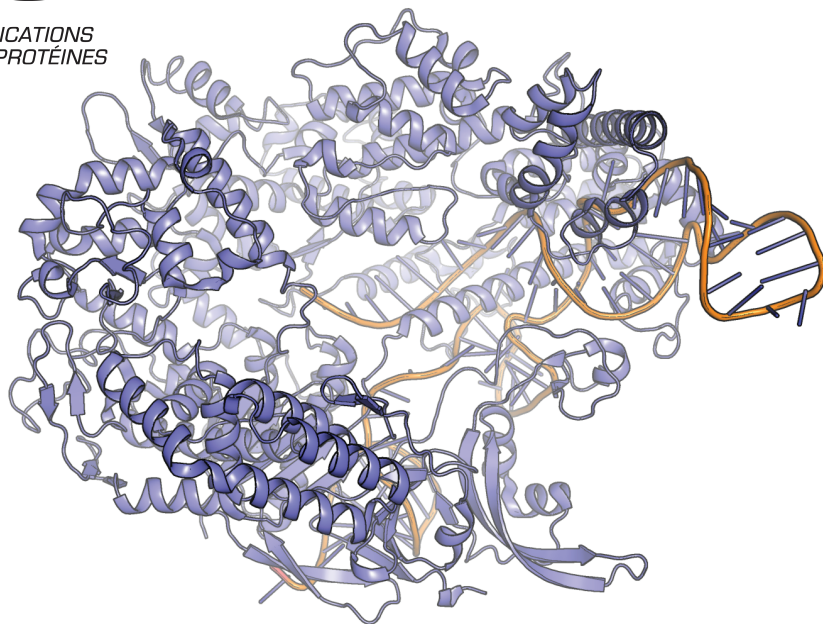




18e Symposium annuel de PROTEO

**Vendredi 18 mai 2018
Friday May 18th 2018**

**Pavillon Alphonse-Desjardins
Université Laval, Québec**

PROGRAMME

Ouverture et bienvenue	
Accueil et inscription	8h00 – 8h30
Première séance : Président de séance : Pr Alexis Vallée-Bélisle	
Nozomu Yachie , University of Tokyo, Japon <i>Chasing Molecular and Cellular Dynamics Using DNA Barcodes</i>	8h30 – 9h20
Ximena Zottig , UQÀM, QC, Canada <i>Guiding Self-assembly and Growth of Amyloid-like Nanoparticles</i>	9h20 – 9h40
Conférencier Thermo-Fisher , Mass Spectrometry Applied to Protein Science	9h40 – 10h00
Pause-café, Atrium	10h00 – 10h20
Timin Hadi , GlaxoSmithKline <i>Biocatalytic Solutions to Chemistry at GSK: Enzyme Applications in Early Discovery through to Route Selection</i>	10h20 – 11h10
Tobin Sosnick , University of Chicago, IL, USA <i>Protein Folding and Dynamics</i>	11h10 – 12h00
Diner, Grand Salon	
Les affiches peuvent être visitées sur l'heure du diner	
Deuxième séance : Président de séance : Pr Charles Calmettes	
Mike Harms , University of Oregon, OR, USA <i>Evolutionary Biochemical Studies of Multifunctional Proteins and High-order Epistasis</i>	13h10 – 14h00
Ugo Dionne , Université Laval, QC, Canada <i>Direct Phosphorylation of SH3 Domains by Tyrosine Kinase Receptors Disassembles Ligand-induced Signaling Networks</i>	14h00 – 14h20
Matthew Benning , Bruker Inc. <i>State of the Art Developments in Protein Structure Characterization using XRD</i>	14h20 – 14h40
Axelle Marchant , Université Laval, QC, Canada <i>Duplication of Homomeric Protein: Retention of Paralogs and Evolution of Protein-protein Interactions</i>	14h40 – 15h00
Pause-café, Atrium	15h00 – 15h20
Audrey Bonin , Chemical Computing Group (CCG) <i>State of the Art Computational Approaches for Protein Studies</i>	15h20 – 15h40
Karen Maxwell , University of Toronto, ON, Canada <i>Outwitting CRISPR-CAS9 in the Evolutionary Arms Race</i>	15h40 – 16h30
Séance de présentation d'affiches	
Séance de présentation d'affiches, Atrium	16h30 – 18h30
Remise des prix pour les meilleures affiches	18h30

