McGill
High Throughput Screening Facility

The 2015 McGill HTS / HCS Conference and Workshop

Appendix 5

March 13th, 2015

McIntyre Building
6th Floor Lobby & Martin Amphitheatre
3655 Promenade Osler
Montreal H3G 1Y6

Speakers

Véronique Birault
GlaxoSmithKline

John Hanrahan
McGill University

Sidong Huang
McGill University

Victoria Muise
McGill University

Jerry Pelletier
McGill University

Anne Roulston
McGill University

Kathryn Skorey
Nuchem Therapeutics

Jian Zhu
University of Rochester Medical Center

Workshops

Beckman-Coulter
Automation

GE HealthCare
High Content Screening

Molecular Devices
High Content Screening

Sophion
Automated Patch-Clamp

Exhibitors

ABIF
Beckman-Coulter
CFTRc
ChemBridge
Eppendorf
Fisher Scientific
GE HealthCare
IDT
Life Chemicals
Sigma-Aldrich
ThermoFisher

SPONSORS


ABIF
Advanced BioImaging Facility


BECKMAN
COULTER
Life Sciences


bionano
CREATE TRAINING PROGRAM IN BIONANOMACHINES


Cystic Fibrosis Translational Research Center
CFTRc
Centre de Recherche Translationnelle sur la Fibrose Kystique


CHEM BRIDGE


eppendorf


Fisher Scientific
Part of ThermoFisher Scientific


GRASP
Groupe de Recherche Axé sur la Structure des Protéines


LIFE CHEMICALS


IDT


MOLECULAR
DEVICES


SIGMA-ALDRICH

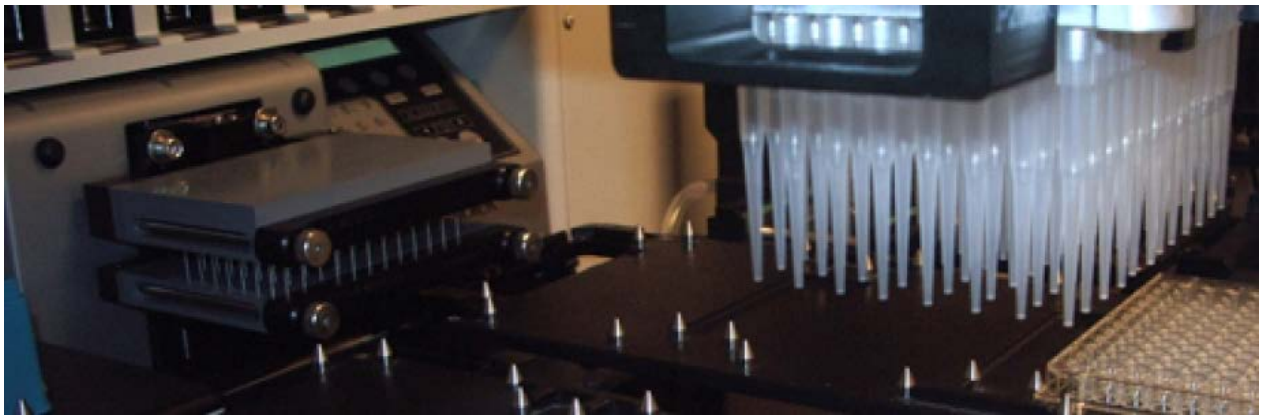

Sophion


ThermoFisher
SCIENTIFIC


VITAS-M
LABORATORY

McGill

High Throughput Screening Facility



Welcome to the **2015 McGill HTS Facility Workshop.**

The Workshop program includes researchers from academia and industry to discuss emerging trends in HTS and drug discovery and available resources at McGill.

This is an excellent opportunity for you to network and to become informed of the infrastructure and opportunities available to you at McGill.

The workshop will bring together experts in HTS and its role in drug discovery. Examples of assay development and successful drug discovery research projects will be presented. The Workshop includes new resources in genome-editing and other technologies that can improve clinical outcomes in drug discovery and development.

