function

Mykhaylo Slobodyanyuk[1], Roberto Chica[1], Corrie daCosta[1]

[1]University of Ottawa

11 - CHARACTERIZATION OF THE TDP-L-VANCOSAMINE BIOSYNTHETIC PATHWAY FROM TDP-4-KETO-6-DEOXY-D-GLUCOSE

Lan Huong Thi Nguyen[1], David Kwan[2]

[1]Concordia University, [2]Concordia University

12 - Clonage, surexpression et purification de la RDH8 en fusion avec plusieurs étiquettes dans le but de mesurer son activité enzymatique

Charlotte Lemay-Lefebvre[1,2,3], Line Cantin[1,2,3], Camille Bérubé[1,2,3], Christian Salesse[1,2,3]

[1]Département d'ophtalmologie, Faculté de médecine, Université Laval, [2]CUO-recherche, Centre de recherche du CHU de Québec, Hôpital du St-Sacrement, [3]Regroupement stratégique PROTEO, Université Laval

13 - Computational modeling of the death complex between glyceraldehyde-3-phosphate dehydrogenase and seven-in-absentia homolog 1 (GAPDH-Siah1)

Ritu Arora[1], Vinod Parmar[1], Ann M. English[1], Gilles H. Peslherbe[1]

[1]Concordia University

14 - Computationally Designed Grafting of a Ru Mediator to Improve Redox Potential of a Laccase

Viviane Robert[1], Emanuele Monza[2], Lionel Tarrago[1], Ferran Sancho[2], Anna De Falco[1], Ludovic Schneider[1], Eloïne Npetgat Ngoutane[1], Yasmina Mekmouche[1], Pierre Rousselot Pailley[1], Jalila Simaan[1], Victor Guallar[2,3], Thierry Tron[1]

[1]Aix Marseille Université, [2]Barcelona Supercomputing Center, [3]ICREA

15 - Conformational landscape of homologous enzymes with distinct biological functions

Chitra Narayanan[1], Pratul K. Agarwal[2], Nicolas Doucet[1,3]

[1]INRS – Centre Armand-Frappier Santé Biotechnologie, Université du Québec, Laval, QC, [2]Department of Biochemistry, Cellular and Molecular Biology, University of Tennessee, Knoxville, TN, [3]PROTEO

16 - Conformational space derived from normal mode analysis: a dynamical metric for scoring 3D predictions of RNA, proteins and their complexes

Olivier Mailhot[1], Vincent Frappier[1], François Major[1], Rafael Najmanovich[1]

[1]Université de Montréal

17 - DESIGNER BIOSENSORS FOR ENGINEERED METABOLIC PATHWAY OPTIMIZATION

Mohamed Nasr[1], David Kwan[1], Vincent Martin[1]

[1]Concordia University

18 - Development of a high-throughput assay to detect fatty acid decarboxylase activity

David Kwan[1], Jama Hagi-Yusuf[1]

[1]Concordia University, [2]Centre for Applied Synthetic Biology

19 - DEVELOPMENT OF CD125-TARGETED ENGINEERED ANTIBODY FRAGMENTS FOR USE IN MUSCELE-INVASIVE BLADDER CANCER THERAPY

Olga Bednova[1], Tim Hercus[2], Angel Lopez[2], Jeffrey V. Leyton[1]

[1]Department of Nuclear Medicine and Radiobiology Faculty of Medicine and Health Sciences Université de Sherbrooke – CHUS, Sherbrooke, QC, Canada, [2]Centre for Cancer Biology, University of South Australia, North Terrace, Adelaide, SA, Australia

20 - Development of sulfahydantoin compound as potential antibiotics and β-lactamase inhibitors

Pierre-Alexandre Paquet-Côté[1,2], Rosalie Lamoureux[1,2], Camille Lapointe Verreault[1,2], Laurie Bédard[1,2], Normand Voyer[1,2]

[1]Université Laval, [2]PROTEO

21 - Devrait-on utiliser la souris comme modèle animal pour caractériser la lécithine rétinol acyltransférase humaine?