PROGRAM

Opening and Registration	
Registration	8:00 – 8:30
Plenary 1 : Chair : Prof Alexis Vallée-Bélisle	
Nozomu Yachie , University of Tokyo, Japan <i>Chasing Molecular and Cellular Dynamics Using DNA Barcodes</i>	8:30 – 9:20
Ximena Zottig , UQÀM, QC, Canada <i>Guiding Self-assembly and Growth of Amyloid-like Nanoparticles</i>	9:20 – 9:40
Conférencier Thermo-Fisher , Mass Spectrometry Applied to Protein Science	9:40 – 10:00
Coffee break, Atrium	10:00 – 10:20
Timin Hadi , GlaxoSmithKline <i>Biocatalytic Solutions to Chemistry at GSK: Enzyme Applications in Early Discovery through to Route Selection</i>	10:20 – 11:10
Tobin Sosnick , University of Chicago, IL, USA <i>Protein Folding and Dynamics</i>	11:10 – 12:00
Lunch, Grand Salon	
Posters can be viewed during lunch time	
Plenary 2: Chair: Prof Charles Calmettes	
Mike Harms , University of Oregon, OR, USA <i>Evolutionary Biochemical Studies of Multifunctional Proteins and High-order Epistasis</i>	1:10 – 2:00
Ugo Dionne , Université Laval, QC, Canada <i>Direct Phosphorylation of SH3 Domains by Tyrosine Kinase Receptors Disassembles Ligand-induced Signaling Networks</i>	2:00 – 2:20
Matthew Benning , Bruker Inc. <i>State of the Art Developments in Protein Structure Characterization using XRD</i>	2:20 – 2:40
Axelle Marchant , Université Laval, QC, Canada <i>Duplication of Homomeric Protein: Retention of Paralogs and Evolution of Protein-protein Interactions</i>	2:40 – 3:00
Coffee break, Atrium	3:00 – 3:20
Audrey Bonin , Chemical Computing Group (CCG) <i>State of the Art Computational Approaches for Protein Studies</i>	3:20 – 3:40
Karen Maxwell , University of Toronto, ON, Canada <i>Outwitting CRISPR-CAS9 in the Evolutionary Arms Race</i>	3:40 – 4:30
Poster Session	
Poster Session, Atrium	4:30 – 6:30
Best Poster Awards Presentation	6:30

**Conférencières et
conférenciers invités**

Keynote Speakers

Chasing Molecular and Cellular Dynamics Using DNA Barcodes

Nozomu Yachie

The University of Tokyo



Beyond its impact on personal genome sequencing, massively parallel DNA sequencing has enabled various high-throughput assays with the idea of DNA barcode. I will first talk about Barcode Fusion Genetics (BFG) technology that we developed for en masse phenotyping of heterogeneous cell pools where each cell has a different combination of two or more genetically engineered loci. We combined this technology with Yeast Two-Hybrid and screened various protein interactomes from up to ~2.5 million protein pairs in 2-3 weeks. I will also introduce about our recent efforts towards high-resolution lineage tracing of dynamic cell population using DNA barcode and genome editing technologies and their potential applications to study cell evolution and development together with various omic information.

Protein folding: “Denatured $\leftrightarrow$ Transition $\leftrightarrow$ Native states” investigated with experiment and simulation

Tobin Sosnick

University of Chicago



I will present a broad view of the protein folding process, describing properties of denatured proteins, the major folding events including rate limiting steps, and conclude with a presentation of our new Upside algorithm that is able to de novo fold proteins in cpu-days

Evolutionary Biochemical Studies of Multifunctional Proteins and High-order Epistasis

Michael J. Harms

University of Oregon



How do protein functions evolve? How does protein biochemistry shape evolution? Our lab tackles protein evolution from both perspectives, and I will draw themes from both in my talk. In the first part, I will discuss our efforts to understand how evolution assembles multi-gene, multi-functional complexes. As a model, we are studying five proteins that play critical roles in vertebrate innate immunity. Three of the proteins form the Toll-like receptor 4 (TLR4) complex, which induces inflammation in response to danger signals. The remaining two proteins form calprotectin, a heterodimer that potently activates the TLR4 complex. Using a combination of phylogenetics and experimental characterization, we found that gene duplication, followed by minor tweaks to each protein—such as changes in dimerization, altered proteolytic susceptibility, and addition of a disordered region—allowed stepwise assembly of new functions without compromising existing functions. In the second part of my talk, I will describe work we've done to understand how the biochemistry of proteins shapes their evolution at a broad scale. We, and others, have noted that proteins exhibit extensive high-order epistasis between mutations—meaning that the effect of each mutation depends on interactions with multiple other mutations. The presence of these high-order interactions profoundly alters the accessibility of evolutionary trajectories. We have found a general explanation for this observation, rooted in protein thermodynamics. This led us to the insight that the simplest way to view this high-order epistasis is as a measure of evolutionary uncertainty.

Outwitting CRISPR-Cas9 in the Evolutionary Arms Race

Karen Maxwell

University of Toronto



The battle between bacteria and the phages that infect them has been ongoing for millions of years. Bacteria have evolved a wide variety of mechanisms to protect themselves against phage predation, including the CRISPR-Cas adaptive immune system. This system captures small fragments of DNA from invading phages and uses them to protect against future attacks. As a countermeasure in this evolutionary arms race, phages have evolved anti-CRISPR proteins. We have identified a number of anti-CRISPR protein families that inactivate CRISPR-Cas9 through a number of distinct mechanisms. These anti-CRISPRs are also able to inhibit genome editing in human cells, providing a sorely needed off switch for CRISPR-Cas9 genome editing technologies.