We are grateful to our sponsors and the exhibitors who will be present to inform you of their new products, and state-of-the-art technologies.

We would also like to thank the speakers and session chairs.

On behalf of the organizing committee, we would like to welcome you for attending and look forward to meeting you.

Enjoy the Workshop!

Renaud Robert & Carmen Lampron
Co-directors of the McGill HTS Facility

Organizing committee:
David Thomas - Annick Guyot - Stevo Radinovic - Carmen Lampron - Renaud Robert

For more information, please contact us at:
Office: 514.398.7284 ; HTS lab: 514.398.3746 ; email: hts.biochem@mcgill.ca
website: http://www.mcgill.ca/lifesciencescomplex/core/hts-hcs

McGill
High Throughput Screening Facility

The 2015 McGill HTS/HCS Conference and Workshop
March 13th, 2015

Schedule

7:45 – 8:20 am Registration, Exhibitors Set-up & Breakfast
McIntyre Building, 6th floor lobby

8:20 – 8:30 am Opening Words and Introduction of the McGill HTS Facility
Renaud Robert & Carmen Lampron, *McGill University*
McIntyre Building, 6th floor, Martin Amphitheater

Session 1 – Session Chair: Gordon Shore, *McGill University*

8:30 – 9:00 am **Kathryn Skorey,** *Nuchem Therapeutics*
Top 10 things you need to know in drug discovery…..Clickbait!

9:00 – 9:30 am **Véronique Birault,** *GlaxoSmithKline*
The importance of medicinal chemistry in drug discovery collaboration. Example of McGill/GSK cystic fibrosis drug discovery program

9:30 – 10:00 am **John Hanrahan,** *McGill University*
The long and winding road from HTS to CF therapy

10:00 – 10:30 am ***Health Break with Exhibitors***
McIntyre Building, 6th floor lobby

Session 2 – Session Chair: Albert Berghuis, *McGill University*

10:30 – 10:45 am **Sidong Huang,** *McGill University*
Vector-based shRNA tools and their application.

10:45 – 11:00 am **Jerry Pelletier,** *McGill University*
Genome editing-enabled assays for genetics and chemical biology

11:00 – 11:30 am **Anne Roulston,** *McGill University*
The use of high-throughput siRNA functional genomic screens to guide oncology drug development.

11:30 – 12:00 pm **Victoria Muise,** *McGill University*
HTS Assay development for anthelmintic discovery

12:00 – 1:00 pm ***Lunch (buffet style with exhibitors)***
McIntyre Building, 6th floor lobby

Session 3 – Session Chair: Jerry Pelletier, *McGill University*

1:00 – 1:30 pm **Jian Zhu,** *University of Rochester Medical Center*
Development and application of PLATO

Workshop: - Session Chair: Kalle Gehring, *McGill University*

1:30 – 2:00 pm **Steve Wiltgen,** *Molecular Devices*
ImageXpress: A high content imaging platform designed to accommodate a full spectrum of imaging applications

2:00 – 2:30 pm **Weifeng Yu,** *Sophion*
Ion channel research: a brief history and its latest development

2:30 – 3:00 pm **Louie Lamorte,** *Beckman Coulter*
Laboratory automation 101

3:00 – 3:30 pm **HaiGuang Zhang -** *GE Healthcare*
High content analysis, imaging cell biology in context

3:30 – 4:00 pm ***Health Break with Exhibitors & Draw***
McIntyre Building, 6th floor lobby

4:00 – 5:00 pm **Demo in the McGill HTS Facility**
McIntyre Building, 9th Floor, Room 930

Fully Integrated Automated System, Biomek FXP dual Arm system

InCell 2200

ImageXpress

QPatch 16X Platform

SPEAKERS

Kathryn Skorey, *Nuchem Therapeutics*

Top 10 Things You Need to Know in Drug Discovery…Clickbait!