Marie-Ève Gauthier[1,2,3,4], Sarah Roy[1,2,3,4], Line Cantin[1,3,4], Christian Salesse[1,3,4]

[1]Département d'ophtalmologie et d'ORL-CCF, Faculté de médecine, Université Laval, [2]Département de biochimie, microbiologie et bio-informatique, Faculté des sciences et de génie, Université Laval, [3]CUO–Recherche, Centre de recherche du CHU de Québec, Hôpital du Saint-Sacrement, CHU de Québec-Université Laval, [4]Regroupement stratégique PROTEO, Université Laval

22 - Direct phosphorylation of SH3 domains by tyrosine kinase receptors disassembles ligand-induced signaling networks

Ugo Dionne[1,2,3], François J. M. Chartier[1,2,3], Kévin Jacquet[1,2,3], Christian R. Landry[3,5,6], Nicolas Bisson[1,2,3,4]

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23 - Effect of spinning rate on the molecular structure and amino acid dynamics in native and supercontracted spider dragline silk: a solid-state NMR and Raman spectroscopic study

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24 - Efficient Site-Specific Antibody-Drug Conjugation by Engineering of a Nature-Derived Recognition Tag for Microbial Transglutaminase

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25 - Efficient Site-Specific Antibody-Drug Conjugation by Engineering of Different Recognition Motifs for Microbial Transglutaminase

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26 - Evolution des complexes protéiques après hybridation entre espèces

Caroline Berger[1], Rohan Dandage[1], Isabelle Gagnon-Arsenault[1], Kyung-Mee Moon[2], Richard Greg Stacey[2], Léonard J. Foster[2], Christian R. Landry[1]

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27 - Evolutionary divergence of conformational exchange phenomena in a host defense enzyme family

David N. Bernard[1], Chitra Narayanan[1], Tim Hempel[2], Myriam Letourneau[1], Purva Prashant Bhojane[3], Khushboo Bafna[3,4], Marie-Christine Groleau[1], Eric Déziel[1], Elizabeth E. Howell[3], Pratul Agarwal[4], Nicolas Doucet[1,5]

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28 - Ex situ and in cell 13C solid-state NMR characterization of starch and glycoprotein-rich cell-wall in microalgae

Alexandre POULHAZAN[1], Alexandre Arnold[1], Dror WARSCHAWSKI[1], Isabelle Marcotte[1]

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29 - Exposing Small-molecule Nano-entities By An NMR Relaxation Assay

Yann Ayotte[1], Victoria Marando[2], Louis Vaillancourt[2], Patricia Bouchard[2], Gregory Heffron[3], Paul W. Coote[2,3], Sacha T. Larda[2], Steven R. LaPlante[1]

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30 - Exposing Small-molecule Nano-entities By An NMR Relaxation Assay

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31 - Expression and purification of CsgA, a functional amyloid composing bacterial biofilm

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32 - Function and engineering of enzymes involved in the glycosylation of natural products

Fathima Mohideen[1], Joel Richard[1], Nathalia Kravchenko[1], David Kwan[1]

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33 - Gesicles: a promising nucleic acid delivery tool

Mathias Mangion[1,2,3], Alexandre Audy[1,2,3], Igor Slivac[1,2,3], Jacques Tremblay[3,4], Rénald Gilbert[5], Bruno Gaillet[1,2,3]

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34 - GFP-based Biosensor to Detect Transiently Expressed Proteins

Matthew G. Eason[1], Antonia T. Pandelieva[1], Safwat T. Khan[1], Guido F. Calderini[1], Hernan G. Garcia[2], Roberto A. Chica[1]

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35 - HOMODIMER INTERFACE MUTATIONS OF HUMAN GALECTIN-7 ALTER ITS BIOLOGICAL ACTIVITY

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36 - Identification de biomarqueurs en relation avec PACE4 pour le cancer de la prostate

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37 - Identification of promising angiogenin allosteric modulators by screening of a chemical compound library

Marie-Aude Pinoteau[1], Myriam Létourneau[1], Steven R.LaPlante[1,2], Nicolas Doucet[1,2]

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38 - Implication des chaines de glycosaminoglycanes membranaires dans la toxicité et l'auto-assemblage d'un peptide amyloïdogénique

Mathilde Fortier[1,2], Noé Quittot[1,2], Mathew Sebastiao[1,2], Phuong Trang[1,2], Steve Bourgault[1,2]

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39 - Increasing the genome-targeting scope of base editing using Streptococcus thermophilus CRISPR1-Cas9

Minja Velimirovic[1], Daniel Agudelo[1], Yannick Doyon[1]

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40 - Influence of nucleotide modifications at the C2′ position on the Hoogsteen base-paired parallel-stranded duplex of poly(A) RNA

William Copp[1], Alexey Denisov[1], Jingwei Xie[2], Anne M. Noronha[1], Kalle Gehring[2], Christopher Wilds[1]

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41 - Inhibition and Activation of Kinases by ADP, Revealed by Isothermal Titration Calorimetry (ITC)

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42 - Investigation of the functional specificity of adaptor proteins NCK1 & NCK2

Kevin Jacquet[1,2], François Chartier[1], Sara Banerjee[1,2], Nicolas Bisson[1,3]

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43 - Is hybridization an adaptive force in response to DNA damage?