Biocatalytic Solutions to Chemistry at GSK: Enzyme Applications in Early Discovery through to Route Selection

Timin Hadi

GlaxoSmithKline



In order to improve sustainability and access to medicines, GSK has made a commitment to incorporating new technologies into the chemical manufacture of active pharmaceutical ingredients. The use of enzymes as catalysts allows for the use of different chemical disconnections while often improving stereoselectivity and atom economy when compared to more traditional synthetic methodology. A strategic partnership with Codexis Inc. during 2014 has broadened the scope of biocatalytic solutions to chemistry at GSK and allowed for the evolution of custom enzyme catalysts for manufacturing-scale processes using the CodeEvolver® directed evolution platform. The incorporation of enzyme catalysis into chemistry at GSK through the use of enzyme panels and high throughput screening methods will be discussed. Case studies detailing the application of the CodeEvolver® platform to the evolution of a transaminase and ketoreductase will be presented.

**Conférencières et
conférenciers étudiants et
stagiaires postdoctoraux**

**Students and Postdocs
Lectures**

Guiding self-assembly and growth of amyloid-like nanoparticles

Ximena Zottig^{1,2}, Soultan Al-Halifa^{1,2}, Margaryta Babych^{1,2}, Noé Quittot^{1,2},
Steve Bourgault^{1,2}

¹Université du Québec à Montréal ²PROTEO

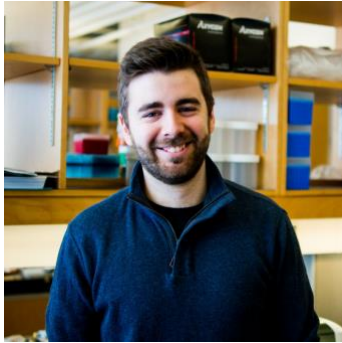


The design of self-assembled supramolecular architecture is of great interest for a variety of applications such as drug and gene delivery, vaccine design, tissue engineering, enzyme catalysis and biosensors. Polypeptides that can self-assemble into amyloid-like assemblies offer many advantages to generate tailored nanoparticles including, functionalization, high mechanical resistance, biocompatibility and enzymatic stability. Nonetheless, the control over the self-assembly and the difficulty of predicting the final supramolecular organization from the peptide sequence constitute major issues. In this study, we develop a novel strategy to control the size, shape and heterogeneity of amyloid-like nanoparticles. This approach is based on electrostatic interactions, which govern nanoparticles growth and morphology. Self-assembling peptides were engineered by end-capping an amyloidogenic peptide with a charged residue. Transmission electron microscopy and atomic force microscopy showed different self-assembled nanostructures, including well-defined rod-like (100 ± 1 nm and 144 ± 4 nm), rope-like (700 - 800 nm) and ribbon-like (3500 - 6500 nm) fibrils. Circular dichroism and Fourier-transform infrared spectroscopy revealed an overall parallel β -sheet fibril structure. Unexpectedly, we found that the rod-like nanofibrils exhibited distinctive properties compared to prototypical amyloids. For instance, lower thermostability and a poor response to the amyloid dye thioflavin T was observed. In addition, cytotoxicity assays demonstrated that these rod-like fibrils are biocompatible. These results highlight the potential of using electrostatic interactions to precisely control the size, shape and surface properties of amyloid-based fibrils, which are important parameters for the design of functional amyloid fibrils in the biomedical field.

Direct Phosphorylation of SH3 Domains by Tyrosine Kinase Receptors Disassembles Ligand-induced Signaling Networks

Ugo Dionne^{1,2,3}, François Chartier^{1,2,3}, Yossef Lopez de los Santos^{3,4}, Noémie Lavoie^{1,2,3}, David N. Bernard^{3,4}, Sara Banerjee^{1,2,3}, François Otis^{3,8}, Kévin Jacquet^{1,2,3}, Michel Tremblay¹, Mani Jain^{3,7}, Sylvie Bourassa¹, Gerald Gish⁵, Jean-Philippe Gagné^{1,2,3}, Guy G. Poirier^{1,2,3,6}, Patrick Laprise^{1,2,6}, Normand Voyer^{3,8}, Christian Landry^{3,7}, Nicolas Doucet^{3,4}, Nicolas Bisson^{1,2,3,6}

¹Centre de recherche du Centre Hospitalier Universitaire (CHU) de Québec-Université Laval, Québec, QC, Canada ²Centre de recherche sur le cancer de l'Université Laval, Québec, QC, Canada ³PROTEO-Quebec Network for Research on Protein Function, Engineering, and Applications ⁴INRS-Institut Armand-Frappier, Université du Québec, Laval, QC, Canada ⁵Lunenfeld-Tanenbaum Research Institute, Mount Sinai Hospital, Joseph and Wolf Lebovic Health Complex, Toronto, ON, Canada ⁶Department of Molecular Biology, Medical Biochemistry and Pathology ⁷Department of Biology, Université Laval, Québec, QC, Canada ⁸Department of Chemistry, Université Laval, Québec, QC, Canada