Discovery of new and novel drugs remains a complex and risky business. Within each phase of drug discovery from target identification, screening for inhibitors or agonists/antagonists, optimization of leads and pre-clinical safety and pharmacokinetics there exist some common practices to improve the probability of success and/or reduce the time and cost of moving a project forward. With the advancement in computational science, the discovery of novel biologics, phenotypical screening etc, some of the original practices in drug discovery are undergoing a re-think including what was once considered as "non-druggable" targets. High throughput screening (HTS) plays a key role in drug discovery at the early stage of basic research and can involve screening for both biologics and small chemical compounds in both cellular and non-cellular assays. A successful HTS campaign provides the lead hits to initiate medicinal chemistry optimization (in the case of small molecules) or biologic optimization. There are several factors that can help drive an HTS campaign towards a higher probablility of success including picking the right target, finding a robust assay readout technology, utilizing a "clean" screening library. Examples of HTS screening programs will be given highlighting a few of the best practices and potential pitfalls that can led to the success or failure of a drug discovery program.

Kathryn is currently the Director of Biology at Nuchem Therapeutics located in Montreal. In her multifaceted role, she is the project manager for several basic research projects between the venture capital fund Amorchem L.P. and universities coordinating the activities between the medicinal chemists from Nuchem Therapeutics and the biologists from the academic collaborator laboratories. Kathryn also conducts due diligence on the various project proposals from academic laboratories throughout Quebec and Canada on behalf of the investment fund managers. She maintains an active presence in the laboratory as an enzymologist and assay development consultant for outside contractors as part of the CRO function of Nuchem Therapeutics. Prior to joining NuChem Therapeutics, Kathryn was Senior Research Associate (Biology) at Merck Frosst Canada in Montreal. She has over 20 years' experience in the pharmaceutical industry with a sound knowledge of the preclinical drug discovery process from target identification to lead optimization. Kathryn has broad expertise in protein chemistry including enzymology, mechanism of action studies and assay development for enzymes and receptors from moderate to high throughput screening in various therapeutic targets including respiratory, inflammation, diabetes, obesity and infectious diseases. She has over 40 publications in peer-reviewed journals. Kathryn received her BSc in organic chemistry from the University of Waterloo and her MSc from the University of Alberta.

Véronique Birault, *GlaxoSmithKline*

The importance of medicinal chemistry in drug discovery collaboration. Example of McGill/GSK cystic fibrosis drug discovery program.

This presentation will talk about successful research collaboration between GSK and the McGill University Cystic Fibrosis Translational Research centre (CFTRc). The primary objective of the collaboration was to discover molecules that correct the underlying trafficking defect of the ΔF508-CFTR protein. The presentation will review briefly cystic fibrosis background and highlights the medicinal chemistry strategy that was applied to the collaboration from hit validation to lead generation.

Dr. Véronique Birault has been working in a drug discovery environment since 2000, in big Pharma (GSK), contract research organisation (BioFocus) providing research to the pharmaceutical industry and in academia as a visiting professor at UCL where she brings her expertise to bear her translational science expertise, bridging the gap between fundamental science and discovering new medicines. Over her career she has worked on projects ranging from target discovery through clinical development across many therapeutic areas (inflammation, oncology, neuroscience). Her research has provided successful candidates selected for development one of which achieved clinical proof of concept study. She has led multidisciplinary team composed of biologists, medicinal chemists; *in-vivo* pharmacologists and physicians. She has established at GSK new areas of science, de-orphanisation of targets and successful partnership with external collaborators. She has been working in partnership with McGill University to discover drugs that correct the trafficking defect of the most common cystic fibrosis mutation, ΔF508. This was supported by a grant from the CIHR and GSK showing she can build effective academia-industry partnerships.

John Hanrahan, McGill University

The long and winding road from HTS to CF therapy.