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44 - Kinetically Programmed, One-Pot DNA Reactions for Molecular Detection Directly in Whole Blood

Guichi Zhu[1], Carl Prévost-Tremblay[2], Dominic Lauzon[3], Alexis Vallée-Bélisle[2]
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45 - La liaison membranaire de la protéine S100A10 et du peptide d'AHNAK intervenant dans la réparation membranaire

Xiaolin YAN[1,2], Marie-France Lebel-Beaucage[3], Samuel Tremblay[1,2], Gary Shaw[4], Dror Warschawski[5], Élodie Boisselier[1,2]

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46 - Laccase identification from the native ligninolytic basidiomycete Dictyopanus pusillus

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47 - Le complexe du pore nucléaire de la levure comme système modèle pour l'étude des déterminants de la trajectoire évolutive suivie par les gènes dupliqués

Simon Aubé[1,3,4], Axelle Marchant[2,3,4], Alexandre Dubé[1,2,3,4], François Rouleau[1,3,4], Isabelle Gagnon-Arsenault[1,2,3,4], Diana Ascencio[2,3,4], Philippe Després[1,3,4], Christian Landry[1,2,3,4]

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48 - Les récepteurs Eph régulent la morphogénèse épithéliale

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49 - Lobaric acid and pseudodepsidones from the lichen Stereocaulon paschale inhibits NF-κB signaling pathway

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50 - Mapping Eph receptor signaling networks via proximity-dependent biotinylation

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51 - Modulation de la multicellularité bactérienne via différents polysaccharides sécrétés

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52 - Molecular fingerprints determining the toxicity-functionality equilibrium of protein amyloid assemblies

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53 - Molecular insights into the bacterial acetylcholinesterase ChoE from Pseudomonas aeruginosa

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54 - Molecular Insights of Val430Ile Mutation Impact on Influenza Neuraminidase Resistance to Zanamivir

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55 - Monitoring Protein Function using Fluorescent Nanoantennas

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56 - New developments of flow biocatalysis systems: Synthesis of indigo and raspberry ketone using cytochrome P450 enzymes

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57 - Optimization of a production and purification process for VSVg pseudotyped gesicles

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58 - Optimization of matriptase-2 inhibitors

Méryl-Farelle Oye mintsa mi-mba[1,2], Pierre-Luc Boudreault[1,2], Antoine Désilets[1,2], Richard Leduc[1,2], Éric Marsault[1,2]

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59 - Origin of Dynamics in a Small Globular Protein

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60 - Peptide-based Drug Discovery: Artificial Selection of Genetically Encoded TB Drugs

Trisha Ghosh[1], Lan Huong Thi Nguyen[1], David Kwan[1], Christopher Hipolito[2]

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61 - Peptoidic Cell-Penetrating Peptides as vectors for efficient intracellular delivery

Etienne Marouseau[1], Andréanne Laniel[1], Marion L'Exact[1], Claire McCartney[1], Christine Lavoie[1], Éric Marsault[1]

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62 - Perturbation de la structure tridimensionnelle du mutant S175R de la lécithine rétinol acyltransférase tronquée par le SDS : une étude par résonance magnétique nucléaire

Marie-Eve Gauthier[1,2,3,4,5], Line Cantin[1,2,3], Stéphane Gagné[3,4,5], Christian Salesse[1,2,3]

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63 - Phase separation and conformational conversion processes drive the self-assembly of non-pathological amyloid in the presence of linear polyanions

Mathew Sebastiao[1], Noé Quittot[1], Isabelle Marcotte[1,2], Steve Bourgault[1,2]

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64 - Phenolic acid decarboxylase structures lead to new insights in its decarboxylation mechanism

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65 - Positive epistasis towards cefotaxime resistance is maintained in highly dynamic, engineered ß-lactamases

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66 - Programming complex regulation mechanisms through simple molecular assembly

Dominic Lauzon[1], Alexis Vallée-Bélisle[1]

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67 - Protein engineering and immobilization of LipA from Pseudomonas aeruginosa to broaden its industrial applications