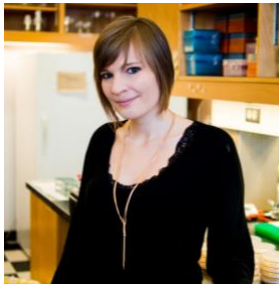


Phosphotyrosine (pTyr) signaling has evolved into a key cell-to-cell communication system in metazoans. In particular, receptor tyrosine kinases (RTKs) initiate several pTyr-dependent signaling events upon their activation by extracellular stimuli. RTK activation creates docking sites required for the assembly of signaling networks on the plasma membrane that drive downstream signaling. However, the mechanisms leading to network disassembly and its consequence remain essentially unknown. We show that activated RTKs terminate downstream signaling via the direct phosphorylation of specific Tyr residues within Src-Homology (SH) 3 domains. The target of the latter events is an evolutionary-conserved Tyr present in most SH3 domains, including the SH2-SH3 adaptor proteins NCK1/2, which are key hubs for the nucleation of RTK-dependent signaling complexes. We show that the EphA4 RTK directly phosphorylates NCK1/2 SH3 domains on this residue, thus entailing the collapse of NCK-dependent signaling networks and the abrogation of their function, both in vitro and in *Drosophila*. Analysis of other RTK-SH3 pairings revealed that this process is a common negative regulation mechanism. Our findings uncover a novel, conserved mechanism through which RTKs rapidly and reversibly terminate downstream signaling while remaining on the plasma membrane in a catalytically active state.

Duplication of homomeric protein: retention of paralogs and evolution of protein-protein interactions

Axelle Marchant, Lou Nielly-Thibault, Alexandre Dubé, Isabelle Gagnon-Arsenault, Yacine Seffar, Christian R. Landry

Institut de Biologie Intégrative et des Systèmes, Département de Biologie, PROTEO



Protein-protein interaction (PPI) network contains significantly more homomers than expected by chance and these homomers have two more partners than proteins that do not interact with themselves (Ispalatov et al 2005). Duplication of a homomer results in a pair of paralogs interacting with each other. The appearance of these pairs happens more frequently than explained by chance and the presence of duplicated proteins self-interacting is higher than singlet proteins suggesting a selective force leading to the retention of both protein copies. Thus, if a homomeric protein is duplicated several times, it would lead to the appearance of a fully interconnected complex. With time, some interactions within the complex evolved due to the divergence of the paralog sequences. Thus, the duplication of proteins forming homomers is suspected of being involved in the appearance of complex networks of proteins. However, the evolutionary path imprinted by PPIs following the duplication of a protein interacting with itself is still poorly understood and several opposing scenarios have been proposed (Kaltenegger and Ober 2015). Here, we studied in *Saccharomyces cerevisiae*, the PPI profile of a large panel of paralogs from small scale (SSD) and whole genome (WGD) duplications to distinguish the different interaction patterns associated with the different evolutionary scenarios. We focus on homomers and interaction between two paralogs of the same pairs using the protein-fragment complementation assay (PCA). To better understand the evolutionary history of PPIs following duplication, we also compare PPI of paralogs observed in *S. cerevisiae* with orthologs proteins duplicated or no in more or less distance yeast species. We observed divergent tendencies of pattern of interactions depending on duplication mechanism (SSD versus WGD), age of duplication and coexpression of paralogs. Thus, evolution of the duplication of homomers seems to depend of the duplication context and probably impact differently the formation of protein complexes depending of origin of duplication. We also proposed a model explaining the retention of paralogs from the duplication of homomeric protein. We showed that the presence of interaction between the two paralogs involved selective force of retention. Thanks to PCA technology allowing a high-throughput approach and modelisation, our study brings new answers on the evolution of protein interactions following the duplication of homomers.

Conférences techniques

Technical Talks

Mass Spectrometry Applied to Protein Science

Thermo-Fisher

State of the Art Developments in Protein Structure Characterization Using XRD

Matthew Benning

Bruker Inc.

State of the Art Computational Approaches for Protein Studies

Audrey Bonin

Chemical Computing Group (CCG)

Présentations d'affiches

Poster presentations

1 - 3D structure prediction of truncated lecithin retinol acyltransferase using bioinformatics 3D prediction tools combined with experimental secondary structure from NMR. Failed successful predictions or successful failed predictions?

Vincent Boulanger, Christian Salesse, Stéphane Gagné

Université Laval

2 - A comprehensive integration of the Residue Interaction Network and NMR relaxation dispersion approaches to understand the dynamic behavior that modulates the catalytic performance of xylanases

Yossef Lopez de los Santos¹, Louise Roux¹, Nicolas Doucet^{2,3}

¹Institut Armand-Frappier (INRS), ²INRS - University of Quebec, ³PROTEO

3 - A fragment screening approach to discover new allosteric modulators of human RNases 3 and 5

Marie-Aude Pinoteau¹, Myriam Letourneau¹, Yossef Lopez de los Santos¹, Donald Gagné¹, Yann Ayotte¹, Steven Laplante^{1,2}, Nicolas Doucet^{1,2}

¹INRS Institut Armand-Frappier, ²PROTEO

4 - Accelerating of the discovery of new monooxygenase variants for industrially relevant oxidation reactions