Most current therapies for cystic fibrosis (CF) are designed to alleviate the symptoms of CF without addressing the underlying cause. Recently the field has entered an exciting new era in which therapies are being developed that target the basic defect, either by increasing the activity of mutant CFTR channels or by promoting their biosynthesis and delivery to the plasma membrane. This has become possible thanks to the identification and cloning of the defective gene and basic research which stemmed from that discovery, and also to the application of high throughput screening (HTS) approaches to identify CFTR modulators. As part of that movement we developed a cell-based assay at McGill to detect trafficking of ER-retained F508del-CFTR, the most frequent CF mutation, and performed unbiased screens of commercial and proprietary libraries and natural product extracts for trafficking "correctors". Cell-based assays are ideal for finding molecules that are biologically active, but finding their targets and mechanisms of action is challenging. Our search for correctors with therapeutic potential led us to a lead series as initially hoped, but also to other weak CFTR correctors with interesting mechanisms of action. So far we have shown that some compounds act as pharmacological chaperones and interact directly with CFTR whilst others, termed proteostasis modulators, appear to act on the protein quality control system and may act on diverse molecular targets including phosphodiesterases, cyclooxygenase 2 and even Na/K ATPase. We have also determined that latonduines, which were originally derived from marine sponge extracts, can improve CFTR trafficking through modulation of the poly(ADP-Ribose)polymerase family of enzymes. Thus HTS hits can lead to new therapeutic candidates and also to the identification and a better understanding of potential drug targets and pathways.

John Hanrahan is a Professor in the Department of Physiology, McGill University, a member of the Research Institute of the MUHC, and an associate member of the Meakins Christie Labs. He is also a member of GEPROM (Groupe d'Etude des PROtéines Membranaires) and the director and co-founder of the McGill Cystic Fibrosis Translational Research centre (CFTRc). Dr. Hanrahan obtained his BSc (Hon) in Biology at Dalhousie, PhD in Zoology (Physiology) at UBC, and Postdoctoral training in the Yale University School of Medicine. He has received Fellowship, Scholar, Scientist and Senior Scientist awards from CIHR, and the Chercheur Boursier Senior II award from FRQS. His research interests relate to epithelial transport and channels at the cellular and molecular level, and are focused on cystic fibrosis and CFTR function. His lab studies basic mechanisms of channel regulation, the role of CFTR in airway epithelial host defense, and the development of new therapeutics for cystic fibrosis.

Sidong Huang, McGill University

Vector-based shRNA tools and their applications.
The discovery that RNA interference (RNAi) can also be used in mammalian cells to suppress gene expression has revolutionized loss-of-function genetics in mammalian biology. Unbiased RNAi-based screens provide a powerful tool to identify novel components of signalling pathways and can help identify effective treatment strategies in preclinical models of cancer. Vector-based shRNA tools available at Life Sciences Complex and examples of pooled shRNA screening will be discussed.

Sidong Huang, is an Assistant Professor in the Department of Biochemistry, Associate Member of the Goodman Cancer Research Centre (GCRC), and holds a Canada Research Chair in Functional Genomics. He uses functional genomic tools to study cancer-relevant pathways and to guide targeted cancer therapy. His laboratory aims to identify novel genes and networks that modulate response to cancer drugs, and to uncover genetic dependencies between the major signaling pathways in cancer that can be exploited therapeutically. One of his works has identified the potential combination therapy targeting both BRAF and EGFR for BRAF mutant colon cancer patients, which is currently being tested in a clinical trial. He is also in charge of managing the latest Mission TRC shRNA genome-wide collections, which have enhanced the research capacity of the community and initiated new projects and collaborations.

Jerry Pelletier, McGill University

Genome editing-enabled assays for genetics and chemical biology.
Once a niche application, genome editing is now a mainstream approach useful for correlating phenotype/genotype relationships, developing novel models of disease, and target identification and validation. Adoption of this technology has been greatly facilitated by CRISPR (clustered regularly interspaced short palindromic repeats)/Cas9, given its facile customizable specificities. I will briefly discuss our efforts at better understanding the Cas9 editing technology as well as our efforts towards implementing it for genetic screens and target validation.