Ingrid Yamile Pulido[1], Lorea Alejaldre[2], Charlotte-Skye Fullerton[2], Rosa E. Prieto[1], Carlos A. Jiménez[1], Joelle N. Pelletier[2]

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68 - Region-focused protein engineering in Cal-A lipase reveals triglyceride-binding hotspot

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69 - Rôle des protéines S100A16 et Annexine A4 dans le maintien de l'intégrité membranaire

Francis Noël[1,2,3], Xiaolin YAN[1,2,3], Stefan Vetter[4], Elodie Boisselier[1,2,3]

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70 - Sequential coselections for CRISPR-driven genome editing in human cells

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71 - Structural changes along the evolutionary trajectory of a de novo designed enzyme

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72 - Structure-self-assembly relationships study of the islet amyloid polypeptide

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73 - Surexpression, purification, caractérisation et liaison membranaire de la sous-unité gamma de la transducine, une protéine de la phototransduction visuelle

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74 - Synthèse de glycopeptides comme outils immunogéniques dans la recherche antifongique et antitumorale

Thomas Tremblay[1], Vincent Denavit[1], Denis Giguere[1]

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75 - Synthèse de nouveaux glucoses trifluorés et analyse de leur lipophilie

Megan Bouchard[1], Jacob St-Gelais[1], Vincent Denavit[1], Denis Giguere[1]

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76 - Synthesis and Modify of Sialyl Lewis X Enable It Attach to Cell Surface ex vivo

Haoyu Wu[1], David Kwan[1]

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77 - Synthesis and NMR-Screening of a Fluorinated Library to be Used in FBDD via 19-F NMR

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78 - Systematic perturbation of the yeast essential proteome using base editing

Philippe C Després[1,2,3,4], Alexandre K Dubé[1,2,3,4,5], Maria Isabel Acosta[1,2,3,4,5], Motoaki Seki[6,7,8,9], Nozomu Yachie[6,7,8,9], Christian R Landry[1,2,3,4,5]

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79 - Systematic perturbation of yeast essential genes using base editing

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80 - Teaching an old dog a new trick: Oxime resin as versatile solid-support towards various cyclic peptide scaffolds

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81 - The Recruitment of Endothelial Progenitor Cells on Bio-memetic Functionalized Surfaces

Mohamed Elkhodiry[1], Omar Bashth[1], Gaétan Laroche[2], Jean-François Tanguay[3], Corinne Hoesli[4]

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82 - The role of structural pleiotropy and regulatory evolution in the retention of heteromers of paralogs

Axelle Marchant[1], Angel Fernando Cisneros Caballero[1], Alexandre Dubé[1], Isabelle Gagnon-Arsenault[1], Diana Ascencio[1], Honey A. Jain[2], Simon Aubé[1], Chris Eberlein[1], Daniel Evans-Yamamoto[3], Nozomu Yachie[3], Christian Landry[1]

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83 - The role of the RhoGEF ARHGEF17 (TEM4) in Mps1 function during mitosis

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84 - Towards the structural characterization of the abortive infection (Abi) system protein AbiV

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85 - Usefulness of Recoverin to express and purify visual proteins

Line Cantin[1], Christian Salesse[1]

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86 - Utilisation d'un support solide pour le développement d'une méthodologie de synthèse de glycopeptides

Gabrielle Robert-Scott[1], Thomas Tremblay[1], Antoine Carpentier[1], Christopher Bérubé[1], Normand Voyer[1], Denis Giguere[1]

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87 - Importance of the β5−β6 Loop for the Structure, Catalytic Efficiency, and Stability of the Carbapenem-Hydrolyzing Class D beta-lactamase Subfamily OXA-143

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88 - Developing a family specific molecular docking energy scoring function to accelerate drug discovery

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89 - Investigation phytochimique de lichens nordiques Cladonia Stellaris et Mitis

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90 - Development of a versatile vaccination platform based on papaya mosaic virus (PapMV) nanoparticles

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91 - Structure et mode d'action des transporteurs membranaires du nickel chez Helicobacter pylori

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92 - Le complexe TAM et son rôle dans la biogenèse des protéines membranaires chez les bactéries Gram-négatif

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93 - Caractérisation fonctionnelle et structurale des transporteurs de nickel chez Helicobacter pylori

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94 - Immune Response of Small Drug-like Molecules: Influence of Self-aggregation

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95 - Identification des protéines TAM dépendantes chez Pseudomonas aeruginosa

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