Olivier Rousseau, Musa Ozboyaci, Maximilian Ebert, Daniela Quaglia, Joelle Pelletier, Sebastian Pechmann

Université de Montréal

5 - Brighter red fluorescent proteins display reduced structural dynamics

Adam M. Damry, Natalie K. Goto, Roberto A. Chica

Université d'Ottawa

6 - Caractérisation structurale de la farnésyle diphosphate synthase de type II chez la tordeuse des bourgeons de l'épinette et évaluation d'inhibiteurs potentiels par arrimage moléculaire

Marie-Ève Picard¹, Audrey Nisole², Catherine Béliveau², Stephanie Sen³, Aline Barbar², Michel Cusson^{1,2}, Rong Shi¹

¹Département de biochimie, de microbiologie et de bio-informatique, Institut de Biologie Intégrative et des Systèmes, PROTEO, Université Laval, ²Ressources Naturelles Canada, Service canadien des forêts, Centre de foresterie des Laurentides, ³Department of Chemistry, The College of New Jersey

7 - Optimisation de l'activité et de la sélectivité d'agonistes des récepteurs neurotensinergiques

Michael Desgagné, Marc Sousbie, Philippe Saret, Eric Marsault

Université de Sherbrooke

8 - ConfBuster Web Server: a free web application for macrocycle conformational search and analysis

Gabriel Bégin¹, Xavier Barbeau¹, Antony Vincent^{1,2}, Patrick Lague¹

¹Université Laval, ²INRS-Institut Armand-Frappier

9 - crystallization of non-structural proteins ORF24 and ORF26 of lactococcal phage p2

XIAOJUN ZHU, DAOWEI ZHU, Jérémie Hamel, Sylvain Moineau, Rong Shi

Université Laval

10 - Dancing Zinc Fingers: How to Reconcile Conformational Exchange Within Zinc Fingers and DNA Binding?

Cynthia Tremblay, Martin Montagne, Danny Letourneau, Pierre Lavigne

IPS - Université de Sherbrooke

11 - Découverte d'AltLMNA, une protéine provenant d'une deuxième séquence codante fonctionnelle dans le gène Lamine A/C

Hélène Mouilleron^{1,3,4}, Vivian Delcourt^{1,2,3,4}, Sondos Samandi^{1,3,4}, Jean-François Jacques^{1,3,4}, Xavier Roucou^{1,3,4}

¹Faculté de Médecine et des Sciences de la Santé, Département de Biochimie, Pavillon de Recherche Appliquée sur le Cancer, Université de Sherbrooke, Québec, Canada,

²Université de Lille, INSERM U1192, Laboratoire Protéomique, Réponse Inflammatoire & Spectrométrie de Masse (PRISM) F-59000 Lille, France, ³Regroupement stratégique PROTEO, Université Laval, Québec, Canada, ⁴PROTEOMEUS, Université de Sherbrooke, Québec, Canada

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

Andréanne Laniel, Étienne Marouseau, Christine Lavoie, Éric Marsault

Université de Sherbrooke

13 - Designer Biosensors for Engineered Metabolic Pathways and Enzyme Evolution

Mohamed Nasr, Logan Timmins, David Kwan, Vincent Martin

Concordia University

14 - Détermination de la structure tridimensionnelle du mutant S175R de la lécithine rétinol acyltransférase tronquée par résonance magnétique nucléaire

Marie-Ève Gauthier^{1,2,3,4,5}, Line Cantin^{1,2,3}, Stephane Gagne^{3,4,5}, Christian Salesse^{1,2,3}

¹Département d'ophtalmologie et d'ORL-CCF, Faculté de médecine, Université Laval,

²CUO-Recherche, Centre de recherche du CHU de Québec, Hôpital du St-Sacrement, CHU de Québec-Université Laval, ³Regroupement stratégique PROTEO, ⁴Département de biochimie, microbiologie et bio-informatique, Faculté des sciences et de génie, Université Laval, ⁵Institut de biologie intégrative et des systèmes, Université Laval

15 - Determining protein-protein interactions and intracellular organisation of the *E.coli* enterobactin metabolon through in vivo chemical crosslinking

Sylvie Ouellette, Peter D. Pawelek

Université Concordia

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

Jama Hagi-Yusuf, David Kwan

Concordia University

17 - Development of a production and purification process for VSVg pseudotyped gesicles

Juliette Champeil^{1,2,3}, Mathias Mangion^{1,2,3}, Rénaud Gilbert^{2,4}, Bruno Gaillet^{1,2,3}

¹Université Laval, ²Thécell : FRQS Cell and Tissue Therapy Network, ³PROTEO,
⁴Human Health Therapeutics Portfolio, National Research Council Canada, Montreal, QC, Canada

18 - Development of a purification strategy for recombinant Vesicular stomatitis virus (rVSV) based HIV vaccine candidates

Anahita Bakhshizadeh Gashti, Alain Garnier

Université Laval

19 - Développement d'une approche à haut débit pour le criblage et la quantification de polyhydroxyalkanoates des bactéries échantillonnées à partir d'huiles usées