Jerry Pelletier, PhD, is a James McGill Professor in the Departments of Biochemistry and Oncology and member of the Rosalind and Morris Goodman Cancer Research Centre. The overarching focus of his research program is to understand how translation, a process fundamental to all cells, becomes deregulated in cancer. Our research has identified unique small molecule inhibitors that interdict a specific nodal point that is frequently dysregulated in neoplasia. We have also developed mouse models that mimic small molecule-mediated targeted inhibition at the organismal level and have used these to validate the concept of targeting translation initiation *in vivo*. We are applying genome engineering technology to suppress gene function in a stable manner as a means of exploring the role of translation in tumor maintenance and treatment response and identifying novel tumor suppressors and/or oncogenes.

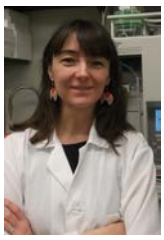
Anne Roulston, McGill University

The use of high-throughput siRNA functional genomic screens to guide oncology drug development.

In oncology, the wide variety of mutations that exist within individual tumors makes a universal approach to successful therapeutic intervention a difficult challenge. Functional genomics using loss of function screens, allows for the systematic examination of cellular gene function in the context of a targeted drug treatment. In oncology, synthetic lethality screens using RNAi technologies have been particularly useful at the pre-clinical stage in the drug development process to guide the clinical development of novel targeted agents. The knowledge generated from these screens provides essential information to uncover biomarkers that will predict patient responders and potential mechanisms of drug resistance; that will identify potential drug combination therapies and most appropriate cancer indication and that will provide key mechanistic information about the compound. Examples of genome-wide siRNA synthetic lethal screens that have generated information key to the clinical development of two candidate oncology agents will be discussed.

Dr. Anne Roulston is the associate director of the Laboratory for Therapeutic Development. Anne accrued more than 15 years of drug development experience prior to launching the LTD in 2010 along with colleague Dr. Gordon Shore. Anne was associate director of biology at Gemin X Pharmaceuticals Inc. where she led a translational research team to support clinical development of drug candidates and to study the mechanism of action of Gemin X compounds. Anne was a post-doctoral fellow at Chiron Corporation (now Novartis) in Emeryville CA. Anne received her Ph. D. from McGill University's department of Microbiology and Immunology and has published research papers in the fields of translational cancer research, apoptosis and virology.

Victoria Muise, McGill University



HTS Assay development for anthelmintic discovery.

Parasitism in humans is not usually a concern in the developed world, because infection is relatively rare, and can be quickly diagnosed and treated. In the developing world, however, morbidity and mortality due to parasites is staggering; it is estimated that >1.5B (or 24%) of the world are infected with soil transmitted helminths alone (WHO, 2015). Drug resistance, tolerance problems, and suboptimal effectiveness all underline our urgent need for new anthelmintics for both human and veterinary use. A yeast based recombinant screen expressing parasite FaRP receptors was donated by Cadus and was used at all centers to screen for potential anthelmintics. This platform was chosen to minimize equipment and training costs, ensure safety of lab personnel, and produce high throughput data with a quantitative endpoint. Assays were run in both agonist and antagonist mode. We had success in establishing a screening program in 5 centers in 4 countries, with hits from a variety of sources. Even in lower capacity labs where assays were run by hand on the benchtop, several interesting hits were found that are being pursued. At McGill, U. South Florida and Michigan U., we modified our SOP to use high-throughput platforms, allowing us to screen up to 20K samples in one day, resulting in 450+ hits. *In vivo* cut-worm testing continues on these hits to determine their activity.