Marianne Héneault^{1,2,3}, Manel Ghribi^{1,2,3}, Fatma Meddeb^{1,2,3}, beauregard marc^{1,2,3}

¹UQTR, ²PROTEO, ³CRML, Centre de Recherche sur les Matériaux Lignocellulosiques, Université du Québec à Trois-Rivières

20 - Développement de nouveaux analogues peptidomimétiques de la lactivicine ayant un potentiel antibiotique et inhibiteur de β -lactamases

Pierre-Alexandre Paquet-Côté^{1,2}, Camille Lapointe Verreault^{1,2}, Laurie Bédard^{1,2}, Normand Voyer^{1,2}

¹Université Laval, ²PROTEO

21 - Directed Evolution of a Triple-Decker Motif Containing Red Fluorescent Protein

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

Faculty of Science, Department of Chemistry and Biomolecular Sciences, University of Ottawa

22 - Discovering Drug Seeds by NMR Fragment-Based Lead Discovery

Luciana Coutinho de Oliveira, Steven Laplante

INRS-IAF

23 - DNA Probes for Monitoring Enzyme Activity

Scott Harroun, Xiaomeng Wang, Arnaud Desrosiers, Alexis Vallée-Bélisle

Université de Montréal

24 - DNA-protein conjugates for electrochemical biosensing applications

xiaomengwang¹ Alexis Vallée-Bélisle

Université de Montréal

25 - Effect of binding interference on the divergence between paralogous genes that encode homodimers

Angel Fernando Cisneros Caballero^{1,2}, Christian Landry^{1,2}

¹ULaval, ²PROTEO

26 - Effet de la vitesse de filage sur la structure moléculaire de fibres de soie d'araignée natives et supercontractées

Jane Gagné, Thierry Lefèvre, Michèle Auger

Université Laval

27 - Elucidating the activation mechanism of Tn7 transposition

Yao Shen¹, Jeremy Caron², Joseph Peters³, Joaquin Ortega¹, Alba Guarne¹

¹McGill University, ²McMaster University, ³Cornell University

28 - Étude de l'expression, de la solubilité, du clivage et de la purification de la rétinol déshydrogénase 8 en fusion avec différentes étiquettes de purification et de solubilisation

Charlotte Lemay-Lefebvre^{1,2,3}, Line Cantin^{1,2,3}, Christian Salesse^{1,2,3}

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

29 - Évolution des complexes protéiques après hybridation entre espèces

Caroline Berger¹, I. Gagnon-Arsenault¹, K-M. Moon², R.G. Stacey², L.J. Foster², C.R. Landry¹

¹Institut de Biologie Intégrative et des Systèmes, Département de Biologie, Regroupement québécois de recherche sur la fonction, l'ingénierie et les applications des protéines, Université Laval., ²Centre for High-Throughput Biology, Michael Smith Laboratories, University of British Columbia.

30 - Evolution of conformational exchange in a host defense enzyme family

David N. Bernard^{1,2}, Myriam Letourneau¹, Purva P. Bhojane³, Khushboo Bafna^{3,4}, Marie-Christine Groleau¹, Éric Déziel¹, Elizabeth E. Howell³, Pratul Argawal^{3,4}, Nicolas Doucet^{1,2,5}

¹INRS-Université du Québec, ²PROTEO, ³University of Tennessee, Knoxville, TN, USA, ⁴Oak Ridge National Laboratory, ⁵GRASP

31 - Expression and purification of immunologic adjuvant P97c protein from *Mycoplasma hyopneumoniae*

Laurie Gauthier, Geneviève Bertheau-Mailhot, Jessica Dion, Denis Archambault, Steve Bourgault

Université du Québec à Montréal

32 - Fluorogenic chemical tools based on cysteine labeling to study oligomer formation in amyloid self-assembly

Guillaume Charron¹, Noé Quittot¹, Steve Bourgault¹

¹Université du Québec à Montréal, ²UQAM, ³Université du Québec à Montréal

33 - Folding and binding act as determinants of environment specific fitness effects

Rohan Dandage^{1,2}, Kausik Chakraborty^{1,2}

¹CSIR- Institute of Genomics and Integrative Biology, Mathura Road Campus, New Delhi, India., ²Academy of Scientific and Innovative Research (AcSIR), New Delhi, India.

34 - Fucosyltransferase Inhibition Assay on a Digital Microfluidics Device

Laura Leclerc¹, Guy Soffer¹, T.W. Tsai², C.C.Yu ², Shih S.C.C.¹, Kwan D.H.¹

¹Concordia University, ²National Chung-Cheng University

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

Fathima Mohideen¹, Joel Richard¹, Nathalia Kravchenko¹, David Kwan¹

¹*Concordia University*

36 - Functional Characterization of AltB2R, an Alternative Protein Encoded in the B2R Gene

Maxime Gagnon^{1,2,3,4,5}, Martin Savard^{1,3}, Jean-François Jacques^{1,2,4,5}, Fernand Gobeil^{1,3}, Xavier Roucou^{1,2,4,5}