Victoria holds an honours degree in Biology from Dalhousie University and a Graduate Certificate in Biotechnology from McGill University. After more than 20 years of experience as a research assistant, she has recently begun teaching the Masters in Biotechnology laboratory at Macdonald Campus, and celebrated 15 years as a McGill employee. Her most recent research involved a 5-year Gates Foundation anthelmintic discovery project led by Drs. T. Geary and E. Ubalijoro at the Institute of Parasitology, with partners at U. Botswana, U. Cape Town, U. of South Florida, and Michigan U. Working with indigenous knowledge holders, botanists, and synthetic chemists, Victoria led technology transfers at each of the centers, adapting the SOPs for a variety of laboratory conditions ranging from basic facilities run by students, to High Throughput Centers with dedicated technical staff.

Jiang Zhu, *University of Rochester Medical Center*

Development and application of PLATO.

Functional characterization of human proteome is currently under active investigation. A variety of proteomic approaches have been developed to facilitate the study of human proteome. However, they suffer from some intrinsic drawbacks. Most display technologies only present partial peptide instead of full-length protein. Other tools such as proteome microarray are labor-intensive to prepare, and proteins may denature during storage. Here we present an *in vitro* method, Parallel Analysis of in vitro Translated ORFs (PLATO), that facilitates protein interaction identification by *in situ* displaying a normalized library of >14,000 full-length human open reading frames (ORFs) on ribosomes followed by massively parallel analysis of bait-prey interactions using DNA sequencing. PLATO allows proteins to be efficiently displayed in full-length and provides kinetic and protein conformation benefits as a solution phase assay. We demonstrate potential applications of PLATO for: 1) identification of protein binding partners for immobilized "bait" proteins or small-molecule compounds, 2) discovery of autoantigens in patients with autoimmune diseases. Convincingly, PLATO is a powerful new tool for proteomic investigations that can be modified for many innovative biomedical studies. Given the recent availability of high quality ORFeome library within the Gateway recombination cloning system and the widespread use of high throughput DNA sequencing, we believe PLATO will be widely employed by other labs. Currently, we are developing the barcoded ORF libraries to simplify and fasten the recovery and recognition of genetic information from PLATO assays. We are also adapting the PLATO protocol compatible for high-throughput screen (HTS) based protein interaction discovery.

Dr. Zhu obtained his Bachelor of Science in Pharmacology from Peking University in China. He moved to USA and pursued his Ph.D. in Pharmacology with Drs. Heng Zhu and Diane Hayward at the Johns Hopkins University School of Medicine with an AHA predoctoral fellowship. Dr. Zhu then completed a NIH/NIAID NRSA (F32) postdoctoral fellowship with Dr. Stephen Elledge at HHMI, Brigham and Women's Hospital of Harvard Medical School. Dr. Zhu is currently an Assistant Professor of Microbiology & Immunology (primary) and Biochemistry & Biophysics (secondary) at the University of Rochester Medical Center (URMC). Dr. Zhu's lab is interested in identifying novel host proteins that associate with viral proteins and modulate viral replications for HIV and herpesviruses, using several *in vitro* synthetic proteomic approaches. During his Ph.D. training, Dr. Zhu applied the protein microarray technology to identify several key host factors involved in the replication of gammaherpesviruses (EBV and KSHV). While as a postdoc in Dr. Stephen Elledge's lab, he developed a new *in vitro* proteomic platform, PLATO (Parallel Analysis of in vitro Translated ORFs), to facilitate protein interaction studies by displaying a normalized library of full-length open reading frames (ORFs) on ribosomes followed by massively parallel analysis of bait-prey interactions using deep DNA sequencing. PLATO is currently being tested for identifying host-virus protein interactions as well as host and viral antigens for several critical autoimmune diseases.

- Canadian graduate program in structural biology, biophysics, and macromolecular chemistry
- Funding for undergraduate and graduate stipends, travel awards, workshops, & international exchanges
- http://bionano.ca

- The *Groupe de Recherche Axé sur la Structure des Protéines* (GRASP) brings together scientists working to understand the molecular basis of diseases and to develop new therapies.
- Areas of interest include cystic fibrosis, long QT syndrome, Parkinson's disease and bacterial infections.
- Funding for infrastructure, trainees and workshops.
- Next Annual Symposium (all welcome, free registration): Monday, November 23, 2015.
- http://grasp.mcgill.ca

Purchase from us:

- small molecule chemical compounds for high-throughput screening
- organic building blocks for combinatorial chemistry

in any format including mg, micromole, dry powder, DMSO solution, dry film.

Inquire us about special projects:

- Scaffolds to synthesize drug-like mini-libraries (Azalea project).
- Fragments collection (Allium Project).
- Preplated Diversity Library

WORKSHOP

Steve Wiltgen, *Molecular Devices*

ImageXpress: A high content imaging platform designed to accommodate a full spectrum of imaging applications.

High content imaging has become more sophisticated in recent years due to increasing pressure to include more biologically relevant samples in the drug discovery process, such as 3D samples and co-cultures. Meeting these demands requires a flexible, yet robust imaging system capable of delivering high-quality data. In this talk, we will cover a broad spectrum of applications that have been imaged on the ImageXpress, as well as the hardware and software specifications that have allowed us to achieve such flexibility.

Weifeng Yu, *Sophion*

Ion channel research: a brief history and its latest development.

Ion channels play vital roles in the information processing in our central nerve system. Understanding ion channels' structure, their functional roles in normal and pathophysiology, their modulations by different cell signaling factors and by drugs has been the major focus of many researchers and pharmaceutical companies in the past several decades. The development of patch clamp recording in early 1980s was a major milestone in the ion channel research field. It allows researchers to study ion channels in fine details, even at single channel level, such as how voltage-gated channels are open and close under different commanding voltages, how ligands interact with their gated channels, and, most important of all for pharmaceutical companies, how drugs interact with different ion channels to exert their effects in alleviating human illness and suffering. With such a broad application, patch clamp technology is often referred as a gold standard in studying pharmacology of different drugs' interaction with their targeted ion channels. On the other hand, a significant drawback of the technology is its slow pace in terms of any patch clamp study and its requirement of long time training for anyone to master it. This makes it extremely hard to adopt the technology in the field of drug research and development (R&D) in pharmaceutical industry. The development of automatic patch clamp (APC) in the past decade dramatically improved its applicability in pharmaceutical R&D. The latest development of 384 format of APC is the first time to allow drug developers to screen ion channel targets under a voltage clamp environment in a high throughput screening (HTS) fashion.

Louie Lamorte, *Beckman Coulter*

Laboratory automation 101.

Laboratory automation, a common staple in the pharmaceutical industry, is growing in popularity within academic laboratories. Increased throughput is only one of several advantages offered through the use of liquid handlers. Other advantages include liberating laboratory personnel from repetitive processes, reducing pipetting errors and eliminating variability amongst different individuals. Various processes can be automated using a liquid handler, alone or in combination with additional devices, such as a plate washer, automated incubator and plate reader. While liquid handlers are often used in high-throughput screening, many other types of protocols can be easily automated. This includes genomic applications such as nucleic acid extractions, PCR setup and next-generation library construction, proteomic applications such as sample preparation for MS analysis and countless numbers of cellular applications.

HaiGuang Zhang, *GE Healthcare*

High content analysis, imaging cell biology in context

IN Cell is a total GE Healthcare imaging solution for cell-based research, assay development and screening. With increased throughput and improved data quality, IN Cell system enhances the productivity of high content analysis (HCA) by combining flexibility with superior image quality. This powerful yet easy to use package has been applied across many areas of research, and is a complementary technology for manual microscopy, flow cytometry and western blotting. Examples of IN Cell application will be presented.