¹*Université de Sherbrooke*, ²*Pavillon de Recherche Appliquée sur le Cancer*, ³*Institut de Pharmacologie de Sherbrooke*, ⁴*PROTEO*, ⁵*Proteomeus*

37 - Functionalization of amyloid-based nanoparticles

Soultan Al-Halifa^{1,2}, Ximena Zottig^{1,2}, Laurie Gauthier^{1,2,3}, Margaryta Babych^{1,2}, Denis Archambault³, Steve Bourgault^{1,2}

¹*Department of Chemistry, Université du Québec à Montréal, Montreal, QC, Canada, H3C 3P8*, ²*Quebec Network for Research on Protein Function, Engineering and Applications, PROTEO*, ³*Department of Biological Sciences, Université du Québec à Montréal, Montreal, QC, Canada, H3C 3P8*

38 - Genetic backgrounds have complex effects on the drug treatment to a human disease mutation

Véronique Hamel^{1,2,3,4}, Marie Filteau⁵, Isabelle Gagnon-Arsenault^{1,2,3,4}, Alexandre K Dubé^{1,2,3,4}, Christian R Landry^{1,2,3,4}

¹*Institut de Biologie Intégrative et des Systèmes*, ²*Département de Biologie, Université Laval*, ³*PROTEO*, ⁴*CRDM*, ⁵*Département des Sciences des Aliments, Université Laval*

39 - Homology modeling and semi-rational protein engineering of a new metagenomic lipase

Ngoc Thu Hang PHAM, Yossef Lopez de los Santos, Guillaume Brault¹, Charles Calmettes, Nicolas Doucet

Université du Québec, INRS - Institut Armand-Frappier

40 - Hybridization as an adaptive force in response to extreme UV conditions

Carla Bautista Rodríguez^{1,2,3,4}, Souhir Marsit^{1,2,3,4}, Christian Landry^{1,2,3,4,5}

¹Université Laval, IBIS, Landry Lab, ²ULaval, ³Département de biologie, ⁴PROTEO, ⁵Département de biochimie, microbiologie et bio-informatique

41 - Identification and characterization of a novel mitotic target site for Haspin on Histone H2B

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42 - Identification of structural determinants of biased signaling of the apelin receptor

Laurent Bruneau Cossette, Éric Marsault, Philippe Sarret, Pierre Lavigne

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43 - Identification protéomique de nouvelles protéines effectrices dans la signalisation des récepteurs Eph

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44 - Impact of the incorporation of a monofluoroalkene moiety on the hydrophobicity of small peptides

José Laxio Arenas, Myriam Drouin, Jean-François Paquin

Université Laval

45 - Inhibition and activation mechanism study of the kinase by isothermal titration calorimetry (ITC)

yun wang, Jinming Guan, Justin M. Di Trani, Karine Auclair, Anthony Mittermaier*

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46 - Interactions of amyloid peptide AS71-82 with model membranes: structural and morphological study via FTIR and ssNMR

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47 - Investigations phytochimiques du Bouleau glanduleux et isolation d'actifs cosméceutiques

Claudia Carpentier^{1,2}, Meggan Beaudoin¹, Gaëlle Simon¹, François Béland², Maxim Maheux³, Normand Voyer¹

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

Guichi Zhu, Alexis Vallée-Bélisle

Université de Montréal

49 - La liaison du tout-trans rétinol avec la lécithine rétinol acyltransférase tronquée et ses mutants n'explique pas la faible activité enzymatique des mutants

Sarah Roy^{1,2,3,4,5}, Ana Coutinho⁶, Line Cantin^{1,3,5}, Marie-Eve Gauthier^{1,2,3,4,5}, Manuel Prieto⁶, Stéphane M. Gagné^{2,4,5}, Christian Salesse^{1,3,5}

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50 - La liaison membranaire de la protéine S100A10 et du peptide d'AHNAK intervenant dans la réparation membranaire

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51 - Le complexe du pore nucléaire de la levure comme système-modèle pour l'étude de la rétention des gènes dupliqués

Simon Aubé^{1,2,3,4}, Axelle Marchant^{1,2,3,4}, Alexandre Dubé^{1,2,3,4}, Isabelle Gagnon-Arsenault^{1,2,3,4}, Philippe Després^{1,3,4}, Christian Landry^{1,2,3,4}

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52 - Lesion Orientation of O4-Alkylthymidine Influences Replication by Human DNA Polymerase η

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53 - Linear and cyclic peptides as green catalysts for chiral epoxidations

Christopher Bérubé, Xavier Barbeau, Patrick Lague, Normand Voyer

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54 - Palladium-Catalyzed Synthesis of Functionalized Monofluoroalkenes

Myriam Drouin, Sébastien Tremblay, Jean-François Paquin

Université Laval

55 - Plasma membrane vesicles derived from mammalian cells to study the perturbative nature of amyloid fibril assembly

Mathew Sebastiao^{1,2}, Noé Quittot^{1,2}, Dror WARSCHAWSKI^{1,3}, Mathilde Fortier^{1,2}, Isabelle Marcotte^{1,2}, Steve Bourgault^{1,2}