Notes

Notes

Notes

Sponsors

ABIF
Claire Brown
claire.brown@mcgill.ca
www.agilent.com/chem

Beckman-Coulter
Louie Lamorte
llamorte@beckman.com
www.beckmancoulter.com

CFTRc
Annick Guyot
annick.guyot@mcgill.ca
www.mcgill.ca/cftrc

ChemBridge
Duncan Beniston
duncan@chembridge.com
www.chembridge.com

Eppendorf
Marc-André Denis
denis.m@eppendorf.com
www.eppendorf.ca

Fisher Scientific
Frank Guarneri
frank.guarneri@thermofisher.com
www.fishersci.ca

GE Healthcare Biosciences
François Veilleux
francois.veilleux@ge.com
www.gelifesciences.com

IDT
Fatima Asad
fasad@idtdna.com
www.idtdna.com

Life Chemicals
Vasily Pinchuk
vasily.pinchuk@lifechemicals.com
www.lifechemicals.com

Molecular Devices
Steve Wiltgen
steve.wiltgen@moldev.com
www.moleculardevices.com

Sigma-Aldrich
Annie Cartman
annie.cartman@sial.com
www.sigma-aldrich.com

Sophion
Rashi Jain
rashi.jain@biolinscientific.com
www.biolinscientific.com/sophion

Thermo Fisher
Isabelle Lemoyne
isabelle.lemoyne@thermofisher.com
www.thermofisher.com

Vitas-M Laboratory
Irina Ryabushenko
irina@vitasmlab.com

McGill

High Throughput Screening Facility

Description

The scientific aim of the McGill HTS Facility is to facilitate the development of chemical biology programs by supporting assay development and HTS of various natures through shared infrastructure, materials and expertise on a fee-for-service basis.

Service offered

- HTS assay development – optimization and validation
- Primary and secondary screening
- Chemical compound libraries from commercial source
- Access to shRNA libraries for genome-scale screening for human or mouse *(only offered to McGill's researchers)*
- *Access to* Liquid-handling workstation and fully integrated robotic system
- *Access to* Plate readers for various applications
- Access to a cell culture room
- Training and assistance

2x robotic workstations

Biomek FX – Beckman Coulter

2x HCS Systems

Molecular Devices ImageXpress

GE InCell2200

1x Automated Patch-clamp

Qpatch Sophion

3x Plate Readers

2x Pherastar FS

1x Synergy MX

For more information, please visit our website:

http://www.mcgill.ca/lifesciencescomplex/core/hts-hcs

Program Schedule 2015 / Programme 2015

7h45 Registration, Exhibitors Set-up & Breakfast (McIntyre Building, 6th floor lobby)

Session 1 – McIntyre Building, 6th floor, Martin Amphitheater

8h20 Opening Words and Introduction of the McGill HTS Facility - Renaud Robert & Carmen Lampron
8h30 Kathryn Skorey, *Nuchem Therapeutics*
9h00 Véronique Birault, *GlaxoSmithKline*
9h30 John Hanrahan, *McGill University*

10h00 Health Break with Exhibitors *(*McIntyre Building, 6th floor lobby)

Session 2 – McIntyre Building, 6th floor, Martin Amphitheater

10h30 Sidong Huang, *McGill University*
10h45 Jerry Pelletier, *McGill University*
11h00 Anne Roulston, *McGill University*
11h30 Victoria Muise, *McGill University*

12h00 Lunch (buffet style with exhibitors ; McIntyre Building, 6th floor lobby)

Session 3 – McIntyre Building, 6th floor, Martin Amphitheater

13h00 Jian Zhu, *University of Rochester Medical Center*

Workshop – McIntyre Building, 6th floor, Martin Amphitheater

13h30 Steve Wiltgen, *Molecular Devices*
14h00 Weifeng Yu, *Sophion*
14h30 Louie Lamorte, *Beckman Coulter*
15h00 HaiGuang Zhang, *GE Healthcare*

15h30 Health Break with Exhibitors & Draw (McIntyre Building, 6th floor lobby)

16h00 Demo in the McGill HTS Facility (McIntyre Building, 9th Floor, Room 930)
Fully Integrated Automated System, Biomek FXP dual Arm system (*Beckman-Coulter*)
InCell 2200 (*GE HealthCare*)
ImageXpress (*Molecular Devices*)
QPatch 16X Platform (*Sophion*)