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56 - Préparation de peptides macrocycliques sur résine oxime

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57 - Proteomic analysis of NCK1/2 adaptors reveals a new NCK2-specific role in cell abscission during cytokinesis

Kévin Jacquet^{1,2,3}, François Chartier^{1,2,3}, Sara L. Banerjee^{1,2,3}, Sabine Elowe^{2,3,4}, Nicolas Bisson^{1,2,3}

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58 - Règles thermodynamiques et cinétiques pour l'assemblage et la régulation de nanomachines polymoléculaires à base d'ADN

Dominic Lauzon, Alexis Vallée-Bélisle

University of Montréal

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

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60 - Rôle des récepteurs Eph dans l'établissement de la polarité des cellules épithéliales

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61 - Self-assembled fibrillar nanostructures for vaccine development

Margaryta Babych^{1,2,3}, Geneviève Bertheau-Mailhot³, Laurie Gauthier^{1,2,3}, Ximena Zottig^{1,2}, Soultan Al-Halifa^{1,2}, Denis Archambault³, Steve Bourgault^{1,2}

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62 - Solid-state NMR study of the microalga *Chlamydomonas reinhardtii* and its constituents

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63 - Structural and (supra)molecular basis of the cellular toxicity of amyloid fibrils

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64 - STRUCTURAL AND BIOPHYSICAL CHARACTERIZATION OF THE HOMODIMERIC INTERFACE OF HUMAN GALECTIN-7

Myriam Letourneau, Nhung Nguyen-Thi, Louise Roux, Donald Gagné, Nicolas Doucet

INRS - University of Quebec

65 - Structural and dynamic characterization of UbKEKS, a newly identified ubiquitin encoded in a pseudogene

Patrick Delattre

Université de Sherbrooke

66 - Structural determinants of conformational exchange in GB1 DANCERS

Mayer Marc, Adam M. Damry, Roberto A. Chica

University of Ottawa

67 - Structure et liaison membranaire de la R9AP, une protéine impliquée dans la phototransduction visuelle

Sarah Bernier^{1,2,3}, Marc-Antoine Millette^{1,2,3}, Sarah Roy^{1,2,3}, Line Cantin^{1,2,3}, Christian Salesse^{1,2,3}

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68 - Surexpression et purification de la sous-unité gamma de la transducine, une protéine de la phototransduction visuelle

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

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70 - Synthesis of poly-fluorinated glucopyranose derivatives from levoglucosan

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71 - Systematic perturbation of yeast essential genes using base editing

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72 - The bacterial protein Curli: expression and characterization for the biomedical application of functional amyloid assemblies

Dominic Arpin, Ximena Zottig, Geneviève Bertheau-Mailhot, Steve Bourgault, Denis Archambault

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73 - The crystal structure of the Cdc5-Dbf4 complex provides insight into Polo-box domain substrate recognition

Ahmad Almawi¹, Stephen Boulton¹, Giuseppe Melacini¹, Alba Guarné²

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74 - The first crystal structure of a bacterial acetylcholinesterase

Van Dung Pham¹, Deqiang Yao², Roger Levesque^{1,3}, Steve Charette¹, Rong Shi¹

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

Louis-Philippe Morency, Rafael Najmanovich

76 - The periplasmic reductase DsbG has a chaperone activity in the elyC mutant of Escherichia coli

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77 - THE SYNTHESIS OF KERATAN SULFATE GLYCOSAMINOGLYCANS BY A GLYCOSYNTHASE APPROACH

Xiaohua Zhang, Gautier Bailleul, Peter Pawelek, David Kwan

Concordia University

78 - Unraveling the controversial role of the pseudokinase domain of BUBR1 in mitosis

Luciano Gama Braga¹, Philippe Thebault¹, Michelle Mathieu¹, SABINE ELOWE²

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79 - Valorisation des huiles usagées à moteur

Manel Ghribi^{1,3,4}, Fatma Meddeb^{2,3,4}, Marc Beauregard^{2,3,4}

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80 - Vers le développement d'une nouvelle génération d'inhibiteurs de l'oncoprotéine c-Myc

Jean-Michel Moreau, Danny Létourneau, Martin Montagne, Pierre Lavigne

Université de Sherbrooke

81 - Identification of a molecular hinge controlling the amyloid self-assembly and cytotoxicity of islet amyloid polypeptide

Elizabeth Godin, Phuong Trang Nguyen, Ximena Zottig, Steve Bourgault

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82 - Développement d'un vecteur viral à double-cassette pour la visualisation en temps réel de l'adhésion et la prolifération des cellules endothéliales progénitrices

Samuel Daigle¹, Mariève Boulanger¹, Mathias Mangion¹, Corinne Hoesli^{1,2},
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83 - Etude des transporteurs de Nickel chez *Helicobacter pylori*

Mirana Mirana Rakotoarivony, Zakaria Orfi, Charles Calmettes

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84 - Measuring Enzyme Kinetics Using Isothermal Titration Calorimetry

Justin Di Trani, Anthony Mittermaier

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